



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 157319

TO: Nita M Minnifield
Location: REM-3C01/3C18
Art Unit: 1645
Thursday, June 30, 2005

Case Serial Number: 08/170344

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: 571-272-2527

Paul.schulwitz@uspto.gov

Search Notes

2 of 2

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-2
Perfect score: 48
Sequence: 1 KLPOLCTEL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	143	2 Q919B6	Q919B6 human papil
2	48	100.0	143	2 Q919C4	Q919C4 human papil
3	48	100.0	151	2 Q778I6	Q778I6 human papil
4	48	100.0	151	2 Q77JC7	Q77JC7 human papil
5	48	100.0	151	2 Q77ZJ5	Q77ZJ5 human papil
6	48	100.0	151	2 Q80963	Q80963 human papil
7	48	100.0	151	2 Q89640	Q89640 human papil
8	48	100.0	151	2 Q89648	Q89648 human papil
9	48	100.0	151	2 Q89755	Q89755 human papil
10	48	100.0	151	2 Q89852	Q89852 human papil
11	48	100.0	151	2 Q8B564	Q8B564 human papil
12	48	100.0	151	2 Q8BB19	Q8BB19 human papil
13	48	100.0	151	2 Q8BB20	Q8BB20 human papil
14	48	100.0	151	2 Q9W8C3	Q9W8C3 human papil
15	48	100.0	151	2 Q9W931	Q9W931 human papil
16	48	100.0	151	2 Q9WMP4	Q9WMP4 human papil
17	48	100.0	151	2 Q9WMP5	Q9WMP5 human papil
18	48	100.0	158	1 V56 HPV16	V56 HPV16
19	48	100.0	158	2 Q8QHP5	Q8QHP5 human papil
20	48	100.0	158	2 Q8QHT0	Q8QHT0 human papil
21	48	100.0	158	2 Q8QRD6	Q8QRD6 human papil
22	48	100.0	158	2 Q8QRD7	Q8QRD7 human papil
23	48	100.0	158	2 Q8QRD8	Q8QRD8 human papil
24	48	100.0	158	2 Q8QRD9	Q8QRD9 human papil
25	48	100.0	158	2 Q8QRE1	Q8QRE1 human papil
26	48	100.0	158	2 Q71BI7	Q71BI7 human papil
27	48	100.0	158	2 Q9QDH3	Q9QDH3 human papil
28	48	100.0	158	2 Q9QDH5	Q9QDH5 human papil
29	48	100.0	158	2 Q9QDH7	Q9QDH7 human papil
30	48	100.0	158	2 Q9QDH9	Q9QDH9 human papil
31	48	100.0	158	2 Q9WH13	Q9WH13 human papil

32 48 100.0 161 2 Q919B1 Q919B1 human papil
33 48 100.0 161 2 Q919C6 Q919C6 human papil
34 48 100.0 161 2 Q919D4 Q919D4 human papil
35 45 93.8 151 2 Q9WMP2 Q9WMP2 human papil
36 45 93.8 158 2 Q8QRE0 Q8QRE0 human papil
37 44 91.7 585 1 DXS_BUCAP DXS_BUCAP human papil
38 43 89.6 25 2 Q8V9R8 Q8V9R8 human papil
39 43 89.6 25 2 Q8V9L1 Q8V9L1 human papil
40 43 89.6 25 2 Q8V9L2 Q8V9L2 human papil
41 43 89.6 25 2 Q8V9L3 Q8V9L3 human papil
42 43 89.6 57 2 Q90133 Q90133 human papil
43 43 89.6 151 2 Q12335 Q12335 human papil
44 43 89.6 151 2 Q12336 Q12336 human papil
45 43 89.6 151 2 Q76TS0 Q76TS0 human papil

ALIGNMENTS

RESULT 1

Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia."
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040702; AAL01361.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 12722 MW; 071F14EE3E6BE2AC CRC64;
Query Match 100.0%; Score 48; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.24; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 KLPOLCTEL 9

Db 3 KLPOLCTEL 11

RESULT 2

Q919C4 PRELIMINARY; PRT; 143 AA.
AC Q919C4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia."
RL Int. J. Cancer 97:868-874(2002).


```

Query Match      100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 KLPOLCTEL 9
Db      11 KLPOLCTEL 19

RESULT 6
ID Q80963      PRELIMINARY;      PRT;      151 AA.
AC Q80963;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DE 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34122; AAA91669.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18231 MW; 97C7028D5169382D CRC64;

Query Match      100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 KLPOLCTEL 9
Db      11 KLPOLCTEL 19

RESULT 7
ID Q89640      PRELIMINARY;      PRT;      151 AA.
AC Q89640;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DE 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.

Query Match      100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 KLPOLCTEL 9
Db      11 KLPOLCTEL 19

RESULT 8
ID Q89648      PRELIMINARY;      PRT;      151 AA.
AC Q89648; O12653; O12654; O12928; O12929;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DE 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34110; AAA91657.1; -.
DR EMBL; U34109; AAA91656.1; -.
DR EMBL; U34113; AAA91660.1; -.
DR EMBL; U34135; AAA91682.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18221 MW; 60CD2A34DAF48CB7 CRC64;

Query Match      100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 KLPOLCTEL 9
Db      11 KLPOLCTEL 19

RESULT 9
ID Q89755      PRELIMINARY;      PRT;      151 AA.

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Qy 1 KLPOLCTEL 9
Db 11 KLPOLCTEL 19

RESULT 13
Q8BB20 PRELIMINARY; PRT; 151 AA.
AC Q8BB20; (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2242222; PubMed=1235268; DOI=10.1007/s00239-002-2344-y;
RA Defilippis V.R., Ayala P.J., Villarreal L.P.;
RT "Evidence of diversifying selection in human papillomavirus type 16 E6
RT but not E7 oncogenes.";
RL J. Mol. Evol. 55:491-499(2002).
DR EMBL; AY089953; AAM1879.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18319 MW; 7CBD23EFCF4F8C17 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPOLCTEL 9
Db 11 KLPOLCTEL 19

RESULT 14
Q9W8C3 PRELIMINARY; PRT; 151 AA.
AC Q9W8C3;
DT 01-NOV-1999 (TREMELrel. 12, Created)
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388064; CAB45120.1; -.
DR EMBL; AJ388062; CAB45116.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18360 MW; FF9A2A3ADDBA7902 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPOLCTEL 9

Db 11 KLPOLCTEL 19

RESULT 15
Q9W931 PRELIMINARY; PRT; 151 AA.
AC Q9W931;
DT 01-NOV-1999 (TREMELrel. 12, Created)
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388059; CAB45110.1; -.
DR EMBL; AJ388058; CAB45108.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18306 MW; 6FB3D9E0F24A5300 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPOLCTEL 9
Db 11 KLPOLCTEL 19

Search completed: June 28, 2005, 19:19:19
Job time : 55.3 secs.

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 Seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-2

Perfect score: 48

Sequence: 1 KLPQLCTEL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	158	1 W6WLHS	protein E6 - human
2	43	89.6	57	2 I56705	E6 protein - human
3	43	89.6	158	1 W6WL18	E6 protein - human
4	43	88.6	158	2 S35561	E6 protein - human
5	38	79.2	625	2 B64172	dxs protein - Haem
6	37	77.1	158	1 W6WL39	E6 protein - human
7	37	77.1	608	2 A84984	dxs protein (impor
8	35	72.9	532	2 T16752	hypothetical prote
9	35	72.9	1150	1 A55289	kinesin-like prote
10	34	70.8	278	2 S17695	chlorophyll a/b-bi
11	34	70.8	328	2 T46001	hypothetical prote
12	34	70.8	341	1 K1BE36	thymidine kinase (
13	34	70.8	341	1 K1BE40	thymidine kinase (
14	34	70.8	341	1 K1BE73	thymidine kinase (
15	34	70.8	341	1 K1BEEL	thymidine kinase (
16	34	70.8	341	1 K1BEGK	thymidine kinase (
17	34	70.8	389	2 S75454	hypothetical prote
18	34	70.8	434	2 I50132	vasotocin receptor
19	34	70.8	471	2 E64223	hypothetical prote
20	34	70.8	486	2 B86611	hypothetical prote
21	34	70.8	486	2 A72014	hypothetical prote
22	34	70.8	564	2 T42695	hypothetical prote
23	34	70.8	567	2 JN0459	transforming growt
24	34	70.8	592	2 S51371	probable iron-sulf
25	34	70.8	1132	2 C75259	E6 protein - human
26	33	68.8	148	2 S36515	hypothetical prote
27	33	68.8	156	2 T20196	hypothetical prote
28	33	68.8	292	2 A64487	modification methy
29	33	68.8	317	2 S01412	hypothetical prote

hypothetical prote
1-deoxy-D-xylose
1-deoxyxylose-5-
dxs protein - Esch
1-deoxy-D-xylose
1-deoxy-D-xylose
1-deoxyxylose-5-
hypothetical prote
probable transketol
ATP-dependent nucl
ATP-dependent heli
kinesin-related pr
glycine cleavage s
hypothetical prote
hypothetical prote
mannose-binding le

30 33 68.8 374 2 T22356
31 33 68.8 619 2 A10385
32 33 68.8 620 2 AF0554
33 33 68.8 620 2 D64771
34 33 68.8 620 2 F85538
35 33 68.8 620 2 B30683
36 33 68.8 626 2 H82286
37 33 68.8 633 2 S76749
38 33 68.8 640 2 F71527
39 33 68.8 822 2 C71633
40 33 69.8 1309 2 F82207
41 32 66.7 147 2 E44259
42 32 66.7 189 2 AF0372
43 32 66.7 215 2 AC1386
44 32 66.7 215 2 AE1761
45 32 66.7 239 1 LNMSMA

ALIGNMENTS

RESULT 1
W6WLHS
protein E6 - human papillomavirus type 16
C:Species: human papillomavirus type 16
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A03682; T10427
R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virolgy 145, 181-185, 1985
A:Title: Human papillomavirus type 16 DNA sequence.
A:Reference number: A22355; MUID:85246220; PMID:2990099
A:Accession: A03682
A:Molecule type: DNA
A:Residues: 1-158 <SEE>
A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A:Reference number: Z17014; MUID:91162763; PMID:1848319
A:Accession: T10427
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-158 <KEN>
A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
C:Genetics:
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:37-73/Region: zinc finger CCCC motif
F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 48; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
Db 18 KLPQLCTEL 26

RESULT 2
I56705
E6 protein - human papillomavirus type 18
C:Species: human papillomavirus type 18
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56705
R:Inagaki, Y.; Tsunokawa, Y.; Takebe, N.; Nawa, H.; Nakanishi, S.; Terada, M.; Sugimura, J. Virol. 62, 1640-1646, 1988
A:Title: Nucleotide sequences of cDNAs for human papillomavirus type 18 transcripts in He
A:Reference number: I56705; MUID:88188247; PMID:2833614
A:Accession: I56705
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA

A;Residues: 1-57 <RES>
A;Cross-references: UNIPROT:Q90133; GB:M20324; PIDN:AAA99512.1; PID:g306834
A;Superfamily: papillomavirus E6 protein

Query Match 89.6%; Score 43; DB 2; Length 57;
Best Local Similarity 88.9%; Pred. No. 0.19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPOLCTEL 9
||| |||||
Db 13 KLPDLCTEL 21

RESULT 3
W6WLJ18
E6 protein - human papillomavirus type 18
C;Species: human papillomavirus type 18
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
A;Accession: A26165; G26251
R;Seedorf, K.; Oltersdorf, T.; Kraemmer, G.; Roewekamp, W.
EMBO J. 6, 139-144, 1987
A;Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)
A;Reference number: A91068; MUID:87218459; PMID:3034571
A;Accession: A26165
A;Molecule type: DNA
A;Residues: 1-158 <SEE>
A;Cross-references: UNIPROT:P06463; GB:X04773; NID:g60876; PIDN:CAA28466.1; PID:g60877
R;Cole, S.T.; Danos, O.
J. Mol. Biol. 193, 593-608, 1987
A;Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 1
A;Reference number: A92937; MUID:87283882; PMID:3039146
A;Accession: G26251
A;Molecule type: DNA
A;Residues: 1-158 <COL>
A;Cross-references: GB:X05015; NID:g60975; PIDN:CAA28664.1; PID:g60976
R;Matlahewski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pim, D.; Crawford, L.
J. Gen. Virol. 67, 1909-1916, 1986
A;Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the p
A;Reference number: A92791; MUID:86306665; PMID:3018129
A;Contents: annotation; identification of the protein
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;32-68/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif

Query Match 89.6%; Score 43; DB 1; Length 158;
Best Local Similarity 88.9%; Pred. No. 0.53;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPOLCTEL 9
||| |||||
Db 13 KLPDLCTEL 21

RESULT 4
S36561
E6 protein - human papillomavirus type 45
C;Species: human papillomavirus type 45
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
A;Accession: S36561
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36561
A;Molecule type: DNA
A;Residues: 1-158
A;Cross-references: UNIPROT:P21735; EMBL:X74479; NID:g397022; PIDN:CAA52573.1; PID:g3970
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 89.6%; Score 43; DB 2; Length 158;
Best Local Similarity 88.9%; Pred. No. 0.53;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPOLCTEL 9
||| |||||
Db 13 KLPDLCTEL 21

RESULT 5
B64172
dxs protein - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: B64172
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: B64172
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-625 <TIGR>
A;Cross-references: UNIPROT:P45205; GB:U32822; GB:L42023; NID:g1574265; PIDN:AAC23088.1;
C;Genetics:
A;Gene: dxs
C;Superfamily: deoxyxylulose-5-phosphate synthase

Query Match 79.2%; Score 38; DB 2; Length 625;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPOLCTEL 9
:|||||
Db 27 QLPOLCQEL 35

RESULT 6
W6WLJ39
E6 protein - human papillomavirus type 39
C;Species: human papillomavirus type 39
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A38502
R;Volpers, C.; Streeck, R.E.
Virology 181, 419-423, 1991
A;Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
A;Reference number: A38502; MUID:91135017; PMID:1847266
A;Accession: A38502
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-158 <VOL>
A;Cross-references: UNIPROT:P24835; GB:M62849; EMBL:M38185; NID:g333245; PIDN:AAA47050.1;
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;32-68/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif

Query Match 77.1%; Score 37; DB 1; Length 158;
Best Local Similarity 77.8%; Pred. No. 7.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLPOLCTEL 9
||| |||||
Db 13 KLPDLCTTL 21

RESULT 7
A84984
dxs protein [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Jun-2003

C:Accession: A84984
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A:Reference number: A84930; MUID:20445173; PMID:10993077
A:Accession: A84984
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-608 <STO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: dxs, BU464
C:Superfamily: deoxyxylulose-5-phosphate synthase

Query Match 77.1%; Score 37; DB 2; Length 608;
Best Local Similarity 77.8%; Pred. No. 29;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
:|||||
Db 27 QLPQLCFEL 35

RESULT 8
T16752
hypothetical protein R144.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16752
R:Favell, T.
submitted to the EMBL Data Library, March 1995
A:Description: The sequence of C. elegans cosmid R144.
A:Reference number: Z18571
A:Accession: T16752
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-532 <FAV>
A:Cross-references: UNIPROT:Q09346; EMBL:U23515; NID:G746492; PID:G746497; PIDN:AA46549
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:R144.5
A:Introns: 56/1; 110/1; 215/1; 264/1; 301/3; 419/3; 426/2; 447/2
C:Superfamily: Caenorhabditis elegans hypothetical protein R144.5

Query Match 72.9%; Score 35; DB 2; Length 532;
Best Local Similarity 77.8%; Pred. No. 61;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
:|||||
Db 309 KLRQLCSEL 317

RESULT 9
A55289
kinesin-like protein KIF1B - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C:Accession: A55289
R:Nangaku, M.; Sato-Yoshitake, R.; Okada, Y.; Noda, Y.; Takemura, R.; Yamazaki, H.; Hiro
Cell 79, 1209-1220, 1994
A:Title: KIF1B, a novel microtubule plus end-directed monomeric motor protein for transp
A:Reference number: A55289; MUID:95094296; PMID:7528108
A:Accession: A55289
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1150 <NAN>
A:Cross-references: GB:D17577; NID:G407338; PIDN:BA04503.1; PID:G407339
C:Superfamily: kinesin-related protein KIF1B; kinesin motor domain homology
C:Keywords: nucleotide binding; P-loop
F:6-354/Domain: kinesin motor domain homology <RMOT>
F:97-104/Region: nucleotide-binding motif A (P-loop)

Query Match 72.9%; Score 35; DB 1; Length 1150;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LPQLCTEL 9
:|||||
Db 119 IPQLCEEL 126

RESULT 10
S17695
chlorophyll a/b-binding protein (clone pINEab 31) - Scotch pine
C:Species: Pinus sylvestris (Scotch pine)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S17695
R:Jansson, S.; Gustafsson, P.
Mol. Gen. Genet. 229, 67-76, 1991
A:Title: Evolutionary conservation of the chlorophyll a/b-binding proteins: cDNAs encod
A:Reference number: S17694; MUID:91375452; PMID:1896022
A:Accession: S17695
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-278 <JAN>
A:Cross-references: UNIPROT:Q02070; EMBL:X58516; NID:G20791; PIDN:CAA41406.1; PID:G20792
C:Superfamily: chlorophyll a/b-binding protein

Query Match 70.8%; Score 34; DB 2; Length 278;
Best Local Similarity 62.5%; Pred. No. 50;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LPQLCTEL 9
:|||||
Db 131 IPELCTKL 138

RESULT 11
T46001
hypothetical protein F9D24.320 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46001
R:D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23011
A:Accession: T46001
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-328 <DAN>
A:Cross-references: UNIPROT:Q9M2H5; EMBL:AL137081
A:Experimental source: cultivar Columbia; BAC clone F9D24
C:Genetics:
A:Map position: 3
A:Introns: 57/2; 100/3; 194/3
A:Note: F9D24.320
C:Superfamily: Arabidopsis thaliana hypothetical protein F9D24.110

Query Match 70.8%; Score 34; DB 2; Length 328;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
:|||||
Db 296 KLRQLCTEL 304

RESULT 12
XIBE36
thymidine kinase (EC 2.7.1.21) - human herpesvirus 3
C:Species: human herpesvirus 3, varicella-zoster virus
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C:Accession: A27341; A45715
R:Davidson, A.J.; Scott, J.E.

J. Gen. Virol. 67, 1759-1816, 1986
 A:Title: The complete DNA sequence of varicella-zoster virus.
 A:Reference number: A27345; MUID:86306657; PMID:3018124
 A:Accession: A27341
 A:Molecule type: DNA
 A:Residues: 1-341 <SAW>
 A:Cross-references: UNIPROT:P09250; EMBL:X04370; NID:G59989; PIDN:CAA27919.1; PID:G60025
 R:Talarico, C.L.; Phelps, W.C.; Biron, K.K.
 J. Virol. 67, 1024-1033, 1993
 A:Title: Analysis of the thymidine kinase genes from acyclovir-resistant mutants of varicella-zoster virus.
 A:Reference number: A45715; MUID:93124537; PMID:8380452
 C:Contents: annotation; analysis of acyclovir-resistant strain mutations
 C:Superfamily: herpesvirus thymidine kinase; herpesvirus thymidine kinase homology
 C:Keywords: ATP; DNA biosynthesis; nucleotide binding; P-loop; phosphotransferase
 F:12-300/Domain: herpesvirus thymidine kinase homology <HTK>
 F:19-26/Region: herpesvirus thymidine kinase homology
 F:125-129/Region: nucleotide-binding motif A (P-loop)
 F:25/Binding site: ATP (Lys) #status predicted

Query Match 70.8%; Score 34; DB 1; Length 341;
 Best Local Similarity 75.0%; Pred. No. 61;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPOLCCTE 8
 |||:|
 Db 262 KLPELCGE 269

RESULT 13
 KIBE40
 thymidine kinase (EC 2.7.1.21) - human herpesvirus 3 (strain 40a2)
 N:Alternate names: pyrimidine deoxyribonucleoside kinase
 C:Species: human herpesvirus 3, varicella-zoster virus
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
 C:Accession: C28930
 R:Sawyer, M.H.; Inchauspe, G.; Biron, K.K.; Waters, D.J.; Straus, S.E.; Ostrove, J.M.
 J. Gen. Virol. 69, 2585-2593, 1988
 A:Title: Molecular analysis of the pyrimidine deoxyribonucleoside kinase gene of wild-type varicella-zoster virus.
 A:Reference number: A32798; MUID:89010695; PMID:2844967
 A:Accession: C28930
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-341 <SAW>
 A:Cross-references: UNIPROT:P14341
 C:Superfamily: herpesvirus thymidine kinase; herpesvirus thymidine kinase homology
 C:Keywords: ATP; DNA biosynthesis; nucleotide binding; P-loop; phosphotransferase
 F:12-300/Domain: herpesvirus thymidine kinase homology <HTK>
 F:19-26/Region: nucleotide-binding motif A (P-loop)
 F:125-129/Region: nucleotide-binding motif B
 F:25/Binding site: ATP (Lys) #status predicted

Query Match 70.8%; Score 34; DB 1; Length 341;
 Best Local Similarity 75.0%; Pred. No. 61;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPOLCCTE 8
 |||:|
 Db 262 KLPELCGE 269

RESULT 14
 KIBE73
 thymidine kinase (EC 2.7.1.21) - human herpesvirus 3 (strain 7-1-3)
 N:Alternate names: pyrimidine deoxyribonucleoside kinase
 C:Species: human herpesvirus 3, varicella-zoster virus
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
 C:Accession: B28930
 R:Sawyer, M.H.; Inchauspe, G.; Biron, K.K.; Waters, D.J.; Straus, S.E.; Ostrove, J.M.
 J. Gen. Virol. 69, 2585-2593, 1988
 A:Title: Molecular analysis of the pyrimidine deoxyribonucleoside kinase gene of wild-type varicella-zoster virus.
 A:Reference number: A32798; MUID:89010695; PMID:2844967
 A:Accession: B28930
 A:Status: nucleic acid sequence not shown

A:Molecule type: DNA
 A:Residues: 1-341 <SAW>
 A:Cross-references: UNIPROT:P14342
 C:Superfamily: herpesvirus thymidine kinase; herpesvirus thymidine kinase homology
 C:Keywords: ATP; DNA biosynthesis; nucleotide binding; P-loop; phosphotransferase
 F:12-300/Domain: herpesvirus thymidine kinase homology <HTK>
 F:19-26/Region: nucleotide-binding motif A (P-loop)
 F:125-129/Region: nucleotide-binding motif B
 F:25/Binding site: ATP (Lys) #status predicted

Query Match 70.8%; Score 34; DB 1; Length 341;
 Best Local Similarity 75.0%; Pred. No. 61;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPOLCCTE 8
 |||:|
 Db 262 KLPELCGE 269

RESULT 15
 KIBEL
 thymidine kinase (EC 2.7.1.21) - human herpesvirus 3 (strains Ellen, Oka, ppIIa, and 5-1-1)
 N:Alternate names: pyrimidine deoxyribonucleoside kinase
 C:Species: human herpesvirus 3, varicella-zoster virus
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
 C:Accession: A28930; A46450
 R:Sawyer, M.H.; Inchauspe, G.; Biron, K.K.; Waters, D.J.; Straus, S.E.; Ostrove, J.M.
 J. Gen. Virol. 69, 2585-2593, 1988
 A:Title: Molecular analysis of the pyrimidine deoxyribonucleoside kinase gene of wild-type varicella-zoster virus.
 A:Reference number: A92798; MUID:89010695; PMID:2844967
 A:Accession: A28930
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-341 <SAW>
 A:Cross-references: UNIPROT:P14344
 R:Mori, H.; Shiraki, K.; Kato, T.; Hayakawa, Y.; Yamanishi, K.; Takahashi, M.
 Intervirology 29, 301-310, 1988
 A:Title: Molecular analysis of the thymidine kinase gene of thymidine kinase-deficient mutant of varicella-zoster virus.
 A:Reference number: A46450; MUID:89154977; PMID:2852653
 A:Accession: A46450
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-341 <WOR>
 A:Cross-references: GB:W36160; NID:G330326; PIDN:AAA45865.1; PID:G330327
 C:Superfamily: herpesvirus thymidine kinase; herpesvirus thymidine kinase homology
 C:Keywords: ATP; DNA biosynthesis; nucleotide binding; P-loop; phosphotransferase
 F:12-300/Domain: herpesvirus thymidine kinase homology <HTK>
 F:19-26/Region: nucleotide-binding motif A (P-loop)
 F:125-129/Region: nucleotide-binding motif B
 F:25/Binding site: ATP (Lys) #status predicted

Query Match 70.8%; Score 34; DB 1; Length 341;
 Best Local Similarity 75.0%; Pred. No. 61;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPOLCCTE 8
 |||:|
 Db 262 KLPELCGE 269

Search completed: June 28, 2005, 19:23:13
 Job time : 13.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-30
Perfect score: 44
Sequence: 1 TLQDIVLHL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	105	1 W7WL18	E7 protein - human
2	40	90.9	106	2 S36562	E7 protein - human
3	37	84.1	447	2 H97146	siderophore/Surfac
4	37	84.1	691	2 G82979	ATP-dependent DNA
5	37	84.1	693	2 A50005	DNA recombinase (E
6	36	81.8	693	1 JH0265	ATP-dependent DNA
7	36	81.8	693	2 AE0969	DNA helicase RecG
8	36	81.8	693	2 G91194	hypothetical prote
9	36	81.8	704	2 H86041	antigen, P35 homol
10	35	79.5	105	2 S36580	transposase (08) /
11	35	79.5	249	2 F70238	E7 protein - human
12	35	79.5	901	2 F83781	nitrogenase (EC 1.
13	34	77.3	101	1 W7WL51	hypothetical prote
14	34	77.3	295	1 JH0039	nitrogenase (EC 1.
15	34	77.3	295	2 JH0888	hypothetical prote
16	33	75.0	187	2 C71317	conserved hypothet
17	33	75.0	299	2 C75514	hypothetical prote
18	33	75.0	312	1 S74332	probable resistanc
19	33	75.0	324	1 C71081	hypothetical prote
20	33	75.0	327	2 D72257	daunorubicin resis
21	33	75.0	328	2 E75108	probable chemotaxi
22	33	75.0	398	2 C69485	Ras GTPase activat
23	33	75.0	490	2 H83286	E7 protein - human
24	33	75.0	1657	2 A54854	E7 protein - human
25	32	72.7	101	1 W7WL13	E7 protein - human
26	32	72.7	103	1 W7WL5	E7 protein - human
27	32	72.7	103	1 W7WL85	E7 protein - rhesu
28	32	72.7	113	1 W7WL81	hypothetical prote
29	32	72.7	265	2 H84128	

30 32 72.7 314 2 AB2409 dTDP-glucose dehyd
31 32 72.7 380 1 C71844 dihydropteroate sy
32 32 72.7 415 2 G83863 threonine dehydrat
33 32 72.7 416 2 C71620 protein with Egl-1
34 32 72.7 447 2 S44809 F4489.8 protein -
35 32 72.7 454 2 A97147 siderophore/Surfac
36 32 72.7 644 2 J00160 3-isopropylmalate
37 32 72.7 692 2 H82041 ATP-dependent DNA
38 31 70.5 93 2 S32553 defensin NP-3a pre
39 31 70.5 98 1 W7WLC1 E7 protein - pygmy
40 31 70.5 98 1 W7WLC1 E7 protein - human
41 31 70.5 98 1 W7WLC1 E7 protein - human
42 31 70.5 102 2 S36486 E7 protein - human
43 31 70.5 109 1 W7WL39 E7 protein - human
44 31 70.5 132 2 H83048 probable transcrip
45 31 70.5 166 2 T47193 yciF protein [impo

ALIGNMENTS

RESULT 1

W7WL18
E7 protein - human papillomavirus type 18
C:Species: human papillomavirus type 18
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: B26165; H26251
R:Seedorf, K.; Olteradorf, T.; Kraemmer, G.; Roewekamp, W.
EMBO J. 6, 139-144, 1987
A:Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)
A:Reference number: A91068; MUID:87219459; PMID:3034571
A:Accession: B26165
A:Molecule type: DNA
A:Residues: 1-105 <SSE>
A:Cross-references: UNIPROT:P06788; GB:X04773; NID:G60876; PIDN:CAA28467.1; PID:G60878
R:Cole, S.T.; Danos, O.
J. Mol. Biol. 193, 599-608, 1987
A:Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 18
A:Reference number: A92937; MUID:87283882; PMID:3039146
A:Accession: H26251
A:Molecule type: DNA
A:Residues: 1-105 <COL>
A:Cross-references: GB:X05015; NID:G60975; PIDN:CAA28665.1; PID:G60977
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 100.0%; Score 44; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
Db 7 TLQDIVLHL 15

RESULT 2

S36562
E7 protein - human papillomavirus type 45
C:Species: human papillomavirus type 45
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36562
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36562
A:Molecule type: DNA
A:Residues: 1-106
A:Cross-references: UNIPROT:P21736; EMBL:X74479; NID:G397022; PIDN:CAA52574.1; PID:G39702;
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 90.9%; Score 40; DB 2; Length 106;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLQDIVLHL 9
|:|:|:|

Db 32 TVQDLLLHL 40

RESULT 7
ATP-dependent DNA helicase (EC 3.6.1.-) [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AE0969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-693 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD03249.1; PID:gl6504871; GSPDB:GN00176
C:Genetics:
A:Gene: STY4048
C:Superfamily: DNA helicase recG
C:Keywords: hydrolase

Query Match 81.8%; Score 36; DB 2; Length 693;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLQDIVLHL 9
|:|:|:|

Db 32 TVQDLLLHL 40

RESULT 8
DNA helicase RecG [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: G91194
R:Hayaashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hatcori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: G91194
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-693 <HAY>
A:Cross-references: UNIPROT:Q8XD86; GB:BA000007; PIDN:BA37950.1; PID:gl3364002; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: EC64527
C:Superfamily: DNA helicase recG

Query Match 81.8%; Score 36; DB 2; Length 693;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLQDIVLHL 9
|:|:|:|

Db 32 TVQDLLLHL 40

RESULT 9
H96041
hypotheoretical protein recG [imported] - Escherichia coli (strain O157:H7, substrain EDL93

C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: H86041
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Roe, D.J.; Mayhew,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dinalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H86041
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-704 <STO>
A:Cross-references: GB:AB005174; NID:gl2518411; PIDN:AG58796.1; GSPDB:GN00145; UMGP:250;
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: recG
C:Superfamily: DNA helicase recG

Query Match 81.8%; Score 36; DB 2; Length 704;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLQDIVLHL 9
|:|:|:|

Db 43 TVQDLLLHL 51

RESULT 10
S36580
E7 protein - human papillomavirus type 56
C:Species: human papillomavirus type 56
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
A:Accession: S36580
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36580
A:Molecule type: DNA
A:Residues: 1-105
A:Cross-references: UNIPROT:P36833; EMBL:X74483; NID:g937053; PIDN:CAA52597.1; PID:g9370;
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 79.5%; Score 35; DB 2; Length 105;
Best Local Similarity 77.8%; Pred. No. 5.3;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLQDIVLHL 9
|:|:|:|

Db 7 TLQDVWLEL 15

RESULT 11
F70238
antigen, P35 homolog - Lyme disease spirochete plasmid H/1p28-3
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: F70238
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: F70238
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-249 <KLE>
A:Cross-references: UNIPROT:O50687; GB:AB000784; NID:g2690041; PIDN:AAC65996.1; PID:g269;
A:Experimental source: strain B31
C:Genetics:

A:Genome: plasmid
C:Superfamily: Lyme disease spirochete plasmid conserved hypothetical protein BB134

Query Match 79.5%; Score 35; DB 2; Length 249;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
Db 153 TLDDVVVHL 161
|||:|:|

RESULT 12
F83781
transposase (08) / ABC transporter (ATP-binding protein) BH1054 [imported] - Bacillus ha
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: F83781
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: F83781
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-901 <STO>
A:Cross-references: UNIPROT:Q9KE04; GB:AP001510; GB:BA000004; NID:G10173440; PIDN:BA047
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1054

Query Match 79.5%; Score 35; DB 2; Length 901;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
Db 886 TLEDVFLHL 894
|||:|:|

RESULT 13
W7WLS1
E7 protein - human papillomavirus type 51
C:Species: human papillomavirus type 51
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: F40415
R;Lungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991
A:Title: Biologic properties and nucleotide sequence analysis of human papillomavirus ty
A:Reference number: A40415; MUID:91303675; PMID:1649326
A:Accession: F40415
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-101 <LUN>
A:Cross-references: UNIPROT:P26558; GB:M62877
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 77.3%; Score 34; DB 1; Length 101;
Best Local Similarity 75.0%; Pred. No. 8.2;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LQDIVLHL 9
Db 8 LKDVVFLHL 15
|||:|:|

RESULT 14
JW0039
nitrogenase (EC 1.18.6.1) iron protein - Rhodospirillum rubrum
N:Alternate names: dinitrogenase reductase
C:Species: Rhodospirillum rubrum

C:Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: JW0039; A61610
R;Lehman, L.J.; Fitzmaurice, W.P.; Roberts, G.P.
Gene 95, 143-147, 1990
A:Title: The cloning and functional characterization of the nifH gene of Rhodospirillum;
A:Reference number: JW0039; MUID:91071597; PMID:1979299
A:Accession: JW0039
A:Molecule type: DNA
A:Residues: 1-295 <LEH>
A:Cross-references: UNIPROT:P22921; GB:M33774; NID:G152609; PIDN:AAA26463.1; PID:G152610
R;Pope, M.R.; Murrell, S.A.; Ludden, P.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 3173-3177, 1985
A:Title: Covalent modification of the iron protein of nitrogenase from Rhodospirillum rub
A:Reference number: A61610; MUID:85216464; PMID:3923473
A:Accession: A61610
A:Molecule type: protein
A:Residues: 101-106 <POP>
C:Comment: This protein is regulated by reversible ADP-ribosylation on a specific Arg res
C:Genetics:
A:Gene: nifH
C:Superfamily: nitrogenase iron protein
C:Keywords: 4Fe-4S; ATP; homodimer; iron-sulfur protein; metalloprotein; nitrogen fixatio
F;11-18/Region: nucleotide-binding motif A (p-loop)
F;17/Binding site: ATP (lys) #status predicted
F;41.45/Active site: Asp #status predicted
F;99,133/Binding site: 4Fe-4S cluster (Cys) (covalent) (shared with dimeric partner) #sta
F;102/Modified site: ADP-ribosylarginine (Arg) (by NAD+-nitrogenase ADP-D-ribosyltransferse

Query Match 77.3%; Score 34; DB 1; Length 295;
Best Local Similarity 87.5%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LQDIVLHL 9
Db 55 LQDTVLHL 62
|||:|:|

RESULT 15
JN0888
nitrogenase (EC 1.18.6.1) iron protein - Rhodobacter capsulatus
N:Alternate names: nitrogenase component II; nitrogenase reductase
C:Species: Rhodobacter capsulatus
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: JN0888; S01411; A29042; S18917
R;Willison, J.C.; Pierrard, J.; Huebner, P.
Gene 133, 39-46, 1993
A:Title: Sequence and transcript analysis of the nitrogenase structural gene operon (nifH
A:Reference number: JN0887; MUID:94040794; PMID:7693551
A:Accession: JN0888
A:Molecule type: DNA
A:Residues: 1-295 <WIL>
A:Cross-references: UNIPROT:P08718; EMBL:X63352; NID:G550144; PIDN:CAA44954.1; PID:G4601;
R;Jones, R.; Haselkorn, R.
Nucleic Acids Res. 16, 8735, 1988
A:Title: The DNA sequence of the Rhodobacter capsulatus nifH gene.
A:Reference number: S01411; MUID:88335644; PMID:3419937
A:Accession: S01411
A:Molecule type: DNA
A:Residues: 1-65, 'V', 67-295 <JON>
A:Cross-references: EMBL:X07866; NID:G46066; PIDN:CAA30716.1; PID:G46067
R;Schumann, J.P.; Waitches, G.M.; Scolnik, P.A.
Gene 48, 81-92, 1986
A:Title: A DNA fragment hybridizing to a nif probe in Rhodobacter capsulatus is homologou
A:Reference number: A91562; MUID:87163519; PMID:3557130
A:Accession: A29042
A:Molecule type: DNA
A:Residues: 1-65, 'V', 67-73, 'L', 75-82, 'R', 84-89, 'S', 91-151, 'C', 153-158, 'V', 160-165, 'P', 167;
A:Cross-references: GB:M15270; NID:G151971; PIDN:AAA26140.1; PID:G151972
C:Genetics:
A:Gene: nifH
C:Superfamily: nitrogenase iron protein
C:Keywords: 4Fe-4S; ATP; iron-sulfur protein; metalloprotein; nitrogen fixation; nucleoti
F;11-18/Region: nucleotide-binding motif A (p-loop)

F:17/Binding site: ATP (Lys) #status predicted
 F:41.45/Active site: Asp #status predicted
 F:99.133/Binding site: 4Fe-4S cluster (Cys) (covalent) (shared with dimeric partner) #status predicted

Query Match 77.3%; Score 34; DB 2; Length 295;
 Best Local Similarity 87.5%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 LQDIVLHL 9
 |||||
 Db 55 LQDTVLHL 62

Search completed: June 26, 2005, 21:27:46
 Job time : 12.15 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)

83.643 Million cell updates/sec

Title: US-08-170-344-30

Perfect score: 44

Sequence: 1 TLQDIVLHL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	105	1 VET_HPV18	P06788 human papil
2	44	100.0	105	2 Q6FGP1	Q6pgp1 homo sapien
3	44	100.0	105	2 Q8V9K9	Q8v9k9 human papil
4	44	100.0	105	2 Q8QNP5	Q8qnp5 human papil
5	44	100.0	105	2 Q8QNP7	Q8qnp7 human papil
6	40	90.9	99	2 Q37386	Q37386 common chim
7	40	90.9	106	1 VET_HPV45	P21736 human papil
8	40	90.9	106	2 Q9Y4Y3	Q9y4y3 homo sapien
9	40	90.9	106	2 O10609	O10609 human papil
10	39	88.6	105	2 Q9QNP6	Q9qnp6 human papil
11	37	84.1	147	2 Q97HK7	Q97hk7 clostridium
12	37	84.1	622	2 Q919J5	Q919j5 hippoglossu
13	37	84.1	626	2 Q6GUK8	Q6guk8 scophthalmu
14	37	84.1	626	2 Q6GUK9	Q6guk9 scophthalmu
15	37	84.1	691	2 Q9HTL3	Q9htl3 pseudomonas
16	37	84.1	693	2 Q66GE9	Q66ge9 yersinia ps
17	37	84.1	693	2 Q8ZJQ6	Q8zjq6 yersinia ps
18	37	84.1	921	2 Q74H42	Q74h42 geobacter s
19	37	84.1	1448	2 Q9XZE9	Q9xze9 hydra atten
20	36	81.8	96	1 VET_HPV24	P50782 human papil
21	36	81.8	101	1 VET_HPV21	P50779 human papil
22	36	81.8	101	2 Q84300	Q84300 human papil
23	36	81.8	102	1 VET_HPV20	P50778 human papil
24	36	81.8	102	2 Q84299	Q84299 human papil
25	36	81.8	267	2 Q8DYH4	Q8dyh4 streptococc
26	36	81.8	267	2 Q8E438	Q8e438 streptococc
27	36	81.8	423	1 FXL3_MOUSE	Q8c4v4 mus musculu
28	36	81.8	693	1 RECG_ECOS7	Q8xd86 escherichia
29	36	81.8	693	1 RECG_ECOLI1	P24230 escherichia
30	36	81.8	693	2 Q8ZT12	Q8zt12 salmonella
31	36	81.8	693	2 Q8ZL39	Q8zl39 salmonella

32 36 81.8 693 2 Q7UB01 Q7ub01 shigella fl
33 36 81.8 693 2 Q6DB64 Q6db64 erwinia car
34 36 81.8 704 2 Q821A1 Q821a1 shigella fl
35 36 81.8 704 2 Q8FC81 Q8fc81 escherichia
36 36 81.8 2516 2 Q9RN43 Q9rn43 photorhabdu
37 36 81.8 2525 2 Q7N7Y9 Q7n7y9 photorhabdu
38 35 79.5 105 1 VET_HPV56 P36833 human papil
39 35 79.5 122 2 Q9CR74 Q9cr74 m mus muscu
40 35 79.5 181 2 Q9ZAD5 Q9zad5 porphyromon
41 35 79.5 249 2 O50687 O50687 borrelia bu
42 35 79.5 300 2 Q9ZS09 Q9zsq9 mesembryant
43 35 79.5 310 2 Q9RC44 Q9rc44 bacillus ha
44 35 79.5 310 2 Q8CUN6 Q8cun6 oceanobacil
45 35 79.5 332 2 Q9CMM7 Q9cmm7 pasteurella

ALIGNMENTS

RESULT 1
VET_HPV18
ID VET_HPV18 STANDARD; PRT; 105 AA.
AC P06788;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87283882; PubMed=3039146;
RA Cole S.T., Danos O.;
RT "Nucleotide sequence and comparative analysis of the human
papillomavirus type 18 genome. Phylogeny of papillomaviruses and
repeated structure of the E6 and E7 gene products.";
RL J. Mol. Biol. 193:599-608(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=8818247; PubMed=2833614;
RA Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M.,
Sugimura T.;
RT "Nucleotide sequences of cDNAs for human papillomavirus type 18
transcripts in HeLa cells";
RL J. Virol. 62:1640-1646(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87053870; PubMed=3023067;
RA Schneider-Gaedcke A., Schwarz E.;
RT "Different human cervical carcinoma cell lines show similar
transcription patterns of human papillomavirus type 18 early genes.";
RL EMO J. 5:2285-2292(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=87218459; PubMed=30345571;
RA Seedorf K., Oltersdorf T., Kraemer G., Roewekamp W.;
RT "Identification of early proteins of the human papilloma viruses type
16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells.";
RL EMO J. 6:139-144(1987).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating
activities.

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DR EMBL; X05015; CAA28665.1; -.
DR EMBL; M20324; AAR9513.1; -.
DR EMBL; M20325; AAR9515.1; -.
DR EMBL; M26798; AAA46947.1; -.
DR EMBL; X04773; CAA28467.1; -.
DR EMBL; A06324; CAA00540.1; -.
DR EMBL; A06328; CAA00543.1; -.
DR PIR; B26165; W7WL18.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW Transcription regulation.
FT SITE 63 66 C-XX-C motif-1.
FT SITE 98 101 C-XX-C motif-2.
FT CONFLICT 73 73 K -> E (in Ref. 1 and 4).
SQ SEQUENCE 105 AA; 11995 MW; 2CDB119534D0186A CRC64;

Query Match 100.0%; Score 44; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
Db 7 TLQDIVLHL 15

RESULT 2
Q6PGP1 PRELIMINARY; PRT; 105 AA.
AC Q6PGP1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056907; AAH56907.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW Hypothetical protein.
SQ SEQUENCE 105 AA; 11995 MW; 2CDB119534D0186A CRC64;

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Query Match 100.0%; Score 44; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
Db 7 TLQDIVLHL 15

RESULT 3
Q8V9K9 PRELIMINARY; PRT; 105 AA.
AC Q8V9K9
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21568387; PubMed=11711624;
RX DOI=10.1128/JVI.75.24.12339-12346.2001;
RA Shera K.A., Shera C.A., McDougall J.K.;
RT "Small Tumor Virus Genomes Are Integrated near Nuclear Matrix
Attachment Regions in Transformed Cells.";
RL J. Virol. 75:12339-12346(2001).
DR EMBL; AF339137; AAL34455.1; -.
DR Pfam; PF00527; E7; 1.
DR PIR; B26165; W7WL18.
SQ SEQUENCE 105 AA; 12036 MW; 2528DEA165850C71 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
Db 7 TLQDIVLHL 15

RESULT 4
Q9QNP5 PRELIMINARY; PRT; 105 AA.
AC Q9QNP5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RA Laassri M., Gul'ko L., Vinokurova S., Kissel'ova N., Veiko V.,
RA Kissel'ev F.;
RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
Transformation Potential of E7 Gene and its Mutants.";
RL Virus Genes 182:139-149(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Veiko V.P.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y18493; CAB53099.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 105 AA; 11952 MW; 247BF448A6BBB4FA CRC64;

Query Match 100.0%; Score 44; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.38;

```

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 TLQDIVLHL 9
Db 7 TLQDIVLHL 15

RESULT 5
Q9QNP7 PRELIMINARY; PRT; 105 AA.
AC Q9QNP7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RA Laasri M., Gul'ko L., Vinokurova S., Kissel'ova N., Veiko V.,
RA Kissel'ev P.;
RT Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
RT Transformation Potential of E7 Gene and its Mutants.";
RL Virus Genes 182:139-149(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Veiko V.P.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y18491; CAB53097.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 105 AA; 12010 MW; 24799BB534D4496A CRC64;

```

Query Match 100.0%; Score 44; DB 2; Length 105;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 TLQDIVLHL 9
Db 7 TLQDIVLHL 15

```

RESULT 6

```

O37386 PRELIMINARY; PRT; 99 AA.
ID O37386;
AC O37386;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE E7.
OS Common chimpanzee papillomavirus type 1.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus; Common chimpanzee papillomavirus.
OX NCBI_TaxID=66261;
RN [1]
RP SEQUENCE FROM N.A.
RA Scinicariello F., Soza I., Brasky K.M., Hilliard J.K.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF020905; AAB71705.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 99 AA; 10858 MW; 7385003547E87AFE CRC64;

```

Query Match 90.9%; Score 40; DB 2; Length 99;
 Best Local Similarity 88.9%; Pred. No. 2.5;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 TLQDIVLHL 9
Db 7 TLQDIVLHL 15

```

RESULT 7

```

VE7 HPV45 STANDARD; PRT; 106 AA.
ID VE7 HPV45
AC P21736;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 45.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10593;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94265501; PubMed=8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Kaplan J.B., Burk R.D.;
RL Submitted (AUG-1990) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X74479; CAA52574.1; -.
CC DR EMBL; M38198; AAA46974.1; -.
CC PIR; S36562; S36562.
CC DR InterPro; IPR000148; Papvi_E7.
CC DR Pfam; PF00527; E7; 1.
CC KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
CC Transcription regulation.
CC FT SITE 64 67 C-XX-C motif-1.
CC FT SITE 99 102 G -> E (in Ref. 2).
CC FT CONFLICT 3 3 R -> Q (in Ref. 2).
CC FT CONFLICT 5 5 R -> Q (in Ref. 2).
CC SQ SEQUENCE 106 AA; 12049 MW; 4C53808A7285AD41 CRC64;

```

Query Match 90.9%; Score 40; DB 1; Length 106;
 Best Local Similarity 88.9%; Pred. No. 2.7;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 TLQDIVLHL 9
Db 7 TLQDIVLHL 15

```

RESULT 8

```

Q9Y4Y3 PRELIMINARY; PRT; 106 AA.
ID Q9Y4Y3
AC Q9Y4Y3;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE E7 protein.
GN Name=HPV45 E7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sastre-Garau X., Favre M., Couturier J., Orth G.;

```

RT "Distinct patterns of alteration of myc genes associated with
 RT integration of human papillomavirus type 16 oe type 45 in two genital
 tumours.";

RL J. Gen. Virol. 81:198-199 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Favre M.G.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ242956; CAB44707.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 106 AA; 11977 MW; 1912D1DE742F6BED CRC64;

Query Match 90.9%; Score 40; DB 2; Length 106;
 Best Local Similarity 88.9%; Pred. No. 2.7;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
 |||:|||||
 Db 7 TLQEIVLHL 15

RESULT 9
 O10609 PRELIMINARY; PRT; 106 AA.
 AC O10609;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Oncoprotein E7.
 OS Human papillomavirus type 45.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sastre-Garau X., Favre M., Couturier J., Orth G.;
 RT "Distinct patterns of alteration of myc genes associated with
 RT integration of HPV16 or HPV45 DNA in two genital tumors.";

RL J. Gen. Virol. 0:0-0(0).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Favre M.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y13218; CA473661.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 106 AA; 11977 MW; 1912D1DE742F6BED CRC64;

Query Match 90.9%; Score 40; DB 2; Length 106;
 Best Local Similarity 88.9%; Pred. No. 2.7;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
 |||:|||||
 Db 7 TLQEIVLHL 15

RESULT 10
 O9QNP6 PRELIMINARY; PRT; 105 AA.
 AC O9QNP6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 18.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10582;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Laasri M., Gul'ko L., Vinokurova S., Kisseljova N., Veiko V.,

RA Kisseljev F.;
 RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
 RT Transformation Potential of E7 Gene and its Mutants.";

RL Virus Genes 182:139-149 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Veiko V.P.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y18492; CAB53098.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 105 AA; 12009 MW; C4979555DAD4A960 CRC64;

Query Match 88.6%; Score 39; DB 2; Length 105;
 Best Local Similarity 88.9%; Pred. No. 4.3;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
 |||:|||||
 Db 7 TLQNVILHL 15

RESULT 11
 Q97HK7 PRELIMINARY; PRT; 447 AA.
 AC Q97HK7;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Siderophore/Surfactin synthetase related protein.
 GN OrderedLocusNames=CAC2004;
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=1359325; PubMed=11466286;
 DOI=10.1128/JB.183.16.4823-4838.2001;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
 RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 183:4823-4838 (2001).
 DR PIR; H97146; AAK79963.1; -;
 DR PIR; H97146; H97146.
 KW Complete proteome.
 SQ SEQUENCE 447 AA; 52723 MW; 95EC53FB2EDDE3EE CRC64;

Query Match 84.1%; Score 37; DB 2; Length 447;
 Best Local Similarity 77.8%; Pred. No. 52;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
 |||:|||||
 Db 254 TINDIVLHL 262

RESULT 12
 Q919J5 PRELIMINARY; PRT; 622 AA.
 AC Q919J5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interferon inducible Mx protein.
 OS Hippoglossus hippoglossus (Atlantic halibut).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;

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OC Pleuronectoidae; Pleuronectidae; Hippoglossus.
OX NCBI_TaxID=8267;
RN [1]
RX MEDLINE=20415962; PubMed=10954913; DOI=10.1089/10799900050116408;
RA Jensen V., Robertsen B.;
RT "Cloning of an Mx cDNA from Atlantic halibut (Hippoglossus
RT hippoglossus) and characterization of Mx mRNA expression in response
RT to double-stranded RNA or infectious pancreatic necrosis virus.";
RL J. Interferon Cytokine Res. 20:701-710(2000).
CC -!- SIMILARITY: Belongs to the dynamin family.
DR EMBL; AF245513; AAF66055.1; -.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR InterPro; IPR001401; Dynamamin.
DR InterPro; IPR003375; Dynamamin_central.
DR Pfam; PF01031; Dynamamin_M; 1.
DR Pfam; PF00350; Dynamamin_N; 1.
DR Pfam; PF02212; GED; 1.
DR PRINTS; PR00195; DYNAMIN.
DR SMART; SM00053; DYNC; 1.
DR SMART; SM00302; GED; 1.
DR GTP-binding.
KW GTP-binding.
SQ SEQUENCE 622 AA; 71205 MW; 8368B668B3DDA9BC CRC64;

Query Match 84.1%; Score 37; DB 2; Length 622;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
Db 535 TLQELILHL 543

RESULT 13
Q6GUK8 PRELIMINARY; PRT; 626 AA.
AC Q6GUK8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mx type 2.
OS Scophthalmus maximus (Turbot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Scophthalmidae; Scophthalmus.
OX NCBI_TaxID=52904;
RN [1]
RP SEQUENCE FROM N.A.
RA Abollo E., Ordas C., Dios S., Figueras A., Novoa B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the dynamin family.
DR EMBL; AY635932; AAT57877.1; -.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR InterPro; IPR001401; Dynamamin.
DR InterPro; IPR003375; Dynamamin_central.
DR InterPro; IPR003130; GED.
DR Pfam; PF01031; Dynamamin_M; 1.
DR Pfam; PF00350; Dynamamin_N; 1.
DR Pfam; PF02212; GED; 1.
DR PRINTS; PR00195; DYNAMIN.
DR SMART; SM00053; DYNC; 1.
DR SMART; SM00302; GED; 1.
DR PROSITE; PS00410; DYNAMIN; 1.
KW GTP-binding.
SQ SEQUENCE 626 AA; 71380 MW; E302204E4B40EA77 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 626;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
Db 539 TLQELILHL 547

RESULT 14
Q6GUK9 PRELIMINARY; PRT; 626 AA.
AC Q6GUK9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mx type 1.
OS Scophthalmus maximus (Turbot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Scophthalmidae; Scophthalmus.
OX NCBI_TaxID=52904;
RN [1]
RP SEQUENCE FROM N.A.
RA Abollo E., Ordas C., Dios S., Figueras A., Novoa B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the dynamin family.
DR EMBL; AY635932; AAT57877.1; -.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR InterPro; IPR001401; Dynamamin.
DR InterPro; IPR003375; Dynamamin_central.
DR InterPro; IPR003130; GED.
DR Pfam; PF01031; Dynamamin_M; 1.
DR Pfam; PF00350; Dynamamin_N; 1.
DR Pfam; PF02212; GED; 1.
DR PRINTS; PR00195; DYNAMIN.
DR SMART; SM00053; DYNC; 1.
DR SMART; SM00302; GED; 1.
DR PROSITE; PS00410; DYNAMIN; 1.
KW GTP-binding.
SQ SEQUENCE 626 AA; 71380 MW; E302204E4B40EA77 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 626;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
Db 539 TLQELILHL 547

RESULT 15
Q9HTL3 PRELIMINARY; PRT; 691 AA.
AC Q9HTL3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ATP-dependent DNA helicase RecG.
GN Name=recG; OrderedLocustNames=PA5345;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

```

RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen";
RL Nature 406:959-964(2000).
DR EMBL; AE004946; AAG08730.1; -.
DR PIR; G82979; G82979.
DR HSRF; Q9WY48; 1GM5.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004003; F:ATP-dependent DNA helicase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0006310; F:DNA recombination; IEA.
DR GO; GO:0006281; F:DNA repair; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH N.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR004609; RecG.
DR InterPro; IPR004365; tRNA_anti.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF01336; tRNA_anti; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
DR TIGRFAMs; TIGR00643; recG; 1.
KW ATP-binding; Complete proteome; Helicase; Hydrolase.
SQ SEQUENCE 691 AA; 76178 MW; 1507D429D5D56F00 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 691;
Best Local Similarity 77.8%; Pred. NO. 82;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLQDIVLHL 9
Db |||||:
30 TLQDILFHL 38

Search completed: June 28, 2005, 21:24:02
Job time : 57.1 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 Seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-1

Perfect score: 48

Sequence: 1 AMFQDPQER 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	158	1 W6LWS	protein E6 - human
2	40	83.3	382	2 JC2091	carboxylesterase (
3	40	83.3	389	2 A4832	esterase esta - Ps
4	38	79.2	149	1 W6LJ35	E6 protein - human
5	37	77.1	150	2 S36544	E6 protein - human
6	36	75.0	191	2 T16545	hypothetical prote
7	36	75.0	555	2 D95377	probable cerebrosi
8	35	72.9	405	2 A88492	protein T07E3.5 [i
9	35	72.9	1025	2 E86355	hypothetical prote
10	34	70.8	401	1 I40208	cyclochrome P450 BJ
11	33	68.8	91	2 C64545	hypothetical prote
12	33	68.8	248	2 AD0395	probable amino aci
13	33	68.8	340	2 H83007	hypothetical prote
14	33	68.8	525	2 T15185	hypothetical prote
15	33	68.8	568	2 C72129	probable outer mem
16	33	68.8	568	2 G86493	probable leader pe
17	33	68.8	663	2 C70838	probable zinc meta
18	33	68.8	859	1 S65938	nitrate reductase
19	33	68.8	2207	2 T24629	glutamate synthase
20	32	66.7	115	2 C64578	conserved hypothet
21	32	66.7	158	1 W6WLP	E6 protein - human
22	32	66.7	160	2 E71560	hypothetical prote
23	32	66.7	195	2 H86141	protein T25K16.15
24	32	66.7	212	2 S28087	gene C protein - y
25	32	66.7	245	2 D70881	hypothetical prote
26	32	66.7	429	2 G97528	citrate synthase [
27	32	66.7	429	2 A42747	citrate synthase [
28	32	66.7	464	2 G84986	cysteine-tRNA liga
29	32	66.7	474	2 F75133	hypothetical prote

ALIGNMENTS

RESULT 1

W6LWS

protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

R:Kennedy, I.M.; Haddock, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10427

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C:Genetics:

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 48; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.022; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9

Db 7 AMFQDPQER 15

RESULT 2

JC2091

carboxylesterase (EC 3.1.1.1) - Pseudomonas fluorescens

N:Alternate names: esterase; esterase III

C:Species: Pseudomonas fluorescens

C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004

C:Accession: JC2091; PC2023

R:Kim, Y.S.; Lee, H.B.; Choi, K.D.; Park, S.; Yoo, O.J.

Biosci. Biotechnol. Biochem. 58, 111-116, 1994

A:Title: Cloning of Pseudomonas fluorescens carboxylesterase gene and characterization of

A:Reference number: JC2091; MUID:94162732; PMID:7764506

A:Accession: JC2091

A:Molecule type: DNA

A;Residues: 1-382 <KIM>
A;Cross-references: UNIPROT:Q53403
A;Accession: PC2023
A;Molecule type: protein
A;Note: the authors translated the codon CGA, TCG, CCG, GTG, TGG, GTT, and TGG 339, 340, 341 and 342 as Gly, Ala, Gly, Gly and Ser
C;Comment: This enzyme catalyzes the hydrolysis of ester bonds.
C;Genetics:
A;Gene: estC
C;Keywords: carboxylic ester hydrolase

Query Match 83.3%; Score 40; DB 2; Length 382;
Best Local Similarity 77.8%; Pred. No. 2.4; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1;

Qy 1 AMFQDPQER 9
Db 20 ALFDDPQER 28

RESULT 3
A44832
esterase estA - Pseudomonas sp.
C;Species: Pseudomonas sp.
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44832
R;McKay, D.B.; Jennings, M.P.; Godfrey, E.A.; MacRae, I.C.; Rogers, P.J.; Beacham, I.R.
J. Gen. Microbiol. 136, 701-708, 1992
A;Title: Molecular analysis of an esterase-encoding gene from a lipolytic psychrotrophic
A;Reference number: A44832; PMID:92268850; PMID:1339464
A;Accession: A44832
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <MCK>
A;Cross-references: UNIPROT:Q52467; GB:M68491; NID:g151213; PIDN:AAA25813.1; PID:g151214
A;Experimental source: LS10782
A;Note: sequence extracted from NCBI backbone (NCBIN:103686, NCBIP:103687)

Query Match 83.3%; Score 40; DB 2; Length 389;
Best Local Similarity 77.8%; Pred. No. 2.5; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1;

Qy 1 AMFQDPQER 9
Db 28 ALFDDPQER 36

RESULT 4
W6WL35
E6 protein - human papillomavirus type 35
C;Species: human papillomavirus type 35
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: E40824; S36521
R;Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A;Title: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35
A;Reference number: A40824; PMID:92124753; PMID:1310198
A;Accession: E40824
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-149 <MAR>
A;Cross-references: UNIPROT:P27228; GB:M74117; NID:g333050; PIDN:AAA46966.1; PID:g333051
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36521
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149
A;Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52561.1; PIDT:g396998

A;Experimental source: strain 35H
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 79.2%; Score 38; DB 1; Length 149;
Best Local Similarity 87.5%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy 2 MFQDPQER 9
Db 1 MFQDPAER 8

RESULT 5
S36544
E6 protein - human papillomavirus type 26
C;Species: human papillomavirus type 26
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36544
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36544
A;Molecule type: DNA
A;Residues: 1-150
A;Cross-references: UNIPROT:P36807; EMBL:X74472; NID:g396956; PIDN:CAA52530.1; PIDT:g39696;
C;Superfamily: papillomavirus E6 protein
C;Keywords: early protein; zinc finger

Query Match 77.1%; Score 37; DB 2; Length 150;
Best Local Similarity 75.0%; Pred. No. 3.5; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 2;

Qy 2 MFQDPQER 9
Db 1 MFEDPRER 8

RESULT 6
T16545
hypothetical protein K03C7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16545
R;Leimbach, D.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid K03C7.
A;Reference number: Z18532
A;Accession: T16545
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-191 <LEI>
A;Cross-references: UNIPROT:Q21188; EMBL:U40059; NID:gi055170; PIDT:gi055173; PIDN:AAA8114
C;Genetics:
A;Gene: CESP:K03C7.3
A;Introns: 80/2; 156/1

Query Match 75.0%; Score 36; DB 2; Length 191;
Best Local Similarity 66.7%; Pred. No. 7.4; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 2;

Qy 1 AMFQDPQER 9
Db 163 ALFQDPDEQ 171

RESULT 7
D95377
probable cerebroside-sulfatase (EC 3.1.6.8) [imported] - Sinorhizobium meliloti (strain 1
C;Species: Sinorhizobium meliloti

A;Residues: I-I025 <StO>
A:Cross-references: UNIPROT:O8LEJ5; UNIPROT:P61430; GB:AE005172; NID:q93922687; PIDN:AAF87;

Query Match	72.9%	Score 35;	DB 2;	Length 1025;
Best Local Similarity	75.0%	Pred. No. 75;		
Matches	6;	Conservative	1;	Mismatches
			1;	Indels
			0;	Gaps

RESULT 10
I40208
Cytochrome P450 BU-1 CYP112 - Bradyrhizobium japonicum
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: Bradyrhizobium japonicum
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004

K;ully, R.E.; Keister, D.L.
Appl. Environ. Microbiol. 59, 4136-4142, 1993
A;Title: Cloning and mutagenesis of a cytochrome P-450 locus from *Bradyrhizobium japonicum*
A;Reference number: I40207
A;Accession: I40208
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-401 <RES>
A;Cross-references: UNIPROT:Q59203; EMBL:U12678; NID:g529961; PIDN:AAC28889.1; PID:g529961
C;Genetics:
A;Gene: CYP112
C;Superfamily: *Bacillus* cytochrome P450 CYP106; cytochrome P450 homology
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;234-372/Domain: cytochrome P450 homology <CYP>
F;350/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 70.8%; Score 34; DB 1; Length 401;
Best Local Similarity 66.7%;
Pred. NO. 42;
Matches 6; Conservative 2; Mismatches 1; Indels 0;
Gaps 0;

```

DO      252 AMFHPQQR 260

RESULT 11
C64545
hypothetical protein HP0203 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: C64545

```

Kotomo, J.F.; White, O.; Keriavage, A.K.; Clayton, R.A.; Sutton, G.G.; Frieschmann, K.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodak, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. N A:Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*. A:Reference number: A64520. MUID: 97394467. PMID: 9252185

```
A;Accession: C64545
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-91 <ROM>
A;Cross-references: UNIPROT:O24995; GB:AE000540; GB:AE000511; NID:g2313287; PIDN:AAD0727

Query Match      68.8%; Score 33; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 13; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy      4 QDPQER 9
      |||||
Db      52 QDPQER 57

RESULT 12
AD0395
A;Title: probable amino acid ABC transporter, ATP-binding protein YPO3254 [imported] - Versinia p
C;Species: Versinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD0395
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Versinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AD0395
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-248 <KUR>
A;Cross-references: UNIPROT:Q82BY0; GB:ALJ590842; PIDN:CAC92488.1; PID:g15981188; GSPDB:C
C;Genetics:
A;Gene: YPO3254
C;Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology

Query Match      68.8%; Score 33; DB 2; Length 248;
Best Local Similarity 66.7%; Pred. No. 40; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AMFQDPQER 9
      |::|||
Db      224 ALFADPQTR 232

RESULT 13
H83007
A;Title: hypothetical protein PA5103 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H83007
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bi
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: AB2950; MUID:20437337; PMID:10984043
A;Accession: H83007
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-340 <STO>
A;Cross-references: UNIPROT:Q9HU80; GB:AE004923; GB:AE004091; NID:g9951395; PIDN:AAG0848
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA5103

Query Match      68.8%; Score 33; DB 2; Length 340;
Best Local Similarity 62.5%; Pred. No. 56; Indels 0; Gaps 0;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AMFQDPQE 8
      |::|||
Db      151 ALFRDPPE 158
```

RESULT 14

```
T15185
A;Title: hypothetical protein C18E3.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15185
R;Connell, M.; Maggi, L.
submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid C18E3.
A;Reference number: Z18304
A;Accession: T15185
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-525 <CON>
A;Cross-references: UNIPROT:O02101; EMBL:AF000265; NID:g1947147; PID:g1947150; PIDN:AAB5;
A;Experimental source: strain Bristol N2; clone C18E3
C;Genetics:
A;Gene: CESP:C18E3.2
A;Map position: 1
A;Introns: 12/1; 70/3; 93/3; 141/3; 503/2

Query Match      68.8%; Score 33; DB 2; Length 525;
Best Local Similarity 100.0%; Pred. No. 91; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 QDPQER 9
      |||||
Db      338 QDPQER 343

RESULT 15
C72129
A;Title: probable outer membrane leader peptide (omp) CPn0021 - Chlamydophila pneumoniae (strains
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: C72129; B81542
R;Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: C72129
A;Molecule type: DNA
A;Residues: 1-568 <ARN>
A;Cross-references: UNIPROT:Q929G0; GB:AE001587; GB:AE001363; NID:g4376271; PIDN:AAD1817;
A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I.
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: AB1500; MUID:20150255; PMID:10684935
A;Accession: B81542
A;Molecule type: DNA
A;Residues: 1-568 <REA>
A;Cross-references: GB:AE002234; GB:AE002161; NID:g7189667; PIDN:AAF38558.1; PID:g718967;
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CPn0021; CP0755

Query Match      68.8%; Score 33; DB 2; Length 568;
Best Local Similarity 100.0%; Pred. No. 99; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 QDPQER 9
      |||||
Db      384 QDPQER 389

Search completed: June 28, 2005, 19:23:11
Job time : 14.2 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-1
Perfect score: 48
Sequence: 1 AMFQDPQER 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	158	1 V56 HPV16	P03126 human papil
2	48	100.0	158	2 Q8JMU8	Q8JMU8 human papil
3	48	100.0	158	2 Q8QHN0	Q8QHN0 human papil
4	48	100.0	153	2 Q8QHP5	Q8QHP5 human papil
5	48	100.0	153	2 Q8QHT0	Q8QHT0 human papil
6	48	100.0	153	2 Q8QRD5	Q8QRD5 human papil
7	48	100.0	158	2 Q8QRD6	Q8QRD6 human papil
8	48	100.0	158	2 Q8QRD7	Q8QRD7 human papil
9	48	100.0	158	2 Q8QRD8	Q8QRD8 human papil
10	48	100.0	158	2 Q8QRD9	Q8QRD9 human papil
11	48	100.0	158	2 Q8QRE0	Q8QRE0 human papil
12	48	100.0	158	2 Q8QRE1	Q8QRE1 human papil
13	48	100.0	158	2 Q71B17	Q71B17 human papil
14	48	100.0	158	2 Q9QDH3	Q9QDH3 human papil
15	48	100.0	158	2 Q9QDH5	Q9QDH5 human papil
16	48	100.0	158	2 Q9QDH7	Q9QDH7 human papil
17	48	100.0	158	2 Q9QDH9	Q9QDH9 human papil
18	48	100.0	158	2 Q9WH13	Q9WH13 human papil
19	48	100.0	161	2 Q919A9	Q919A9 human papil
20	48	100.0	161	2 Q919B1	Q919B1 human papil
21	48	100.0	161	2 Q919C6	Q919C6 human papil
22	48	100.0	161	2 Q919D4	Q919D4 human papil
23	44	91.7	151	2 O12335	O12335 human papil
24	44	91.7	151	2 O12336	O12336 human papil
25	44	91.7	151	2 Q76TS0	Q76TS0 human papil
26	44	91.7	151	2 Q778I6	Q778I6 human papil
27	44	91.7	151	2 Q778L6	Q778L6 human papil
28	44	91.7	151	2 Q77JC7	Q77JC7 human papil
29	44	91.7	151	2 Q77ZJ5	Q77ZJ5 human papil
30	44	91.7	151	2 Q80963	Q80963 human papil
31	44	91.7	151	2 Q80966	Q80966 human papil

32	44	91.7	151	2	Q89640	human papil
33	44	91.7	151	2	Q89648	human papil
34	44	91.7	151	2	Q89708	human papil
35	44	91.7	151	2	Q89755	human papil
36	44	91.7	151	2	Q89852	human papil
37	44	91.7	151	2	Q89887	human papil
38	44	91.7	151	2	Q8B564	human papil
39	44	91.7	151	2	Q8BB19	human papil
40	44	91.7	151	2	Q8BB20	human papil
41	44	91.7	151	2	Q8BB21	human papil
42	44	91.7	151	2	Q9W8C3	human papil
43	44	91.7	151	2	Q9W931	human papil
44	44	91.7	151	2	Q9WMP2	human papil
45	44	91.7	151	2	Q9WMP3	human papil

ALIGNMENTS

RESULT 1
VE6 HPV16 STANDARD; PRT; 158 AA.
AC P03126;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85246220; PubMed=2990099;
RA Schneider-Maunoury S., Pehau-Arnauudet G., Breitburd F., Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-v cells,
J. Gen. Virol. 71:809-817(1990)."
RN [3]
RP INTERACTION WITH FBLN1, AND INHIBITION OF E6-MEDIATED TRANSFORMATION.
RX MEDLINE=22188366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;
RA Du M., Fan X., Hong E., Chen J.J.;
RT "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";
Biochem. Biophys. Res. Commun. 296:962-969(2002).
CC -!- FUNCTION: This protein has transforming activity in vitro.
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double
CC stranded DNA (in vitro).
CC -!- SUBUNIT: Interacts with FBLN1.
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -!- MISCELLANEOUS: HPV16, in comparison to HPV types 6 and 11, is more
CC often associated with malignant genital cancers in humans.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; K02718; AAA46939.1; --
CC EMBL; D00735; BAA00632.1; --
CC PIR; A03682; W6WHS.
CC InterPro; IPR001334; E6.
CC Pfam; PF00519; E6; 1.
CC DNA-binding; Early protein; Nuclear protein; Oncogene; Zinc-finger.

```
FT ZN_FING 37 73 Potential.
FT ZN_FING 110 146 Potential.
SQ SEQUENCE 158 AA; 19187 MW; 01FEF5ADCDFDB37EB CRC64;

Query Match 100.0%; Score 48; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 7 AMFQDPQER 15

RESULT 2
ID Q8JMU8 PRELIMINARY; PRT; 158 AA.
AC Q8JMU8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]

SEQUENCE FROM N.A.
RP Terai M., Fu L., Ma Z., Burk R.D.;
RA Cruz M.R., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
RA Martins C.R.F.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]

RP SEQUENCE FROM N.A.
RA Terai M., Fu L., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY098922; AAM29170.1; -.
DR EMBL; AF536180; AAQ10720.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19145 MW; CB70F51C00F867DC CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 7 AMFQDPQER 15

RESULT 3
ID Q8QHN0 PRELIMINARY; PRT; 158 AA.
AC Q8QHN0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]

SEQUENCE FROM N.A.
RP Terai M., Ma Z., Burk R.D.;
RA Cruz M.R., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
RA Martins C.R.F.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]

RP SEQUENCE FROM N.A.
RA Terai M., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY098922; AAM29170.1; -.
DR EMBL; AF536180; AAQ10720.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19145 MW; CB70F51C00F867DC CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 7 AMFQDPQER 15

RESULT 4
ID Q8QHP5 PRELIMINARY; PRT; 158 AA.
AC Q8QHP5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]

SEQUENCE FROM N.A.
RP STRAIN=E-G276T, and E-G276G442T;
RC MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486315; AAL96620.1; -.
DR EMBL; AF486323; AAL96628.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19160 MW; AFF015533FC7FAP7 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 7 AMFQDPQER 15

RESULT 5
ID Q8QHT0 PRELIMINARY; PRT; 158 AA.
AC Q8QHT0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transforming protein E6.
RN [2]
```

```
RP SEQUENCE FROM N.A.
RA Terai M., Ma Z., Burk R.D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]

SEQUENCE FROM N.A.
RA Cruz M.R., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
RA Martins C.R.F.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF486314; AAL96619.1; -.
DR EMBL; AF472509; AAL15705.1; -.
DR EMBL; AF486324; AAL96629.1; -.
DR EMBL; AY098918; AAM29166.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19157 MW; FI40F509DAC794F6 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 7 AMFQDPQER 15

RESULT 4
ID Q8QHP5 PRELIMINARY; PRT; 158 AA.
AC Q8QHP5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]

SEQUENCE FROM N.A.
RP STRAIN=E-G276T, and E-G276G442T;
RC MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486315; AAL96620.1; -.
DR EMBL; AF486323; AAL96628.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19160 MW; AFF015533FC7FAP7 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 7 AMFQDPQER 15

RESULT 5
ID Q8QHT0 PRELIMINARY; PRT; 158 AA.
AC Q8QHT0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transforming protein E6.
RN [2]
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OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ag-P, As-C193, and As-A178;
 RX MEDLINE=22182962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RA "Human papillomavirus type 16 intratypic variant infection and risk
 RT for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Terai M., Fu L., Ma Z., Burk R.D.;
 RA Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF486229; AAL96604.1; -
 DR EMBL; AF486300; AAL96605.1; -
 DR EMBL; AF486301; AAL96606.1; -
 DR EMBL; AF486302; AAL96607.1; -
 DR EMBL; AF486306; AAL96611.1; -
 DR EMBL; AF486308; AAL96613.1; -
 DR EMBL; AF534061; AAL10403.1; -
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 DR PIR; P00018; E6; 1.
 SQ SEQUENCE 158 AA; 19201 MW; 004EF5ADCE6B375B CRC64;
 Query Match 100.0%; Score 48; DB 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.092;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AMFQDPQER 9
 Db |||||
 7 AMFQDPQER 15
 RESULT 6
 ID Q8QRD5 PRELIMINARY; PRT; 158 AA.
 AC Q8QRD5;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Transforming protein E6.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NAL;
 RX MEDLINE=22182962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RA "Human papillomavirus type 16 intratypic variant infection and risk
 RT for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Terai M., Burk R.D.;
 RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RP SEQUENCE FROM N.A.
 RA Cruz M.R., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
 RA Martins C.R.F.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Cruz Mr., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
 RA Martins C.R.F.;

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Cruz M.R., Martins C.R.F.;
 RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF486325; AAL96630.1; -
 DR EMBL; AF486278; AAO85408.1; -
 DR EMBL; AY098923; AAM29171.1; -
 DR EMBL; AY112662; AAM51853.1; -
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 158 AA; 19208 MW; B8E47F57F22EC2E1 CRC64;
 Query Match 100.0%; Score 48; DB 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.092;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AMFQDPQER 9
 Db |||||
 7 AMFQDPQER 15
 RESULT 7
 ID Q8QRD6 PRELIMINARY; PRT; 158 AA.
 AC Q8QRD6;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-T360T;
 RX MEDLINE=22182962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RA "Human papillomavirus type 16 intratypic variant infection and risk
 RT for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700(2002).
 DR EMBL; AF486319; AAL96624.1; -
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 158 AA; 19246 MW; 01FEF70F45F137EB CRC64;
 Query Match 100.0%; Score 48; DB 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.092;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AMFQDPQER 9
 Db |||||
 7 AMFQDPQER 15
 RESULT 8
 ID Q8QRD7 PRELIMINARY; PRT; 158 AA.
 AC Q8QRD7;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E-C442T;
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486318; AAL96623.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19173 MW; 14EBF5ADCDFB3640 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
| | | | |
Db 7 AMFQDPQER 15

RESULT 9

Q8QRD8 ID Q8QRD8 PRELIMINARY; PRT; 158 AA.
AC Q8QRD8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E-G449T;
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486316; AAL96621.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19188 MW; 01FEF5B1D21AF7EB CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
| | | | |
Db 7 AMFQDPQER 15

RESULT 10

Q8QRD9 ID Q8QRD9 PRELIMINARY; PRT; 158 AA.
AC Q8QRD9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.

OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AS-A267;
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486309; AAL96614.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19173 MW; 161AD3EFAA4D636B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
| | | | |
Db 7 AMFQDPQER 15

RESULT 11

Q8QRE0 ID Q8QRE0 PRELIMINARY; PRT; 158 AA.
AC Q8QRE0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AS-G137;
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486307; AAL96612.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19187 MW; 005E2FC1E617C55B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
| | | | |
Db 7 AMFQDPQER 15

RESULT 12

Q8QRE1 ID Q8QRE1 PRELIMINARY; PRT; 158 AA.
AC Q8QRE1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

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OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AS-CL31;
RX MEDLINE=2182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF496303; AAL96608.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19146 MW; CB6EFA91548727C CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 7 AMFQDPQER 15

RESULT 13
Q71B17 PRELIMINARY; PRT; 158 AA.
AC Q71B17;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Putative transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Terai M., Fu L., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF536179; AAQ10712.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19074 MW; 9BECF5B6DB95D75E CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 7 AMFQDPQER 15

RESULT 14
Q9QDH3 PRELIMINARY; PRT; 158 AA.
AC Q9QDH3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
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RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187869; AAF13398.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19210 MW; 004BF5ADD6FABESB CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 7 AMFQDPQER 15

RESULT 15
Q9QDH5 PRELIMINARY; PRT; 158 AA.
AC Q9QDH5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187868; AAF13396.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19195 MW; 00564E1A8994CB0B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 7 AMFQDPQER 15
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Search completed: June 28, 2005, 19:19:19
Job time : 57.3 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 Seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-10
Perfect score: 48
Sequence: 1 FAFRDLICV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	48	100.0	158	1 W6WLS	protein E6 - human
2	45	93.8	158	2 S36561	E6 protein - human
3	42	87.5	148	2 S36515	E6 protein - human
4	37	77.1	471	1 KHRZOB	oryzain (EC 3.4.22
5	36	75.0	109	2 AH0544	hypothetical prote
6	36	75.0	522	2 H82486	probable response
7	36	75.0	934	2 T01796	hypothetical prote
8	35	72.9	155	1 W6WL43	E6 protein - human
9	35	72.9	274	2 E95500	protein T27A10.2 [
10	35	72.9	402	2 B95354	hypothetical prote
11	34	70.8	250	2 S56156	Rieske iron-sulfur
12	34	70.8	264	2 PD0019	mistletoe lectin I
13	34	70.8	265	2 JW0090	lectin-I B chain -
14	34	70.8	363	2 G83079	hypothetical prote
15	34	70.8	1651	2 T25038	hypothetical prote
16	33	68.8	149	1 W6WL35	E6 protein - human
17	33	68.8	158	1 W6WL18	E6 protein - human
18	33	68.8	164	2 S27650	2,3,4,5-tetrahydro
19	33	68.8	219	2 S47177	lactoylglutathione
20	33	68.8	295	2 T00725	hypothetical prote
21	33	68.8	313	2 D86219	protein F22O13.19
22	33	68.8	415	2 D95248	conserved hypothe
23	33	68.8	415	2 A98113	conserved hypothe
24	33	68.8	614	2 A88466	protein B0244.2 [i
25	33	68.8	915	2 T19692	hypothetical prote
26	32	66.7	149	1 W6WL31	E6 protein - human
27	32	66.7	154	2 S36555	E6 protein - human
28	32	66.7	154	2 S36584	E6 protein - human
29	32	66.7	157	2 S55956	probable membrane

ALIGNMENTS

RESULT 1

W6WLS

Protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virol. 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

R:Kennedy, I.M.; Haddock, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human papillomavirus type 16 genome acts at the level

A:Reference number: 217014; MUID:91162763; PMID:1848319

A:Accession: T10427

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C:Genetics:

A:Gene: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 48; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.027;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFRDLICV 9

Db 52 FAFRDLICV 60

RESULT 2

S36561

E6 protein - human papillomavirus type 45

C:Species: human papillomavirus type 45

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S36561

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36561

A:Molecule type: DNA

A:Residues: 1-158

A;Cross-references: UNIPROT:P21735; EMBL:X74479; NID:g397022; PIDN:CAA52573.1; PID:g3970
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 93.8%; Score 45; DB 2; Length 158;
Best Local Similarity 88.9%; Pred. No. 0.11;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAFRDLCLIV 9
|:|:|:|:|:
DB 47 FAFKDLCLIV 55

RESULT 3

E6 protein - human papillomavirus type 34
C;Species: human papillomavirus type 34
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36515
R;Delius H.; Hofmann B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36515
A;Molecule type: DNA
A;Residues: 1-148
A;Cross-references: UNIPROT:P36911; EMBL:X74476; NID:g396989; PIDN:CAA52555.1; PID:g3969
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 87.5%; Score 42; DB 2; Length 148;
Best Local Similarity 77.8%; Pred. No. 0.41;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAFRDLCLIV 9
|:|:|:|:|:
DB 46 FIFRDLCLIV 54

RESULT 4

KRZOB
oryzain (EC 3.4.22.-) beta precursor - rice
C;Species: Oryza sativa (rice)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: JU0389; B40053
R;Watanabe, H.; Abe, K.; Emori, Y.; Hosoyama, H.; Arai, S.
submitted to JIPID, May 1991
A;Reference number: JU0389
A;Accession: JU0389
A;Molecule type: mRNA
A;Residues: 1-471 <WAT1>
A;Cross-references: UNIPROT:P25777
R;Watanabe, H.; Abe, K.; Emori, Y.; Hosoyama, H.; Arai, S.
J. Biol. Chem. 266, 16897-16902, 1991
A;Title: Molecular cloning and gibberellin-induced expression of multiple cysteine prote
A;Reference number: A40053; MUID:91358494; PMID:1885617
A;Accession: B40053
A;Molecule type: mRNA
A;Residues: 1-471 <WAT2>
A;Cross-references: GB:D90407; NID:g218182; PIDN:BAA14403.1; PID:g218183
C;Superfamily: papain
C;Keywords: cysteine proteinase; glycoprotein; hydrolase; seed
F;1-21/Domain: signal sequence #status predicted <SIG>
F;122-139/Domain: amino-terminal propeptide #status predicted <PRO>
F;140-360/Product: oryzain beta #status predicted <MAT>
F;361-471/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;161-204, 195-237, 295-346/Disulfide bonds: #status predicted
F;164, 301, 321/Active site: Cys, His, Asn #status predicted
F;340, 388/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 77.1%; Score 37; DB 1; Length 471;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFRDLCLIV 9
|:|:|:|:|:
DB 401 FGFRNLCLIV 409

RESULT 5

AH0544
hypothetical protein STY0375 [imported] - Salmonella enterica subsp. enterica serovar Ty
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AH0544
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
Th, T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0544
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08800.1; PID:g16501616; GSPDB:GN00176
C;Genetics;
A;Gene: STY0375

Query Match 75.0%; Score 36; DB 2; Length 109;
Best Local Similarity 75.0%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFRDLCLIV 8
|:|:|:|:|:
DB 28 FFRDLCLIV 35

RESULT 6

H82486
probable response regulator VCA0210 [imported] - Vibrio cholerae (strain N16961 serogrou
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: H82486
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chadson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: H82486
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-522 <HEI>
A;Cross-references: UNIPROT:Q9KMV8; GB:AE004361; GB:AE003853; NID:g9657600; PIDN:AAF9612;
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics;
A;Gene: VCA0210
A;Map position: 2

Query Match 75.0%; Score 36; DB 2; Length 522;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 AFRLCLIV 9
|:|:|:|:|:
DB 163 AYRDLCLIV 170

RESULT 7

T01796
hypothetical protein A_TM021B04.10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004

```
C:Accession: T01796
R:Dante, M.; Wansley, P.; Gibson, A.
submitted to the EMBL Data Library, June 1997
A:Description: The sequence of A. thaliana TW021B04.
A:Reference number: Z14440
A:Accession: T01796
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-934 <DAN>
A:Cross-references: UNIPROT:O04647; EMBL:AF007271; NID:g2191181; PID:g2191192; GSPDB:GN000
C:Genetics:
A:Gene: ATSP:A.TM021B04.10
A:Map position: 5
A:Introns: 167/1; 640/1; 744/1; 775/3

Query Match      75.0%; Score 36; DB 2; Length 934;
Best Local Similarity 62.5%; Pred. No. 39;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy  2  AFRDLCLIV 9
Db  154  SFRDNCVV 161

RESULT 8
W6WL43
E6 protein - human papillomavirus type 43
C:Species: human papillomavirus type 43
A:Note: host Homo sapiens (man)
C:Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C:Accession: A34144
R:Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; Schmidt, B.J.; Temple, G.F.
J. Virol. 63, 2829-2834, 1989
A:Title: Cloning and partial DNA sequencing of two new human papillomavirus types associated with cervical intraepithelial neoplasia
A:Reference number: A34144; MUID:89259065; PMID:2542593
A:Accession: A34144
A:Molecule type: DNA
A:Residues: 1-155 <LOS>
A:Cross-references: UNIPROT:P19709; GB:M27022; NID:g341596; PIDN:AAA63453.1; PID:g703247
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:31-67/Region: zinc finger CCCC motif
F:104-140/Region: zinc finger CCCC motif

Query Match      72.9%; Score 35; DB 1; Length 155;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy  1  FAFRDLCLIV 9
Db  46  FAFRDLRVV 54

RESULT 9
E89500
protein T27A10.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: E89500
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2104, 1999
A:Accession: E89500
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-274 <STO>
A:Cross-references: UNIPROT:Q22821; GB:chr.X; PIDN:AAB52501.1; PID:g1326287; GSPDB:GN000
A:Note: coded for by C. elegans cDNA CEESD86F
C:Genetics:
A:Gene: T27A10.2
```

```
A:Map position: X

Query Match      72.9%; Score 35; DB 2; Length 274;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  FAFRDLCL 7
Db  224  FKFRDLCL 230

RESULT 10
B95354
hypothetical protein Sma1351 [imported] - Sinorhizobium meliloti (strain 1021) magaplasma
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: B95354
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowsby, J.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: B95354
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-402 <KUR>
A:Cross-references: UNIPROT:Q92YX4; GB:AB006469; PIDN:AAK65396.1; PID:g14523859; GSPDB:G14523859
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, F.; Pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, H.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Sma1351
A:Genome: plasmid

Query Match      72.9%; Score 35; DB 2; Length 402;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy  1  FAFRDLCLIV 9
Db  285  FAFRDLAVL 293

RESULT 11
S56156
Rieske iron-sulfur protein soxF - Sulfolobus acidocaldarius
N:Alternate names: Rieske iron-sulfur protein II
C:Species: Sulfolobus acidocaldarius
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S56156; S56173
R:Castresana, J.; Luebben, M.; Saraste, M.
J. Mol. Biol. 250, 202-210, 1995
A:Title: New archaeobacterial genes coding for redox proteins: implications for the evolution of the iron-sulfur cluster
A:Reference number: S56155; MUID:9533177; PMID:7608970
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-250 <CAS>
A:Cross-references: UNIPROT:Q53766; EMBL:Z48338; NID:g927521; PID:g927524
A:Accession: S56173
A:Molecule type: protein
A:Residues: 1-24 <CA2>
C:Keywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein
F:130-190/Domain: Rieske [2Fe-2S] homology #status atypical <RSK>
F:140,142,170,173/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status p
```

Query Match 70.8%; Score 34; DB 2; Length 250;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFRDLCI 8
: |||||
Db 134 FAFSDVCV 141

RESULT 12

PD0019
Mistletoe lectin I B chain - Viscum album (fragment)
C:Species: Viscum album
C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
R:Accession: PD0019
R:Eschenburg, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelter, W.
Biochem. Biophys. Res. Commun. 247, 367-372, 1998
A:Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum album
A:Reference number: PD0018; MUID:98308123; PMID:9642133
A:Accession: PD0019
A:Molecule type: protein
A:Residues: 1-264 <ESC>
A:Cross-references: UNIPROT:P81830
C:Superfamily: ricin; rRNA N-glycosidase homology

Query Match 70.8%; Score 34; DB 2; Length 264;
Best Local Similarity 62.5%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFRDLCI 8
: |||||
Db 146 YGFRDLCM 153

RESULT 13

JW0090
lectin-I B chain - European mistletoe
N:Alternate names: ML-I
C:Species: Viscum album (European mistletoe)
C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000
R:Accession: JW0090
R:Soler, M.H.; Stoeva, S.; Voelter, W.
Biochem. Biophys. Res. Commun. 246, 596-601, 1998
A:Title: Complete amino acid sequence of the B chain of mistletoe lectin I.
A:Reference number: JW0090; MUID:98289575; PMID:9618256
A:Accession: JW0090
A:Molecule type: protein
A:Residues: 1-265 <SOL>
C:Superfamily: ricin; rRNA N-glycosidase homology
C:Keywords: glycoprotein
F:61.96.136/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 70.8%; Score 34; DB 2; Length 265;
Best Local Similarity 62.5%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFRDLCI 8
: |||||
Db 146 YGFRDLCM 153

RESULT 14

G83079
hypothetical protein PA4539 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
R:Accession: G83079
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: G83079
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-363 <STO>
A:Cross-references: UNIPROT:Q9HVN8; GB:AE004867; GB:AE004091; NID:g9950769; PIDN:AAG0792;
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4539
C:Superfamily: Neisseria meningitidis probable nucleotide-binding protein NMA1520

Query Match 70.8%; Score 34; DB 2; Length 363;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFRDLCL 7
: |||||
Db 269 FAFADLCL 275

RESULT 15

T25038
hypothetical protein Y106G6G.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25038; T26426
R:Kershaw, J.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19972
A:Accession: T25038
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1651 <WIL>
A:Cross-references: UNIPROT:O18093; EMBL:Z81594; PIDN:CAB04748.1; GSPDB:GN00019; CESP:Y106G6G.2
A:Experimental source: clone T20F10
R:McMurray, A.
submitted to the EMBL Data Library, November 1998
A:Reference number: Z20213
A:Accession: T26426
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1651 <WIL>
A:Cross-references: EMBL:AL033508; PIDN:CAA22058.1; CESP:Y106G6G.2
C:Genetics:
A:Gene: CESP:Y106G6G.2
A:Map position: 1
A:Introns: 26/1; 70/3; 114/3; 137/3; 237/2; 296/2; 392/3; 427/1; 490/3; 533/1; 655/1; 712/1

Query Match 70.8%; Score 34; DB 2; Length 1651;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 AFRDLCLIV 9
: |||||
Db 1599 AYRDICLI 1606

Search completed: June 28, 2005, 19:23:24
Job time : 12.2 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-10
Perfect score: 48
Sequence: 1 FAFRDLCTIV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	81	2 Q80886	Q80886 human papil
2	48	100.0	84	2 Q80882	Q80882 human papil
3	48	100.0	90	2 Q80883	Q80883 human papil
4	48	100.0	90	2 Q80885	Q80885 human papil
5	48	100.0	91	2 Q80887	Q80887 human papil
6	48	100.0	99	2 Q81982	Q81982 human papil
7	48	100.0	130	2 Q919B4	Q919B4 human papil
8	48	100.0	130	2 Q919B8	Q919B8 human papil
9	48	100.0	130	2 Q919C0	Q919C0 human papil
10	48	100.0	130	2 Q919C2	Q919C2 human papil
11	48	100.0	130	2 Q919C8	Q919C8 human papil
12	48	100.0	130	2 Q919D0	Q919D0 human papil
13	48	100.0	138	2 Q919D2	Q919D2 human papil
14	48	100.0	143	2 Q919B6	Q919B6 human papil
15	48	100.0	151	2 Q12335	Q12335 human papil
16	48	100.0	151	2 Q12336	Q12336 human papil
17	48	100.0	151	2 Q76TS0	Q76TS0 human papil
18	48	100.0	151	2 Q77E16	Q77E16 human papil
19	48	100.0	151	2 Q77E16	Q77E16 human papil
20	48	100.0	151	2 Q77JC7	Q77JC7 human papil
21	48	100.0	151	2 Q77ZJ5	Q77ZJ5 human papil
22	48	100.0	151	2 Q80963	Q80963 human papil
23	48	100.0	151	2 Q80966	Q80966 human papil
24	48	100.0	151	2 Q89640	Q89640 human papil
25	48	100.0	151	2 Q89648	Q89648 human papil
26	48	100.0	151	2 Q89708	Q89708 human papil
27	48	100.0	151	2 Q89755	Q89755 human papil
28	48	100.0	151	2 Q89852	Q89852 human papil
29	48	100.0	151	2 Q89887	Q89887 human papil
30	48	100.0	151	2 Q8B564	Q8B564 human papil
31	48	100.0	151	2 Q8BB19	Q8BB19 human papil

32	48	100.0	151	2 Q8BB20	Q8BB20 human papil
33	48	100.0	151	2 Q8BB21	Q8BB21 human papil
34	48	100.0	151	2 Q8W8C3	Q8W8C3 human papil
35	48	100.0	151	2 Q9WMP2	Q9WMP2 human papil
36	48	100.0	151	2 Q9WMP3	Q9WMP3 human papil
37	48	100.0	151	2 Q9WMP4	Q9WMP4 human papil
38	48	100.0	151	2 Q9WMP5	Q9WMP5 human papil
39	48	100.0	158	1 VE6 HPV16	P03126 human papil
40	48	100.0	158	2 Q8JMU8	Q8JMU8 human papil
41	48	100.0	158	2 Q8QHN0	Q8QHN0 human papil
42	48	100.0	158	2 Q8QHP5	Q8QHP5 human papil
43	48	100.0	158	2 Q8QHT0	Q8QHT0 human papil
44	48	100.0	158	2 Q8QRD5	Q8QRD5 human papil
45	48	100.0	158	2 Q8QRD6	Q8QRD6 human papil

ALIGNMENTS

RESULT 1
Q80886 PRELIMINARY; PRT; 81 AA.
AC Q80886; (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galuira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14515; AAB60569.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00519; E6; 1.
FT NON_TER 1
FT NON_TER 81
/SQ SEQUENCE 81 AA; 9784 MW; DD5FEDBC9F845B97 CRC64;
Query Match 100.0%; Score 48; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.075; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;
Qy 1 FAFRDLCTIV 9
Db 4 FAFRDLCTIV 12
RESULT 2
Q80882 PRELIMINARY; PRT; 84 AA.
AC Q80882; (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical;
RA Haegert D.G., Galuira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14511; AAB60565.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

DR GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 FT NON_TER 84
 SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;
 Query Match 100.0%; Score 48; DB 2; Length 84;
 Best Local Similarity 100.0%; Pred. NO. 0.078; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FAFRDLCLIV 9
 Db 1 FAFRDLCLIV 9

RESULT 3
 Q80883 PRELIMINARY; PRT; 90 AA.
 AC Q80883; (Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HPV16; TISSUE=Cervical tissue;
 RA Haegert D.G., Galutira D.F., Younghusband B.H.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U14512; AAB60566.1; -.
 DR GO:0042025; C:host cell nucleus; IEA.
 DR GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 FT NON_TER 90
 SQ SEQUENCE 90 AA; 10904 MW; 5D3ADF843AD6060B CRC64;
 Query Match 100.0%; Score 48; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 0.084; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FAFRDLCLIV 9
 Db 4 FAFRDLCLIV 12

RESULT 4
 Q80885 PRELIMINARY; PRT; 90 AA.
 AC Q80885; (Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HPV16; TISSUE=Cervical tissue;
 RA Haegert D.G., Galutira D.F., Younghusband B.H.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U14514; AAB60568.2; -.
 DR GO:0042025; C:host cell nucleus; IEA.
 DR GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 FT NON_TER 99

FT NON_TER 1
 FT NON_TER 90
 SQ SEQUENCE 90 AA; 10964 MW; BC2531643ACBA76C CRC64;
 Query Match 100.0%; Score 48; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. NO. 0.084; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FAFRDLCLIV 9
 Db 4 FAFRDLCLIV 12

RESULT 5
 Q80887 PRELIMINARY; PRT; 91 AA.
 AC Q80887; (Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HPV16; TISSUE=Cervical tissue;
 RA Haegert D.G., Galutira D.F., Younghusband B.H.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U14516; AAB60570.1; -.
 DR GO:0042025; C:host cell nucleus; IEA.
 DR GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 FT NON_TER 91
 SQ SEQUENCE 91 AA; 11136 MW; 22FDF3EA185ACBA7 CRC64;
 Query Match 100.0%; Score 48; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. NO. 0.084; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FAFRDLCLIV 9
 Db 4 FAFRDLCLIV 12

RESULT 6
 Q919B2 PRELIMINARY; PRT; 99 AA.
 AC Q919B2; (Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370; Rose B.R.;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404704; AAL01365.1; -.
 DR GO:0042025; C:host cell nucleus; IEA.
 DR GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 FT NON_TER 99

QY	1	FAFRDLCIV 9	Matches	9;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
DB	24	FAFRDLCIV 32	Matches	9; <td>Conservative</td> <td>0;<td>Mismatches</td><td>0;<td>Indels</td><td>0;<td>Gaps</td><td>0;</td></td></td></td>	Conservative	0; <td>Mismatches</td> <td>0;<td>Indels</td><td>0;<td>Gaps</td><td>0;</td></td></td>	Mismatches	0; <td>Indels</td> <td>0;<td>Gaps</td><td>0;</td></td>	Indels	0; <td>Gaps</td> <td>0;</td>	Gaps	0;
<p>RESULT 9</p> <p>Q919C0 PRELIMINARY; PRT; 130 AA.</p> <p>AC Q919C0; MEDLINE=21846229; Pubmed=11857370;</p> <p>DT 01-DEC-2001 (TrEMBLrel. 19, Created)</p> <p>DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)</p> <p>DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)</p> <p>DE E6 protein (Fragment).</p> <p>OS Human papillomavirus type 16.</p> <p>OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;</p> <p>OC Papillomavirus.</p> <p>OX NCBI_TaxID=10581;</p> <p>RN [1]</p> <p>RP SEQUENCE FROM N.A.</p> <p>RX MEDLINE=21846229; Pubmed=11857370;</p> <p>RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;</p> <p>RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";</p> <p>RL Int. J. Cancer 97:868-874 (2002).</p> <p>DR EMBL; AF404700; AAL01357.1; -</p> <p>DR GO; GO:0042025; C:host cell nucleus; IEA.</p> <p>DR GO; GO:0003677; F:DNA binding; IEA.</p> <p>DR Pfam; PF00518; E6; 1.</p> <p>DR NON TER</p> <p>FT</p> <p>SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;</p> <p>Query Match 100.0%; Score 48; DB 2; Length 130;</p> <p>Best Local Similarity 100.0%; Pred. No. 0.12;</p> <p>Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0</p>												
QY	1	FAFRDLCIV 9	Matches <th>9;</th> <th>Conservative</th> <th>0;</th> <th>Mismatches</th> <th>0;</th> <th>Indels</th> <th>0;</th> <th>Gaps</th> <th>0;</th>	9;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
DB	24	FAFRDLCIV 32	Matches <th>9;</th> <th>Conservative</th> <th>0;</th> <th>Mismatches</th> <th>0;</th> <th>Indels</th> <th>0;</th> <th>Gaps</th> <th>0;</th>	9;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
<p>RESULT 10</p> <p>Q919C2 PRELIMINARY; PRT; 130 AA.</p> <p>AC Q919C2; MEDLINE=21846229; Pubmed=11857370;</p> <p>DT 01-DEC-2001 (TrEMBLrel. 19, Created)</p> <p>DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)</p> <p>DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)</p> <p>DE E6 protein (Fragment).</p> <p>OS Human papillomavirus type 16.</p> <p>OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;</p> <p>OC Papillomavirus.</p> <p>OX NCBI_TaxID=10581;</p> <p>RN [1]</p> <p>RP SEQUENCE FROM N.A.</p> <p>RX MEDLINE=21846229; Pubmed=11857370;</p> <p>RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;</p> <p>RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";</p> <p>RL Int. J. Cancer 97:868-874 (2002).</p> <p>DR EMBL; AF404699; AAL01355.1; -</p> <p>DR GO; GO:0042025; C:host cell nucleus; IEA.</p> <p>DR GO; GO:0003677; F:DNA binding; IEA.</p> <p>DR Pfam; PF00518; E6; 1.</p> <p>DR NON TER</p> <p>FT</p> <p>SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;</p> <p>Query Match 100.0%; Score 48; DB 2; Length 130;</p> <p>Best Local Similarity 100.0%; Pred. No. 0.12;</p> <p>Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0</p>												

Qy 1 FAFRDLClv 9
Db 24 FAFRDLClv 32

RESULT 11

Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404696; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFRDLClv 9
Db 24 FAFRDLClv 32

RESULT 12

Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404695; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFRDLClv 9
Db 24 FAFRDLClv 32

RESULT 13

Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404694; AAL01345.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFRDLClv 9
Db 32 FAFRDLClv 40

RESULT 14

Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404702; AAL01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match 100.0%; Score 48; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFRDLClv 9
Db 37 FAFRDLClv 45

RESULT 15

O12335
ID O12335 PRELIMINARY; PRT; 151 AA.
AC O12335;
DT 01-JUL-1997 (TREMELrel. 04, Created)
DT 01-JUL-1997 (TREMELrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003015; AAB70732.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR SEQUENCE 151 AA; 18238 MW; BFP32A8B016CC88B CRC64;
Query Match 100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FAFRDLClV 9
DB 45 FAFRDLClV 53

Search completed: June 28, 2005, 19:19:22
Job time : 55.3 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 Seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-11

Perfect score: 54

Sequence: 1 KISEYRHYC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	158	1 W6WLS	protein E6 - human
2	45	83.3	148	2 A61237	E6 protein - human
3	45	83.3	148	2 S36573	E6 protein - human
4	45	83.3	149	1 W6WL33	E6 protein - human
5	45	83.3	149	1 W6WL58	E6 protein - human
6	41	75.9	294	2 A40993	H+/K+-exchanging A
7	41	75.9	370	2 E42951	long-chain-fatty-a
8	40	74.1	275	2 T32010	hypothetical prote
9	40	74.1	291	2 A36051	H+/K+-exchanging A
10	38	70.4	155	1 W6WL43	E6 protein - human
11	38	70.4	211	2 B82901	hypothetical prote
12	37	68.5	332	1 F69508	N-acetyl-gamma-glu
13	37	68.5	430	2 D83977	hypothetical prote
14	36	66.7	115	2 T31781	hypothetical prote
15	36	66.7	146	2 S42570	flavodoxin - Desul
16	36	66.7	203	2 H85563	hypothetical prote
17	36	66.7	203	2 D90713	phosphohistidine p
18	36	66.7	205	2 H69854	hypothetical prote
19	36	66.7	890	2 T21000	hypothetical prote
20	35	64.8	68	2 T17702	hypothetical prote
21	35	64.8	149	1 W6WL35	E6 protein - human
22	35	64.8	150	1 W6WL11	E6 protein - human
23	35	64.8	150	1 W6WL6	E6 protein - human
24	35	64.8	177	2 A37408	betacellulin precu
25	35	64.8	178	2 JCI467	betacellulin precu
26	35	64.8	298	2 AC0838	probable transcrip
27	35	64.8	934	2 B29838	paraspasal crystal
28	35	64.8	1028	2 B86473	113.9K hypothetical
29	34	63.0	150	1 W6WLC1	E6 protein - pygmy

ALIGNMENTS

RESULT 1

W6WLS

protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virolgy 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

J.Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

R. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human papillomavirus type 16 genome acts at the level

A:Reference number: 217014; MUID:91162763; PMID:1848319

A:Accession: T10427

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C:Genetics:

A:Gene: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 54; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.015; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0;

Oy 1 KISEYRHYC 9

Db 79 KISEYRHYC 87

RESULT 2

A61237

E6 protein - human papillomavirus type 52

C:Species: human papillomavirus type 52

C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996

C:Accession: A61237

R:Takami, Y.; Kondoh, G.; Saito, K.; Sudiro, T.M.; Sjahrurachman, A.; Warsa, U.

Int. J. Cancer 48, 516-522, 1991

A:Title: Cloning and characterization of human papillomavirus type 52 from cervical carci

A:Reference number: A61237; MUID:91258022; PMID:1646174

A:Accession: A61237

A>Status: preliminary

A:Molecule type: DNA

A;Residues: 1-148 <TAK>
C:Superfamily: papillomavirus E6 protein

Query Match 83.3%; Score 45; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KISEYRHY 8
|||||
Db 72 KISEYRHY 79

RESULT 3

E6 protein - human papillomavirus type 52
C:Species: human papillomavirus type 52
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36573

submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36573
A:Molecule type: DNA

A;Residues: 1-148
A:Cross-references: UNIPROT:P36814; EMBL:X74481; NID:G397038; PIDN:CAA52585.1; PID:G397038
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 83.3%; Score 45; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KISEYRHY 8
|||||
Db 72 KISEYRHY 79

RESULT 4

E6 protein - human papillomavirus type 33
C:Species: human papillomavirus type 33
C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A03683

R:Cole, S.T.; Strebeck, R.E.
J. Virol. 58, 991-995, 1986
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 33, which is related to the type 33A virus.
A:Reference number: A93020; MUID:86200464; PMID:3009902

A;Accession: A03683
A:Molecule type: DNA
A;Residues: 1-149 <COL>
A:Cross-references: UNIPROT:P06427; GB:M12732; NID:G333049; PIDN:AAA46958.1; PID:G463177
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 83.3%; Score 45; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KISEYRHY 8
|||||
Db 72 KISEYRHY 79

RESULT 5

E6 protein - human papillomavirus type 58
C:Species: human papillomavirus type 58
A:Note: host Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: E36779

R:Kirii, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
A:Title: Human papillomavirus type 58 DNA sequence.
A:Reference number: A36779; MUID:92024102; PMID:1656594
A:Accession: E36779
A>Status: translation not shown
A:Molecule type: DNA
A;Residues: 1-149 <KIR>
A:Cross-references: UNIPROT:P26555; GB:D90400; NID:G222386; PIDN:BA31845.1; PID:G3337098
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 83.3%; Score 45; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KISEYRHY 8
|||||
Db 72 KISEYRHY 79

RESULT 6

A40993
H+/K+-exchanging ATPase (EC 3.6.3.10) beta chain - mouse
C:Species: Mus musculus (house mouse)

C>Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 09-Jul-2004
C:Accession: A40993; A41777; I49512
R:Canfield, V.A.; Levenson, R.
Proc. Natl. Acad. Sci. U.S.A. 88, 8247-8251, 1991

A:Title: Structural organization and transcription of the mouse gastric H(+),K(+) -ATPase
A:Reference number: A40993; MUID:91376121; PMID:1654563
A;Accession: A40993
A:Molecule type: DNA

A;Residues: 1-294 <CAN>
A:Cross-references: UNIPROT:P50992; GB:M64688; NID:G192079; PIDN:AAA37269.1; PID:G192081
R:Morley, G.P.; Callaghan, J.M.; Rose, J.B.; Toh, B.H.; Gleeson, P.A.; van Driel, I.R.
J. Biol. Chem. 267, 1165-1174, 1992
A:Title: The mouse gastric H,K-ATPase beta subunit. Gene structure and co-ordinate expression of the beta subunit and the alpha subunit.
A:Reference number: A41777; MUID:92112757; PMID:1370459
A;Accession: A41777
A:Molecule type: DNA

A;Residues: 1-294 <MOR>
A:Cross-references: GB:M80251; NID:G192086; PIDN:AAA37270.1; PID:G192088
A:Experimental source: gastric mucosal parietal cells
A:Note: sequence extracted from NCBI backbone (NCBIN:76277, NCBIN:76281, NCBIN:76285, NCBI:Genetics)

A;Introns: 38/1; 81/1; 119/1; 185/3; 204/3; 241/3
C:Superfamily: Na+/K+-exchanging ATPase beta-3 chain
C:Keywords: hydrolase; membrane protein

Query Match 75.9%; Score 41; DB 2; Length 294;
Best Local Similarity 55.6%; Pred. No. 5.9;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 KISEYRHYC 9
:::|||||
Db 13 RMAEFHYC 21

RESULT 7

E42951
long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) luxE - Xenorhabdus luminescens
N:Alternate names: fatty acid reductase complex synthetase
C:Species: Xenorhabdus luminescens

C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: E42951; E38448; D35411; D37898
R:Meighen, E.A.; Sztitner, R.B.
J. Bacteriol. 174, 5371-5381, 1992

A:Title: Multiple repetitive elements and organization of the lux operons of luminescent bacteria.
A:Reference number: A42951; MUID:92355513; PMID:1644764
A;Accession: E42951

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-370 <MEI>
A:Cross-references: UNIPROT:Q56823; GB:M90092; NID:g155411; PIDN:AA05359.1; PID:g155416
A:Experimental source: strain Hw
A>Note: sequence extracted from NCBI backbone (NCBIN:110516, NCBIP:110525)
R:Xi, L.; Cho, K.W.; Tu, S.C.
J. Bacteriol. 173, 1399-1405, 1991
A:Title: Cloning and nucleotide sequences of lux genes and characterization of luciferase
A:Reference number: A38448; MUID:91139581; PMID:1995589
A:Accession: E38448
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-27, 'CA', 30-116 <XIA>
A:Cross-references: GB:M62917; GB:M38525; NID:g155427; PIDN:AAA63567.1; PID:g155432
R:Johnston, T.C.; Rucker, E.B.; Cochrum, L.; Hruska, K.S.; Vandegrift, V.
Biochem. Biophys. Res. Commun. 170, 407-415, 1990
A:Title: The nucleotide sequence of the luxA and luxB genes of Xenorhabdus luminescens H
A:Reference number: A35411; MUID:90343746; PMID:2383248
A:Accession: D35411
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-27, 'CA', 30-37 <JOH>
A:Cross-references: GB:M55977; NID:g155422; PIDN:AAA27628.1; PID:g155426
R:Sztittner, R.; Meighen, E.
J. Biol. Chem. 265, 16581-16587, 1990
A:Title: Nucleotide sequence, expression, and properties of luciferase coded by lux gene
A:Reference number: A37898; MUID:90375532; PMID:2204626
A:Accession: D37898
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <S21>
A:Cross-references: GB:M57416; GB:J05625; NID:g155417
A>Note: this translation is not annotated in GenBank entry XENLUXAB, release 113.0
C:Genetics:
A:Gene: luxE
C:Keywords: acid-thiol ligase
F:360/Active site: Cys (covalent substrate-binding) #status predicted

Query Match 75.9%; Score 41; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 7.2; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0

Qy 4 EYRHYC 9
Db 54 EYRHYC 59

RESULT 8
T32010
hypothetical protein K10G6.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32010
R:Davidson, S.; Wohldmann, P.; Mullen, G.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid K10G6.
A:Reference number: Z2111
A:Accession: T32010
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-275 <DAV>
A:Cross-references: UNIPROT:Q16627; EMBL:AF016669; PIDN:AAB66097.1; GSPDB:GN00020; CESP:
A:Experimental source: strain Bristol N2; clone K10G6
C:Genetics:
A:Gene: CESP:K10G6.2
A:Map position: 2
A:Introns: 22/1; 66/2; 102/3; 136/2; 208/1

Query Match 74.1%; Score 40; DB 2; Length 275;
Best Local Similarity 62.5%; Pred. No. 8.4; 1; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 1

Qy 2 ISEYRHYC 9
Db 62 VNYRHYC 69

RESULT 9
A36051
H+/K+-exchanging ATPase (EC 3.6.3.10) beta chain - rabbit
N:Alternate names: H+/K+-transporting ATPase beta chain
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 09-Jul-2004
C:Accession: A36051
R:Reuben, M.A.; Lasater, L.S.; Sachs, G.
Proc. Natl. Acad. Sci. U.S.A. 87, 6767-6771, 1990
A:Title: Characterization of a beta subunit of the gastric H+/K+-transporting ATPase.
A:Reference number: A36051; MUID:90370865; PMID:2168558
A:Accession: A36051
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-291 <REU>
A:Cross-references: UNIPROT:P18597; GB:M35544; NID:g165031; PIDN:AAA31256.1; PID:g165032
C:Superfamily: Na+/K+-exchanging ATPase beta-3 chain
C:Keywords: hydrolase; transmembrane protein

Query Match 74.1%; Score 40; DB 2; Length 291;
Best Local Similarity 55.6%; Pred. No. 8.8; 1; Indels 0; Gaps 0;
Matches 5; Conservative 3; Mismatches 3

Qy 1 KISEYRHYC 9
Db 13 RMEEFHYC 21

RESULT 10
W6ML43
E6 protein - human papillomavirus type 43
C:Species: human papillomavirus type 43
A>Note: host Homo sapiens (man)
C:Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C:Accession: A34144
R:Lozinckz, A.T.; Quinn, A.P.; Goldsborough, M.D.; Schmidt, B.J.; Temple, G.F.
J. Virol. 63, 2829-2834, 1989
A:Title: Cloning and partial DNA sequencing of two new human papillomavirus types associ
A:Reference number: A34144; MUID:89259065; PMID:2542593
A:Accession: A34144
A:Molecule type: DNA
A:Residues: 1-155 <LOE>
A:Cross-references: UNIPROT:P19709; GB:M27022; NID:g341596; PIDN:AAA63453.1; PID:g703247
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:31-67/Region: zinc finger CCCC motif
F:104-140/Region: zinc finger CCCC motif

Query Match 70.4%; Score 38; DB 1; Length 155;
Best Local Similarity 75.0%; Pred. No. 12; 2; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 2

Qy 1 KISEYRHY 8
Db 73 KISQYRHP 80

RESULT 11
B82901
hypothetical protein U0366 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: B82901
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mini
A:Reference number: A82870
A:Accession: B82901

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-211 <GLA>
A;Cross-references: GB:AE002133; GB:AF222894; NID:G6899339; PIDN:AAF30775.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: UU366
A;Genetic code: SGC3

Query Match 70.4%; Score 38; DB 2; Length 211;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KISEYRHYC 9
:|:|:|
Db 37 KTIENHYC 45

RESULT 12

F69508
N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: F69508
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: F69508
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-332 <KLE>
A;Cross-references: UNIPROT:O28208; GB:AE000961; GB:AE000782; NID:G2689284; PIDN:AAB6918
C;Superfamily: N-acetyl-gamma-glutamyl-phosphate reductase
C;Keywords: oxidoreductase

Query Match 68.5%; Score 37; DB 1; Length 332;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KISEYRHY 8
:|:|:|
Db 197 KITERRY 204

RESULT 13

D83977
Hypothetical protein BH2620 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: D83977
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83977
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-430 <STO>
A;Cross-references: UNIPROT:Q9K9M5; GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BA8063
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2620
C;Superfamily: iucD protein

Query Match 68.5%; Score 37; DB 2; Length 430;
Best Local Similarity 71.4%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SEYRHYC 9
:|:|:|
Db 98 TEYNYHC 104

RESULT 14

T31781
Hypothetical protein F13H6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31781
R;Jones, K.; Wohldmann, P.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid F13H6.
A;Reference number: Z21085
A;Accession: T31781
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-115 <JON>
A;Cross-references: UNIPROT:O16349; EMBL:AF016437; PIDN:AAB65884.1; GSPDB:GN00023; CESP:I
A;Experimental source: strain Bristol N2; clone F13H6
C;Genetics:
A;Gene: CESP:F13H6.2
A;Map position: 5
A;Introns: 52/1; 92/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F13H6.2

Query Match 66.7%; Score 36; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YRHYC 9
:|:|:|
Db 7 YRHYC 11

RESULT 15

S42570
Flavodoxin - Desulfovibrio desulfuricans (ATCC 27774)
C;Species: Desulfovibrio desulfuricans
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C;Accession: S42570
R;Caldeira, J.; Palma, P.N.; Regalla, M.; Lampreia, J.; Calvete, J.; Schaefer, W.; Legall
Eur. J. Biochem. 220, 987-995, 1994
A;Title: Primary sequence, oxidation-reduction potentials and tertiary-structure predicti
A;Reference number: S42570; MUID:94192692; PMID:8143752
A;Accession: S42570
A;Molecule type: protein
A;Residues: 1-146 <CAL>
A;Cross-references: UNIPROT:P80312
A;Experimental source: strain ATCC 27774
C;Superfamily: flavodoxin; flavodoxin homology
C;Keywords: electron transfer; flavoprotein; FMN
F;6-145/Domain: flavodoxin homology <FLX>

Query Match 66.7%; Score 36; DB 2; Length 146;
Best Local Similarity 83.3%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 EYRHYC 9
:|:|:|
Db 97 EYHYC 102

Search completed: June 28, 2005, 19:23:26
Job time : 13.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-11
Perfect score: 54
Sequence: 1 KISEYRHYC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	84	2 Q80882	Q80882 human papil
2	54	100.0	90	2 Q80883	Q80883 human papil
3	54	100.0	90	2 Q80884	Q80884 human papil
4	54	100.0	99	2 Q819B2	Q819B2 human papil
5	54	100.0	103	2 Q819D6	Q819D6 human papil
6	54	100.0	130	2 Q819B4	Q819B4 human papil
7	54	100.0	130	2 Q819B8	Q819B8 human papil
8	54	100.0	130	2 Q819C0	Q819C0 human papil
9	54	100.0	130	2 Q819C2	Q819C2 human papil
10	54	100.0	130	2 Q819C8	Q819C8 human papil
11	54	100.0	130	2 Q819D0	Q819D0 human papil
12	54	100.0	138	2 Q819D2	Q819D2 human papil
13	54	100.0	143	2 Q819B6	Q819B6 human papil
14	54	100.0	143	2 Q819C4	Q819C4 human papil
15	54	100.0	151	2 Q812335	Q812335 human papil
16	54	100.0	151	2 Q812336	Q812336 human papil
17	54	100.0	151	2 Q77816	Q77816 human papil
18	54	100.0	151	2 Q777J5	Q777J5 human papil
19	54	100.0	151	2 Q772J07	Q772J07 human papil
20	54	100.0	151	2 Q80963	Q80963 human papil
21	54	100.0	151	2 Q89640	Q89640 human papil
22	54	100.0	151	2 Q89648	Q89648 human papil
23	54	100.0	151	2 Q89755	Q89755 human papil
24	54	100.0	151	2 Q89852	Q89852 human papil
25	54	100.0	151	2 Q8B564	Q8B564 human papil
26	54	100.0	151	2 Q8BB19	Q8BB19 human papil
27	54	100.0	151	2 Q8BB20	Q8BB20 human papil
28	54	100.0	151	2 Q8W931	Q8W931 human papil
29	54	100.0	151	2 Q9WMP4	Q9WMP4 human papil
30	54	100.0	151	2 Q9WMP5	Q9WMP5 human papil
31	54	100.0	158	1 VE6_HPV16	P03126 human papil

32 54 100.0 158 2 Q8QHP5 Q8qhp5 human papil
33 54 100.0 158 2 Q8QHT0 Q8qht0 human papil
34 54 100.0 158 2 Q8QRD6 Q8qrd6 human papil
35 54 100.0 158 2 Q8QRD7 Q8qrd7 human papil
36 54 100.0 158 2 Q8QRD8 Q8qrd8 human papil
37 54 100.0 158 2 Q8QRD9 Q8qrd9 human papil
38 54 100.0 158 2 Q8QRE0 Q8qre0 human papil
39 54 100.0 158 2 Q8QRE1 Q8qre1 human papil
40 54 100.0 158 2 Q71B17 Q71bi7 human papil
41 54 100.0 158 2 Q8QDH3 Q8qdh3 human papil
42 54 100.0 158 2 Q8QDH5 Q8qdh5 human papil
43 54 100.0 158 2 Q8QDH7 Q8qdh7 human papil
44 54 100.0 158 2 Q8QDH9 Q8qdh9 human papil
45 54 100.0 158 2 Q9WH13 Q9wh13 human papil

ALIGNMENTS

RESULT 1
Q80882 PRELIMINARY; PRT; 84 AA.
AC Q80882;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14511; AAB60565.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 84 84
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;
Query Match Similarity 100.0%; Score 54; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KISEYRHYC 9
DB 28 KISEYRHYC 36
RESULT 2
Q80883 PRELIMINARY; PRT; 90 AA.
AC Q80883;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14512; AAB60566.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

```

DR GO: 0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10904 MW; 5D3ADF843AD6060B CRC64;

Query Match      100.0%; Score 54; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 31 KISEYRHYC 39

RESULT 3
Q80884
ID Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Youngusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DDJB databases.
DR EMBL; U14513; AA860567.2; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFAFACCC01 CRC64;

Query Match      100.0%; Score 54; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 31 KISEYRHYC 39

RESULT 4
Q919B2
ID Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404704; AAL01365.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.

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DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;

Query Match      100.0%; Score 54; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 48 KISEYRHYC 56

RESULT 5
Q919D6
ID Q919D6 PRELIMINARY; PRT; 103 AA.
AC Q919D6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404692; AAL01342.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 103
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;

Query Match      100.0%; Score 54; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 24 KISEYRHYC 32

RESULT 6
Q919B4
ID Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01363.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1

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SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227BEDDC CRC64;
 Query Match 100.0%; Score 54; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
 Db 51 KISEYRHYC 59

RESULT 7
 Q919B8 PRELIMINARY; PRT; 130 AA.
 AC Q919B8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404701; AAL01357.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match 100.0%; Score 54; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
 Db 51 KISEYRHYC 59

RESULT 8
 Q919C0 PRELIMINARY; PRT; 130 AA.
 AC Q919C0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404700; AAL01357.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
 Db 51 KISEYRHYC 59

RESULT 9
 Q919C2 PRELIMINARY; PRT; 130 AA.
 AC Q919C2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404699; AAL01355.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
 Db 51 KISEYRHYC 59

RESULT 10
 Q919C8 PRELIMINARY; PRT; 130 AA.
 AC Q919C8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404696; AAL01349.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
 Db 51 KISEYRHYC 59

Qy 1 KISEYRHYC 9
Db 51 KISEYRHYC 59

RESULT 11

Q919D0 ID Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT "Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404695; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15735 MW; 95FB30EEDCA21AF3 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 51 KISEYRHYC 59

RESULT 12

Q919D2 ID Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT "Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404694; AAL01345.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481ESA90895FC2 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 59 KISEYRHYC 67

RESULT 13

Q919B6 ID Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT "Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404702; AAL01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match 100.0%; Score 54; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 64 KISEYRHYC 72

RESULT 14

Q919C4 ID Q919C4 PRELIMINARY; PRT; 143 AA.
AC Q919C4;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT "Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404696; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 64 KISEYRHYC 72

RESULT 15

012335
ID O12335 PRELIMINARY; PRT; 151 AA.
AC O12335;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2195-2208 (1997).
DR EMBL; AF003015; AAB70732.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;

Query Match 100.0%; Score 54; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 72 KISEYRHYC 80

Search completed: June 28, 2005, 19:19:23
Job time : 56.3 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 Seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-12

Perfect score: 52

Sequence: 1 PLCDLLIRC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	158	1 W6WLHS	protein E6 - human
2	45	86.5	155	1 W6WL56	E6 protein - human
3	45	86.5	918	2 A1667	nitrate reductase
4	43	82.7	149	1 W6WL31	E6 protein - human
5	42	80.8	917	1 RDMUNH	nitrate reductase
6	40	76.9	150	2 S36544	E6 protein - human
7	38	73.1	148	2 S36515	E6 protein - human
8	38	73.1	149	1 W6WL35	E6 protein - human
9	38	73.1	518	1 S27381	probable serine/th
10	38	73.1	528	2 T52101	probable nuclear t
11	38	73.1	538	2 T86225	hypothetical prote
12	37	71.2	527	2 T04329	importin alpha - t
13	37	71.2	532	2 T52102	probable nuclear t
14	37	71.2	532	2 T52268	importin alpha [va
15	37	71.2	535	2 T52098	probable nuclear t
16	36	69.2	180	2 E71337	hypothetical prote
17	36	69.2	219	2 A35650	Sur protein - chic
18	36	69.2	258	2 T41936	hypothetical prote
19	36	69.2	433	2 T33108	hypothetical prote
20	36	69.2	441	2 A83370	probable MPS trans
21	36	69.2	471	2 A81680	conserved hypothet
22	36	69.2	595	2 S37057	parafagellar rod
23	35	67.3	60	2 B82795	hypothetical prote
24	35	67.3	148	2 S36590	E6 protein - human
25	35	67.3	311	2 A95342	hypothetical prote
26	35	67.3	337	2 T19651	hypothetical prote
27	35	67.3	416	2 B84710	probable C3HC4 zin
28	35	67.3	471	2 T25455	hypothetical prote
29	35	67.3	472	2 A83331	probable two-compo

30 35 67.3 476 2 E97631 probable membrane
31 35 67.3 636 2 G97029 nH(3)-dependent NA
32 35 67.3 716 2 H84421 probable receptor-
33 35 67.3 1161 2 B96368 protein F28C11.9 l
34 34 65.4 149 1 W6WL33 E6 protein - human
35 34 65.4 153 2 S36503 E6 protein - human
36 34 65.4 240 2 T46180 hypothetical prote
37 34 65.4 263 2 S47086 pir7a protein - ri
38 34 65.4 276 2 T44181 hypothetical prote
39 34 65.4 276 2 T43994 virion protein (im
40 34 65.4 279 2 T09328 probable membrane-
41 34 65.4 308 2 E81288 hypothetical prote
42 34 65.4 321 2 A87668 conserved hypothet
43 34 65.4 330 2 S75496 hypothetical prote
44 34 65.4 331 2 E85878 sucrose specific t
45 34 65.4 331 2 D91034 sucrose operon rep

ALIGNMENTS

RESULT 1

W6WLHS

protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virolgy 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P03126; GB:K02719; NID:G333031; PIDN:AAA46939.1; PID:G333032

R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: 217014; MUID:91162763; PMID:1848319

A:Accession: T10427

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C:Genetics:

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match

Best Local Similarity 100.0%; Score 52; DB 1; Length 158;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy

1 PLCDLLIRC 9

|||||||

Db 102 PLCDLLIRC 110

RESULT 2

W6WL56

E6 protein - human papillomavirus type 56

C:Species: human papillomavirus type 56

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C:Accession: A33377; S36579

R:Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; McAllister, P.; Temple, G.F.

J. Gen. Virol. 70, 3099-3104, 1989

A:Title: Human papillomavirus type 56: a new virus detected in cervical cancers.

A:Reference number: A33377; MUID:90063558; PMID:2555440

A:Accession: A33377

A:Molecule type: DNA

A:Residues: 1-155 <LOE5>

A;Cross-references: UNIPROT:P24836
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36579
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-155
A;Cross-references: EMBL:X74483; NID:G397053; PIDN:CAA52596.1; PID:G397054
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;33-69/Region: zinc finger CCCC motif
F;106-142/Region: zinc finger CCCC motif

Query Match 86.5%; Score 45; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LCDDLIRC 9
Db 99 LCDDLIRC 106
|||||

RESULT 3
A1667
nitrate reductase (NADH) (EC 1.7.1.1) - winter squash
C;Species: Cucurbita maxima (winter squash)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: A41667
R;Hyde, G.E.; Crawford, N.M.; Campbell, W.H.
J. Biol. Chem. 266, 23542-23547, 1991
A;Title: The sequence of squash NADH:nitrate reductase and its relationship to the sequ
A;Reference number: A41667; MUID:92084635; PMID:1748631
A;Accession: A41667
A;Molecule type: mRNA
A;Residues: 1-918 <HYD>
A;Cross-references: UNIPROT:P17569; GB:M33154; NID:G167498; PIDN:AAA33114.1; PID:G167499
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 red
C;Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron;
F;91-483/Domain: molybdopterin-binding domain homology <PCO>
F;543-617/Domain: cytochrome b5 core homology <CB5>
F;668-918/Domain: cytochrome-b5 reductase homology <CBR>
F;195/Binding site: molybdoplerin (Cys) (covalent) #status predicted
F;434/Disulfide bonds: interchain #status predicted
F;578,601/Binding site: heme iron (His) (axial ligands) #status predicted
F;733,890/Binding site: NAD(P) (Lys, Cys) #status predicted
F;773/Binding site: FAD (Tyr) #status predicted

Query Match 86.5%; Score 45; DB 2; Length 918;
Best Local Similarity 88.9%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 228 PLCDDLKRC 236
|||||

RESULT 4
W6WL31
E6 protein - human papillomavirus type 31
C;Species: human papillomavirus type 31
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A32444
R;Goldsbrough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associ
A;Reference number: A94398; MUID:89299478; PMID:2545036
A;Accession: A32444
A;Status: translation not shown
A;Molecule type: DNA

A;Residues: 1-149 <GOL>
A;Cross-references: UNIPROT:P17386; GB:J04353; NID:G333048; PIDN:AAA46950.1; PID:G459916
C;Comment: This protein may be involved in the oncogenic potential of this virus.
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 82.7%; Score 43; DB 1; Length 149;
Best Local Similarity 87.5%; Pred. No. 1.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LCDDLIRC 9
Db 96 ICDDLIRC 103
|||||

RESULT 5
RDMUNH
nitrate reductase (NADH) (EC 1.7.1.1) 2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: A31821; S01641
R;Crawford, N.M.; Smith, M.; Bellissimo, D.; Davis, R.W.
Proc. Natl. Acad. Sci. U.S.A. 85, 5006-5010, 1988
A;Title: Sequence and nitrate regulation of the Arabidopsis thaliana mRNA encoding nitrat
A;Reference number: A31821; MUID:88276888; PMID:3393528
A;Accession: A31821
A;Molecule type: mRNA
A;Residues: 1-917 <CRA>
A;Cross-references: UNIPROT:P11035; GB:J03240; NID:G166781; PIDN:AAA32830.1; PID:G166782
R;Cheng, C.; Dewdney, J.; Nam, H.; den Boer, B.G.W.; Goodman, H.M.
EMBO J. 7, 3309-3314, 1988
A;Title: A new locus (NRA1) in Arabidopsis thaliana encoding nitrate reductase.
A;Reference number: S01640; MUID:89091069; PMID:2905260
A;Accession: S01641
A;Molecule type: mRNA
A;Residues: 522-917 <CHE>
A;Cross-references: EMBL:X13435; NID:G16403; PIDN:CAA31787.1; PID:G930002
A;Note: the translation of the nucleotide sequence is not complete
C;Comment: This enzyme catalyzes the reduction of nitrate to nitrite in cytoplasm; each c
me involved in the first step of nitrate assimilation in plants, fungi, and bacteria.
C;Genetics:
A;Gene: NIA2
A;Map position: 1
C;Complex: homodimer
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reduc
C;Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron; n
F;87-482/Domain: molybdopterin-binding domain homology <PCO>
F;542-616/Domain: cytochrome b5 core homology <CB5>
F;667-917/Domain: cytochrome-b5 reductase homology <CBR>
F;191/Binding site: molybdoplerin (Cys) (covalent) #status predicted
F;433/Disulfide bonds: interchain #status predicted
F;577,600/Binding site: heme iron (His) (axial ligands) #status predicted
F;731,889/Binding site: NAD (Lys, Cys) #status predicted
F;771/Binding site: FAD (Tyr) #status predicted

Query Match 90.8%; Score 42; DB 1; Length 917;
Best Local Similarity 77.8%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 224 PLCDVLKRC 232
|||||

RESULT 6
S36544
E6 protein - human papillomavirus type 26
C;Species: human papillomavirus type 26
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36544
R;Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469

A:Accession: S36544
A:Molecule type: DNA
A:Residues: 1-150
A:Cross-references: UNIPROT:P36807; EMBL:X74472; NID:G396956; PIDN:CAA52530.1; PID:G3969
C:Superfamily: papillomavirus E6 protein
C:Keywords: early protein; zinc finger

Query Match 76.9%; Score 40; DB 2; Length 150;
Best Local Similarity 87.5%; Pred. No. 4.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LCDLLIRC 9
||:|||||
DB 96 LCNLLIRC 103

RESULT 7
S36515
E6 protein - human papillomavirus type 34
C:Species: human papillomavirus type 34
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36515
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36515
A:Molecule type: DNA
A:Residues: 1-148
A:Cross-references: UNIPROT:P36811; EMBL:X74476; NID:G396989; PIDN:CAA52555.1; PID:G3969
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 73.1%; Score 38; DB 2; Length 148;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LCDLLIRC 9
||:|||||
DB 97 LCNLLIRC 104

RESULT 8
W6WLJ35
E6 protein - human papillomavirus type 35
C:Species: human papillomavirus type 35
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: E40824; S36521
R:Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillo
A:Reference number: A40824; MUID:92124753; PMID:1310198
A:Accession: E40824
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-149 <MAR>
A:Cross-references: UNIPROT:P27228; GB:M74117; NID:G333050; PIDN:AAA46966.1; PID:G333051
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36521
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149
A:Cross-references: EMBL:X74477; NID:G396997; PIDN:CAA52561.1; PID:G396998
A:Experimental source: strain 35H
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger

F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 73.1%; Score 38; DB 1; Length 149;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCDLLIRC 9
||:|||||
DB 96 LCHLLIRC 103

RESULT 9
S27381
probable serine/threonine-specific protein kinase (EC 2.7.1.1.-) YKL116c - yeast (Saccharon
N:Alternate names: probable protein kinase YKL516
C:Species: Saccharomyces cerevisiae
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S27381; S37944
R:Jacquier, A.; Legrain, P.; Dujon, B.
Yeast 8, 121-132, 1992
A:Title: Sequence of a 10.7 kb segment of yeast chromosome XI identifies the APN1 and the

S
A:Reference number: S22267; MUID:92221689; PMID:1561835
A:Accession: S27381
A:Molecule type: DNA
A:Residues: 1-518 <JAC>
A:Cross-references: UNIPROT:P28708; GB:S93804; NID:G248391; PIDN:AAB21999.1; PID:G248393
A:Experimental source: strain S288C
R:Jacquier, A.; Legrain, P.; Colleaue, L.; Richard, G.F.; Thierry, A.; Dujon, B.
submitted to the Protein Sequence Database, March 1994
A:Reference number: S37938
A:Accession: S37944
A:Molecule type: DNA
A:Residues: 1-518 <JAC>

A:Cross-references: EMBL:Z28115; NID:G486193; PIDN:CAA81955.1; PID:G486194; GSPDB:GN00011
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:PRR1; MIPS:YKL116C
A:Cross-references: SGD:S0001599
A:Map position: 11L
C:Superfamily: yeast probable serine/threonine-specific protein kinase YKL116c; protein 1
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:190-499/Domain: protein kinase homology <KIN>
F:354/Active site: Asp #status predicted

Query Match 73.1%; Score 38; DB 1; Length 518;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLCDLIR 8
||:|||||
DB 288 PLCDLIR 295

RESULT 10
T52101
Probable nuclear transport factor importin alpha-like protein [imported] - Arabidopsis t
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C:Accession: T52101
R:Merkle, T.
submitted to the EMBL Data Library, March 1998

A:Reference number: Z25955
A:Accession: T52101
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-528 <MER>
A:Cross-references: UNIPROT:O49602; EMBL:Y14616; PIDN:CAA74966.1
A:Experimental source: ecotype Columbia; vegetative tissue; 3 weeks old
C:Genetics:
A:Gene: Impa-4
C:Superfamily: pendulin

```
Query Match      73.1%; Score 38; DB 2; Length 528;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLI 7
Db 413 PLCDLLI 419

RESULT 11
F86225
Hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86225
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.;
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F86225
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-538 <STO>
A:Cross-references: UNIPROT:O80480; GB:AE005172; NID:g3249096; PIDN:AAC24079.1; GSPDB:GN
C:Genetics:
A:Map position: 1
A:Superfamily: pendulin

Query Match      73.1%; Score 38; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLI 7
Db 423 PLCDLLI 429

RESULT 12
T04329
Importin alpha - tomato
N:Alternate names: KAP alpha protein
C:Species: Lycopersicon esculentum (tomato)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04329
R:Kunik, T.; Mizrachi, L.; Citovsky, V.; Gafni, Y.
submitted to the EMBL Data Library, June 1998
A:Reference number: Z15286
A:Accession: T04329
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-527 <KUN>
A:Cross-references: UNIPROT:O22478; EMBL:AF017252; NID:g3228369; PIDN:AAC23722.1; PID:g3
C:Genetics:
A:Gene: KAP
C:Superfamily: pendulin

Query Match      71.2%; Score 37; DB 2; Length 527;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLI 7
Db 417 PLCDLLV 423
```

RESULT 13

```
T52102
Probable nuclear transport factor importin alpha-like protein [imported] - Arabidopsis th
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C:Accession: T52102
R:Merkle, T.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z25955
A:Accession: T52102
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-532 <MER>
A:Cross-references: UNIPROT:Q96321; EMBL:Y15224; PIDN:CAA75513.1
A:Experimental source: ecotype Columbia; vegetative; 3 weeks old
C:Genetics:
A:Gene: Impal
C:Superfamily: pendulin

Query Match      71.2%; Score 37; DB 2; Length 532;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLI 7
Db 416 PLCDLLV 422

RESULT 14
T52268
Importin alpha [validated] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C:Accession: T52268
R:Smith, H.M.; Hicks, G.R.; Raikhel, N.V.
Plant Physiol. 114, 411-417, 1997
A:Title: Importin alpha from Arabidopsis thaliana is a nuclear import receptor that recog
A:Reference number: Z26010; MUID:97336305; PMID:9193081
A:Accession: T52268
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-532 <SMI>
A:Cross-references: UNIPROT:Q96321; EMBL:AF077528; PIDN:AAC27644.1
A:Experimental source: cultivar Columbia
C:Function:
A:Description: involved in protein import in nucleus; binds to nuclear localization sign
C:Superfamily: pendulin

Query Match      71.2%; Score 37; DB 2; Length 532;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLI 7
Db 416 PLCDLLV 422

RESULT 15
T52098
Probable nuclear transport factor importin alpha [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C:Accession: T52098
R:Schledz, M.; Leclerc, D.; Neuhaus, G.; Merkle, T.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z25951
A:Accession: T52098
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-535 <SCH>
A:Cross-references: UNIPROT:O49600; EMBL:Y14615; PIDN:CAA74965.1
A:Experimental source: ecotype Columbia; vegetative tissue; 3 weeks old
C:Genetics:
```


A:Gene: Impa-2
C:Superfamily: pendulin

Query Match 71.2%; Score 37; DB 2; Length 535;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLI 7
| | | | |
Db 421 PLCDLIV 427

Search completed: June 28, 2005, 19:23:27
Job time : 12.2 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-28
Perfect score: 45
Sequence: 1 DTLEKLTWT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03: +
1: uniprot_sprot: +
2: uniprot_trembl: +

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB	ID	Description
1	45	100.0	158	1	VE6	HPV18	P06463 human papillomavirus type 18
2	45	100.0	158	2	Q9QNP8		Q9QNP8 human papillomavirus type 18
3	39	86.7	158	1	VE6	HPV45	P21735 human papillomavirus type 45
4	39	86.7	158	2	Q9Y4Y4		Q9Y4Y4 homo sapiens
5	39	86.7	158	2	O10608		O10608 human papillomavirus type 18
6	38	84.4	553	1	MIS	RAT	P49000 rattus norvegicus
7	37	82.2	157	2	Q9WHG0		Q9WHG0 human papillomavirus type 18
8	37	82.2	549	2	Q8AYZ2		Q8AYZ2 porcine lymphoma
9	36	80.0	170	2	Q6A862		Q6A862 propionibacterium
10	36	80.0	173	2	Q8AY95		Q8AY95 arabidopsis thaliana
11	36	80.0	173	2	Q9SV38		Q9SV38 arabidopsis thaliana
12	36	80.0	682	2	Q6CX99		Q6CX99 kluyveromyces fragilis
13	36	80.0	772	2	Q8MQK1		Q8MQK1 drosophila melanogaster
14	36	80.0	772	2	Q92X30		Q92X30 rhizobium meliloti
15	36	80.0	1087	2	Q86BS5		Q86BS5 drosophila melanogaster
16	36	80.0	1124	2	Q8MQJ8		Q8MQJ8 drosophila melanogaster
17	36	80.0	1532	2	Q8PLD6		Q8PLD6 xanthomonas campestris
18	35	77.8	93	2	Q997G5		Q997G5 bovine adenovirus type 1
19	35	77.8	115	2	Q9BRT3		Q9BRT3 homo sapiens
20	35	77.8	164	2	Q8RH02		Q8RH02 fusobacterium nucleatum
21	35	77.8	266	2	Q97S05		Q97S05 streptococcus pneumoniae
22	35	77.8	271	2	Q8CWT0		Q8CWT0 streptococcus pneumoniae
23	35	77.8	303	1	KINE	METTH	Q50559 methanobacterium thermoautotrophicum
24	35	77.8	327	2	Q92XR9		Q92XR9 rhizobium meliloti
25	35	77.8	342	2	Q6R7L3		Q6R7L3 ostreid her
26	35	77.8	420	2	Q7P2D2		Q7P2D2 fusobacterium nucleatum
27	35	77.8	515	2	Q7OTM2		Q7OTM2 giardia lamblia
28	35	77.8	522	2	Q7QWN9		Q7QWN9 giardia lamblia
29	35	77.8	583	2	Q8RFT9		Q8RFT9 fusobacterium nucleatum
30	35	77.8	603	1	RAEP	YEAST	P32864 saccharomyces cerevisiae
31	35	77.8	947	2	Q86H44		Q86H44 dictyostelium discoideum

RESULT 1				
VE6	HPV18	STANDARD;	PRT;	158 AA.
ID	VE6 HPV18			
AC	P06463;			
DT	01-JAN-1988 (Rel. 06, Created)			
DT	01-JAN-1988 (Rel. 06, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	E6 protein.			
GN	Name=E6;			
OS	Human papillomavirus type 18.			
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;			
OC	Papillomavirus.			
OX	NCBI_TaxID=10582;			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87283882; PubMed=3039146;			
RA	Cole S.T., Danos O.;			
RT	"Nucleotide sequence and comparative analysis of the human papillomavirus type 18 genome. Phylogeny of papillomaviruses and repeated structure of the E6 and E7 gene products.";			
RL	J. Mol. Biol. 193:599-608(1987).			
LN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86306665; PubMed=3018129;			
RA	Matlashewski G., Banks L., Wu-Liao J., Spence P., Pim D., Crawford L.;			
RT	"The expression of human papillomavirus type 18 E6 protein in bacteria and the production of anti-E6 antibodies.";			
RL	J. Gen. Virol. 67:1909-1916(1986).			
LN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88188247; PubMed=2833614;			
RA	Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M.,			
RA	Sugimura T.;			
RT	"Nucleotide sequences of cDNAs for human papillomavirus type 18 transcripts in HeLa cells.";			
RL	J. Virol. 62:1640-1646(1988).			
LN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87053870; PubMed=3023067;			
RA	Schneider-Gaeddicke A., Schwarz E.;			
RT	"Different human cervical carcinoma cell lines show similar transcription patterns of human papillomavirus type 18 early genes.";			
RL	EMBO J. 5:2285-2292(1986).			
LN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87218459; PubMed=3034571;			
RA	Seedorf K., Oltersdorf T., Kraemer G., Roewekamp W.;			
RT	"Identification of early proteins of the human papilloma viruses type 16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells.";			
RL	EMBO J. 6:139-144(1987).			
LN	[6]			
RP	ZINC-BINDING.			
RX	MEDLINE=89385606; PubMed=2550872;			
RA	Grossman S.R., Laimins L.A.;			

Q87ym9 pseudomonas
Q881b1 pseudomonas
Q9waj4 human immun
Q9sch7 betula verr
Q9ac11 betula verr
P17386 human papill
Q9adn0 listeria in
Q722c7 listeria in
P15494 betula verr
P43177 betula verr
P43178 betula verr
P43179 betula verr
P43180 betula verr
P43183 betula verr

Qy 1 DTLEKLTNT 9
:|||||

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Q9WHG0
ID Q9WHG0 PRELIMINARY; PRT; 157 AA.
AC Q9WHG0;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative transforming protein E6.
OS Human papillomavirus candHPV85.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus; Human papillomavirus unidentified type.
OX NCBI_TaxID=151757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20047972; PubMed=10580054;
RA Chow V.T.K., Leong P.W.;
RT "Complete nucleotide sequence, genomic organization and phylogenetic
RT analysis of a novel genital human papillomavirus type, HLT7474-S.";
RL J. Gen. Virol. 80:2923-2929(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Chow V.T.K., Leong W.F.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF131950; AAD24181.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 157 AA; 18450 MW; 1B154BA2C49EED7 CRC64;

Query Match 82.2%; Score 37; DB 2; Length 157;
Best Local Similarity 77.8%; Pred. No. 39;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTLEKLTNT 9
Db 88 ETLEKLTNS 96

RESULT 8
Q9AY22
ID Q9AY22 PRELIMINARY; PRT; 549 AA.
AC Q9AY22;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Tegument protein.
OS Porcine lymphotropic herpesvirus 2.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae.
OX NCBI_TaxID=91741;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22594013; PubMed=12706081; DOI=10.1016/S0042-6822(03)00006-0;
RA Chmielewicz B., Goltz M., Franz T., Bauer C., Brena S., Ellerbok H.,
RA Beckmann S., Rziha H.-J., Lahrmann K.-H., Romero C., Ehlers B.;
RT "A novel porcine gammaherpesvirus.";
RL Virology 308:317-329(2003).
DR EMBL; AY170314; AAO12289.1; -.
DR EMBL; AY170317; AAO12361.1; -.
DR InterPro; IPR002493; UL25.
DR Pfam; PF01499; Herpes_UL25; 1.
SQ SEQUENCE 549 AA; 62473 MW; 9ACBF84178093B35 CRC64;

Query Match 82.2%; Score 37; DB 2; Length 549;
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTLEKLTNT 9
Db 89 DTLEKLTNT 97

RESULT 9
Q6A862
ID Q6A862 PRELIMINARY; PRT; 170 AA.
AC Q6A862;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Conserved protein.
GN OrderedLocusNames=PPA1304;
OS Propionibacterium acnes.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Propionibacteriaceae; Propionibacteriaceae; Propionibacterium.
OX NCBI_TaxID=1747;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=KPA171202 / DSM 16379;
RC PubMed=15286373; DOI=10.1126/science.1100330;
RA Brueggemann H., Henne A., Hofer F., Liesegang H., Wierer A.,
RA Strittmatter A., Hufner S., Duerre P., Gottschalk G.;
RT "The complete genome sequence of Propionibacterium acnes, a commensal
RT of human skin.";
RL Science 305:671-673(2004).
RN EMBL; AB017283; AATB3053.1; -.
KW Complete proteome.
SQ SEQUENCE 170 AA; 17992 MW; CB08F928CDD69184 CRC64;

Query Match 80.0%; Score 36; DB 2; Length 170;
Best Local Similarity 77.8%; Pred. No. 66;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DTLEKLTNT 9
Db 146 DLSKLTNT 154

RESULT 10
Q84Y95
ID Q84Y95 PRELIMINARY; PRT; 173 AA.
AC Q84Y95;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CAXIPI protein.
GN Name=CAXIPI;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22476970; PubMed=12480930; DOI=10.1074/jbc.M210883200;
RA Cheng N.-H., Hirschi K.D.;
RT "Cloning and characterization of CXIPI A novel PICOT domain-containing
RT Arabidopsis protein that associates with CAX1.";
RL J. Biol. Chem. 278:6503-6509(2003).
DR EMBL; AY157988; AAO19647.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR002109; Glutaredoxin.
DR InterPro; IPR004480; Glutaredox-rel.
DR Pfam; PF00462; Glutaredoxin; 1.
DR TIGRFAMs; TIGR00365; Glutaredox-rel; 1.
SQ SEQUENCE 173 AA; 19319 MW; 2DE24EE2A276D727 CRC64;

Query Match 80.0%; Score 36; DB 2; Length 173;
Best Local Similarity 77.8%; Pred. No. 67;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DTLEKLTNT 9
Db 73 DTLEKLVNS 81

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DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)	
DE	Similarities with sp P53331 Saccharomyces cerevisiae YGR276c RNH70	
DE	ribonuclease H.	
GN	ORFNames=KLLA0A10065g;	
OS	Kluyveromyces lactis NRRL Y-1140.	
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;	
OC	Saccharomycetales; Saccharomycetaceae; Kluyveromyces.	
OC	NCBI_TaxID=284590;	
RP	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=NRRL Y-1140;	
RG	Genolevures;	
RA	Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,	
RA	Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,	
RA	Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,	
RA	Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,	
RA	Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,	
RA	Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,	
RA	Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,	
RA	Kerstet A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,	
RA	Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,	
RA	Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,	
RA	Swennene D., Tekaja F., Wesolowski-Louvel M., Westhof E., Wirth B.,	
RA	Zenou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,	
RA	Bouchier C., Caudron B., ScarPELLI C., Gaillardin C., Weissenbach J.,	
RT	Wincker P., Souciet J.L.;	
RL	"Genome evolution in Yeasts.";	
RL	Nature 430:35-44 (2004).	
RP	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=NRRL Y-1140;	
RG	Genoscope;	
RA	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.	
RL	EMBL; CR382121; CAH03028.1; -;	
DR	GO; GO:0005622; C:intracellular; IEA.	
DR	GO; GO:0004527; F:exonuclease activity; IEA.	
DR	InterPro; IPR006055; Exonuclease.	
DR	Pfam; PF00929; Exonuc X-T; 1.	
DR	SMART; SM00479; EXOIII; 1.	
SQ	SEQUENCE 682 AA; 75993 MW; 1AED20DBF7F961A0 CRC64;	
Query Match	80.0%; Score 36; DB 2; Length 682;	
Best Local Similarity	77.8%; Pred. No. 2.6e+02;	
Matches	7; Conservative 1; Mismatches 1; Indels 0; Gaps	
Qy	1 DTLEKLTNT 9	
Db	218 ENLEKLTNT 226	
RESULT 13		
Q8MQK1		
ID	Q8MQK1 PRELIMINARY; PRT; 751 AA.	
AC	Q8MQK1;	
DT	01-OCT-2002 (TrEMBLrel. 22, Created)	
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)	
DE	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	LD08185P.	
GN	ORFNames=CG10971;	
OS	Drosophila melanogaster (Fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Ephydroidea; Drosophilidae; Drosophila.	
OC	NCBI_TaxID=7227;	
RP	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Berkely;	
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,	
RA	Champe M., Chavez C., Dorsett V., Dreenek D., Farfan D., Frise E.,	
RA	George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,	
RA	Miranda A., Mungall C.J., Nunoo J., Facle J., Paragas V., Park S.,	
RA	Fatel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,	
RA	Celniker S.;	

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY129439; AAM76181.1; -
 DR FlyBase: FBgn036309; CG10971.
 DR GO: GO:0003779; F:actin binding; IEA.
 DR InterPro: IPR002558; ILWEQ.
 DR Pfam: PF01608; I LWEQ; 1.
 DR PROSITE: PS0945; I LWEQ; 1.
 SQ SEQUENCE 751 AA; 85362 MW; 7EFBC7661CE8AA0 CRC64;

Query Match 80.0%; Score 36; DB 2; Length 751;
 Best Local Similarity 87.5%; Pred. No. 2.8e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTLEKLTN 8
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 Db 168 DTLEKLSN 175

RESULT 14
 Q92X30 PRELIMINARY; PRT; 772 AA.
 AC Q92X30;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Probable aldehyde oxidase and xanthine dehydrogenase family protein
 DE TRANSMEMBRANE
 GN ORFNames=SM20132;
 OS Rhizobium meliloti (sinorhizobium meliloti).
 OG Plasmid pSymB.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396508; PubMed=11481431; DOI=10.1073/pnas.161294698;
 RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
 RA Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie J.,
 RA Golding B., Puchler A.;
 RA "The complete sequence of the 1,693-kb pSymB megaplasmid from the N2-
 RT fixing endosymbiont sinorhizobium meliloti";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
 DR EMBL: AL51985; CAC48532.1; -
 DR PIR: D95858; D95858.
 DR HSP; Q46509; I LWB.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR InterPro: IPR000674; Aldxan_dh_bind.
 DR Pfam: PF01315; Ald_Xan_dh_C; 1.
 DR Pfam: PF02738; Ald_Xan_dh_C2; 1.
 KW Complete proteome; plasmid; Transmembrane.
 SQ SEQUENCE 772 AA; 83462 MW; 148E8377FF591CAA CRC64;

Query Match 80.0%; Score 36; DB 2; Length 772;
 Best Local Similarity 77.8%; Pred. No. 2.9e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DTLEKLTNT 9
 |||||:
 Db 27 DTLEKVTGT 35

RESULT 15
 Q86BS5 PRELIMINARY; PRT; 1087 AA.
 AC Q86BS5;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE CG10971-PB.

GN ORFNames=CG10971;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Frannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle B.J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacle B.J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
 RN (5)
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN (6)
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003540; AAF49884.1; -;
 DR FlyBase: FBgn0036309; CG10971.
 DR GO: GO:0003779; F:actin binding; IEA.
 DR GO: GO:0005543; F:phospholipid binding; IEA.
 DR InterPro: IPR011417; ANTH.
 DR InterPro: IPR001026; Epsin_N.
 DR InterPro: IPR002558; ILWEQ_N.
 DR InterPro: IPR008943; PI_bind_N.
 DR Pfam: PF07651; ANTH; 1.
 DR Pfam: PF01608; ILWEQ; 1.
 DR ProDom: PD011820; ILWEQ; 1.
 DR PROSITE: PS50942; ENTH; 1.
 DR PROSITE: PS50945; ILWEQ; 1.
 SQ SEQUENCE 1087 AA; 124298 MW; C83E709907DFE8E8 CRC64;

Query Match 80.0%; Score 36; DB 2; Length 1087;
 Best Local Similarity 87.5%; Pred. No. 4e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTLEKLTN 8
 Db 504 DTLEKLSN 511

Search completed: June 28, 2005, 21:23:58
 Job time : 57.1 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-28
Perfect score: 45
Sequence: 1 DTLEKLTNT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	158	1 W6WL18	E6 protein - human
2	39	86.7	158	2 S36561	E6 protein - human
3	38	84.4	553	1 A24299	mullerian inhibiti
4	36	80.0	173	2 T06730	hypothetical prote
5	36	80.0	772	2 D95858	probable aldehyde
6	35	77.8	266	2 C95072	hypothetical prote
7	35	77.8	271	2 A97940	hypothetical prote
8	35	77.8	303	2 B69160	mevalonate kinase
9	35	77.8	327	2 D95408	probable oxidoredu
10	35	77.8	603	2 S47917	rab geranylgeranyl
11	34	75.6	149	1 W6WL31	E6 protein - human
12	34	75.6	158	2 AG1530	transcription regu
13	34	75.6	160	2 C55699	major pollen aller
14	34	75.6	160	2 F55699	major pollen aller
15	34	75.6	160	2 I55699	major pollen aller
16	34	75.6	160	2 G55699	major pollen aller
17	34	75.6	160	2 G55699	major pollen aller
18	34	75.6	160	2 D55699	major pollen aller
19	34	75.6	160	2 S05376	major pollen aller
20	34	75.6	260	2 E70578	probable wagl pro
21	34	75.6	447	2 S37844	molybdopterin-conv
22	34	75.6	2802	2 F97686	cyclic beta-(1-2)
23	34	75.6	2831	2 A12911	beta (1-2) glucan
24	33	73.3	185	2 AH3399	hypothetical cytos
25	33	73.3	234	2 T31753	hypothetical prote
26	33	73.3	454	2 G35047	aspartate kinase
27	33	73.3	454	2 F97918	aspartate kinase
28	33	73.3	1383	2 T06091	hypothetical prote
29	33	73.3	2186	2 H89960	hypothetical prote

fatty-acid synthas
E6 protein - human
gene 1 sc2 protein
major pollen aller
major pollen aller
major pollen aller
major pollen aller
gene 1-sci protein
major pollen aller
ABC transporter (s
ABC transporter pe
probable replicati
histidyl-cRNA synt
lipoprotein homolo
probable cytosolic
hypothetical prote
hypothetical prote

ALIGNMENTS

RESULT 1

W6WL18
E6 protein - human papillomavirus type 18
C:Species: human papillomavirus type 18
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: A26165; G26251
R:Seedorf, K.; Olterodorf, T.; Kraemmer, G.; Roewekamp, W.
EMBO J. 6, 139-144, 1987
A:Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)
A:Reference number: A91068; MUID:87218459; PMID:3034571
A:Accession: A26165
A:Molecule type: DNA
A:Residues: 1-158 <SEE>
A:Cross-references: UNIPROT:P06463; GB:X04773; NID:G60876; PIDN:CAA28466.1; PID:G60877
R:Coile, S.T.; Danos, O.
J. Mol. Biol. 193, 599-608, 1987
A:Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 18
A:Reference number: A92937; MUID:87283882; PMID:3039146
A:Accession: G26251
A:Molecule type: DNA
A:Residues: 1-158 <COL>
A:Cross-references: GB:X05015; NID:G60975; PIDN:CAA28664.1; PID:G60976
R:Matlashewski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pim, D.; Crawford, L.
J. Gen. Virol. 67, 1909-1916, 1986
A:Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the p
A:Reference number: A92791; MUID:86306665; PMID:3018129
A:Contents: annotation; identification of the protein
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:32-68/Region: zinc finger CCCC motif
F:105-141/Region: zinc finger CCCC motif

Query Match 100.0%; Score 45; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTLEKLTNT 9
| | | | |
Db 88 DTLEKLTNT 96

RESULT 2

S36561
E6 protein - human papillomavirus type 45
C:Species: human papillomavirus type 45
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36561
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36561

A:Molecule type: DNA
A:Residues: 1-158
A:Cross-references: UNIPROT:P21735; EMBL:X74479; NID:G397022; PIDN:CAAS2573.1; PID:G3970
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 86.7%; Score 39; DB 2; Length 158;
Best Local Similarity 77.8%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 2

QY 1 DTLEKLTNT 9
|||:||||
Db 88 ETELEKLTNT 96
|||:||||

RESULT 3
A42499
mullerian inhibiting factor precursor - rat
N:Alternate names: anti-mullerian hormone; mullerian inhibiting substance (MIS)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A42499
R:Haq, C.; Lee, M.M.; Tizard, R.; Wysk, M.; DeMarinis, J.; Donahoe, P.K.; Cate, R.L.
Genomics 12, 665-669, 1992
A:Title: Isolation of the rat gene for Mullerian inhibiting substance.
A:Reference number: A42499; MUID:92241861; PMID:1572639
A:Accession: A42499
A:Molecule type: DNA
A:Residues: 1-553 <HAQ>
A:Cross-references: UNIPROT:P49000; GB:S98336; NID:G248896; PIDN:AAB22104.1; PID:G248897
A>Note: sequence extracted from NCBI backbone (NCBIN:98336, NCBIP:98343)
C:Superfamily: inhibin
C:Keywords: cytotoxin; glycoprotein; gonadal differentiation; testis

Query Match 84.4%; Score 38; DB 1; Length 553;
Best Local Similarity 77.8%; Pred. No. 10; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 2

QY 1 DTLEKLTNT 9
|||:||||
Db 23 DTVEELTNT 31
|||:||||

RESULT 4
T06730
hypothetical protein F28P10.120 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06730
R:Quetier, F.; Cholsne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artigou
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15793
A:Accession: T06730
A:Molecule type: DNA
A:Residues: 1-173 <QUE>
A:Cross-references: UNIPROT:Q9SV38; EMBL:AL049655; GSPDB:GN00061; ATSP:F28P10.120
A:Experimental source: cultivar Columbia; BAC clone F28P10
C:Genetics:
A:Gene: ATSP:F28P10.120
A:Map position: 3
C:Superfamily: conserved hypothetical protein HI1165

Query Match 80.0%; Score 36; DB 2; Length 173;
Best Local Similarity 77.8%; Pred. No. 7.6; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1

QY 1 DTLEKLTNT 9
|||:||||
Db 73 DTLEKLVNS 81
|||:||||

RESULT 5
D95858
hypothetical protein ABC-SBP [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

probable aldehyde oxidase and xanthine dehydrogenase family protein [imported] - Sinorhiz
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: D95858
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmaster, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endos
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: D95858
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-772 <KUR>
A:Cross-references: UNIPROT:Q92X30; GB:AL591985; PIDN:CAC48532.1; PID:G15140004; GSPDB:G
A:Experimental source: strain 1021, megaplasmid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMB20132
A:Genome: Plasmid
C:Superfamily: carbon monoxide dehydrogenase molybdoprotein

Query Match 80.0%; Score 36; DB 2; Length 772;
Best Local Similarity 77.8%; Pred. No. 38; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1

QY 1 DTLEKLTNT 9
|||:||||
Db 27 DTLEKVTGT 35
|||:||||

RESULT 6
C95072
hypothetical protein SP0620 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: C95072
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I.
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: C95072
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <KUR>
A:Cross-references: UNIPROT:Q97S05; GB:AE005672; PIDN:AAK74772.1; PID:G14972096; GSPDB:G
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0620

Query Match 77.8%; Score 35; DB 2; Length 266;
Best Local Similarity 87.5%; Pred. No. 19; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1

QY 2 TLEKLTNT 9
|||:||||
Db 245 TLEKLSNT 252
|||:||||

RESULT 7
A97940
hypothetical protein ABC-SBP [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C:Accession: A97940
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
 r, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A:Reference number: A97872; MUID:21429245; PMID:11544234
 A:Accession: A97940
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-271 <KUR>
 A:Cross-references: UNIPROT:Q8CWT0; GB:AE007317; PIDN:AAK99349.1; PID:g15458121; GSPDB:G
 C:Genetics:
 A:Gene: ABC-SBP

Query Match 77.8%; Score 35; DB 2; Length 271;
 Best Local Similarity 87.5%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLEKLTNT 9
 |||||:
 Db 250 TLEKLSNT 257

RESULT 8
 B69160
 mevalonate kinase - Methanobacterium thermoautotrophicum (strain Delta H)
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
 A:Accession: B69160
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
 A:Reference number: A69000; MUID:98037514; PMID:9371463
 A:Accession: B69160
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-303 <MTH>
 A:Cross-references: UNIPROT:Q50559; GB:AE000796; GB:AE000666; NID:g2621057; PIDN:AAB8455
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH46
 A:Start codon: TTG
 C:Superfamily: Mevalonate kinase/phosphomevalonate kinase

Query Match 77.8%; Score 35; DB 2; Length 303;
 Best Local Similarity 66.7%; Pred. No. 22;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DTLEKLTNT 9
 |||||:
 Db 203 DTVESITNT 211

RESULT 9
 D95408
 probable oxidoreductase Sma2157 [imported] - Sinorhizobium meliloti (strain 1021) magap1
 C:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 16-Aug-2004
 A:Accession: D95408
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
 ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: D95408
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-327 <KUR>
 A:Cross-references: UNIPROT:Q92XR9; GB:AE006469; PIDN:AAK65830.1; PID:g14524335; GSPDB:G

A:Experimental source: strain 1021, megaplasmid pSymA
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler,
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Pederspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kies, E.; Komp, C.; Lelaure,
 hebaull, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: Sma2157
 A:Genome: plasmid
 C:Superfamily: Aldehyde reductase

Query Match 77.8%; Score 35; DB 2; Length 327;
 Best Local Similarity 66.7%; Pred. No. 24;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DTLEKLTNT 9
 |||||:
 Db 170 DTMERLVNT 178

RESULT 10
 S47917
 rab geranylgeranyl transferase component A - Yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein 06676; protein YOR370C
 C:Species: Saccharomyces cerevisiae
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 A:Accession: S47917; S48222; S27431; S67282; S43545
 R:Fujimura, K.; Tanaka, K.; Nakano, A.; Toh-e, A.
 J. Biol. Chem. 269, 9205-9212, 1994
 A:Title: The Saccharomyces cerevisiae MS14 gene encodes the yeast counterpart of componer
 A:Reference number: S47917; MUID:94179341; PMID:8132658
 A:Accession: S47917
 A:Molecule type: DNA
 A:Residues: 1-603 <FUJ>
 A:Cross-references: UNIPROT:P32864; EMBL:D26441; NID:g4522240; PIDN:BAA05460.1; PID:g45222
 R:Ragnini, A.; Teply, R.; Waldherr, M.; Voskova, A.; Schweyen, R.J.
 Curr. Genet. 26, 308-314, 1994
 A:Title: The yeast protein Mrsp6, a homologue of the rabGDI and human choroideaemia prot
 A:Reference number: S48222; MUID:95188267; PMID:7882424
 A:Accession: S48222
 A:Molecule type: DNA
 A:Residues: 1-299, 'P', 301-603 <RAG>
 A:Cross-references: EMBL:X70339; NID:g473150; PIDN:CAA49804.1; PID:g473151
 R:Waldherr, M.; Voskova, A.; Schweyen, R.J.
 submitted to the EMBL Data Library, April 1992
 A:Reference number: S27431
 A:Accession: S27431
 A:Molecule type: DNA
 A:Residues: 'MIFPRV', 138-299, 'P', 301-594 <WAL>
 A:Cross-references: EMBL:M90844; NID:g171989; PID:g171990
 R:Delius, H.; Hebling, U.; Hofmann, B.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67261
 A:Accession: S67261
 A:Molecule type: DNA
 A:Residues: 1-603
 A:Cross-references: EMBL:D75278; NID:g1420799; PID:e252194; PID:g1420800; MIPS:YOR370C
 A:Experimental source: strain S288C
 C:Genetics:
 A:Gene: SGD:MR56; MS14
 A:Cross-references: SGD:S0005897; MIPS:YOR370C
 A:Map position: 15R
 C:Keywords: transmembrane protein
 P:49-65/Domain: transmembrane #status predicted <TM>

Query Match 77.8%; Score 35; DB 2; Length 603;
 Best Local Similarity 77.8%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DTLEKLTNT 9
| | | | |
Db 171 DCFEKLNT 179

RESULT 11
W6WL31
C:Species: human papillomavirus type 31
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: A32444
R:Goldsbrough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virolgy 171, 306-311, 1989
A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated
A:Reference number: A94398; MUID:89299478; PMID:2545036
A:Accession: A32444
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-149 <GL>
A:Cross-references: UNIPROT:P17386; GB:J04353; NID:G333048; PIDN:AAA46950.1; PID:G459916
C:Comment: This protein may be involved in the oncogenic potential of this virus.
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 75.6%; Score 34; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLEKLTN 8
| | | | |
Db 87 TLEKLTN 93

RESULT 12
AG1530
Transcription regulator (EbsC from Enterococcus faecalis) homolog lin0783 [imported] - I
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AG1530
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A:Authors: Kref, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1530
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-158 <GLA>
A:Cross-references: UNIPROT:Q92DN0; GB:AL592022; PIDN:CAC96015.1; PID:G16413234; GSPDB:G
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lin0783
C:Superfamily: conserved hypothetical protein HI1434

Query Match 75.6%; Score 34; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTLEKLT 7
| | | | |
Db 90 DTLEKLT 96

RESULT 13
C55699
major pollen allergen Bet v 1d/h - European white birch
C:Species: Betula pendula (European white birch)

C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C:Accession: C55699; S41901; S41898
R:Swoboda, I.; Jilek, A.; Ferreira, F.; Engel, E.; Hoffmann-Sommergruber, K.; Scheiner, C
ch, M.
J. Biol. Chem. 270, 2607-2613, 1995
A:Title: Isoforms of Bet v 1, the major birch pollen allergen, analyzed by liquid chromat
A:Reference number: A55699; MUID:95155322; PMID:7852325
A:Accession: C55699
A:Molecule type: mRNA
A:Residues: 1-160 <SWO>
A:Cross-references: UNIPROT:P43177; EMBL:X77266; NID:G452731; PIDN:CAAS4482.1; PID:G45273
A:Note: the source is designated as Betula verrucosa
R:Swoboda, I.; Jilek, A.; Ferreira, F.; Vicente, O.; Hoffmann-Sommergruber, K.; Heberle-B
submitted to the EMBL Data Library, January 1994
A:Reference number: S41896
A:Accession: S41901
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-160 <SW2>
A:Cross-references: EMBL:X77270; NID:G452737; PIDN:CAA54486.1; PID:G452738
A:Note: the source is designated as Betula verrucosa
C:Superfamily: pathogenesis-related protein
C:Keywords: pollen
F:2-160/Product: major pollen allergen Bet v 1d/h #status experimental <MAT>
F:83/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 75.6%; Score 34; DB 2; Length 160;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTLEKLTN 8
| | | | |
Db 94 DTLEKISN 101

RESULT 14
F55699
major pollen allergen Bet v 1g - European white birch
C:Species: Betula pendula (European white birch)
C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C:Accession: F55699; S41896
R:Swoboda, I.; Jilek, A.; Ferreira, F.; Engel, E.; Hoffmann-Sommergruber, K.; Scheiner, C
ch, M.
J. Biol. Chem. 270, 2607-2613, 1995
A:Title: Isoforms of Bet v 1, the major birch pollen allergen, analyzed by liquid chromat
A:Reference number: A55699; MUID:95155322; PMID:7852325
A:Accession: F55699
A:Molecule type: mRNA
A:Residues: 1-160 <SWO>
A:Cross-references: UNIPROT:P43180; EMBL:X77269; NID:G452727; PIDN:CAAS4485.1; PID:G45273
A:Note: the source is designated as Betula verrucosa
C:Superfamily: pathogenesis-related protein
C:Keywords: pollen
F:2-160/Product: major pollen allergen Bet v 1g #status experimental <MAT>
F:83/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 75.6%; Score 34; DB 2; Length 160;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTLEKLTN 8
| | | | |
Db 94 DTLEKISN 101

RESULT 15
I55699
major pollen allergen Bet v 1l - European white birch
C:Species: Betula pendula (European white birch)
C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C:Accession: I55699; S41904
R:Swoboda, I.; Jilek, A.; Ferreira, F.; Engel, E.; Hoffmann-Sommergruber, K.; Scheiner, C
ch, M.

J. Biol. Chem. 270, 2607-2613, 1995
 A;Title: Isoforms of Bet v 1, the major birch pollen allergen, analyzed by liquid chroma
 A;Reference number: A55699; MUID:95155322; PMID:7852325
 A;Accession: I55699
 A;Molecule type: mRNA
 A;Residues: 1-160 <SWO>
 A;Cross-references: UNIPROT:P43185; EMBL:X77273; NID:G452743; PIDN:CAA54489.1; PID:G4527
 A;Note: the source is designated as Betula verrucosa
 C;Superfamily: pathogenesis-related protein
 C;Keywords: pollen
 F;2-160/Product: major pollen allergen Bet v 1l #status experimental <MAT>
 F;83/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 75.6%; Score 34; DB 2; Length 160;
 Best Local Similarity 75.0%; Pred. NO. 18;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTLEKLTN 8
 Db 94 DTLEKISN 101

Search completed: June 28, 2005, 21:27:43
 Job time : 12.15 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-27

Perfect score: 45

Sequence: 1 FAFKDLFVV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	45	100.0	158	1	VE6_HPV18	P06463 human papillomavirus type 18
2	45	100.0	158	2	Q9QNP8	Q9QNP8 human papillomavirus type 18
3	44	97.8	158	2	Q9V4Y4	Q9V4Y4 homo sapiens
4	44	97.8	158	2	O10608	O10608 human papillomavirus type 18
5	39	86.7	157	2	Q9WHG0	Q9WHG0 human papillomavirus type 18
6	39	86.7	158	1	VE6_HPV70	P50804 human papillomavirus type 18
7	39	86.7	160	2	Q81964	Q81964 human papillomavirus type 18
8	38	84.4	1192	2	Q7XE21	Q7XE21 oryza sativa
9	37	82.2	144	1	VE6_HPV54	Q81018 human papillomavirus type 18
10	37	82.2	158	1	VE6_HPV39	P24835 human papillomavirus type 18
11	37	82.2	383	2	Q81370	Q81370 plasmodium
12	36	80.0	59	2	Q64MQ3	Q64MQ3 bacteroides
13	36	80.0	90	2	Q80884	Q80884 human papillomavirus type 18
14	36	80.0	158	1	VE6_HPV45	P21735 human papillomavirus type 18
15	36	80.0	225	2	Q815N4	Q815N4 bacillus cereus
16	36	80.0	225	2	Q81XA9	Q81XA9 bacillus anthracis
17	36	80.0	260	2	Q7VM54	Q7VM54 haemophilus influenzae
18	36	80.0	389	2	Q9FXT7	Q9FXT7 chlamydomonas reinhardtii
19	36	80.0	697	2	Q9TIV5	Q9TIV5 ellisia nyc
20	36	80.0	953	1	Q8YX84	Q8YX84 anabaena sp
21	35	77.8	153	1	VE6_HPV2A	P25484 human papillomavirus type 18
22	35	77.8	154	1	VE6_HPV07	P36800 human papillomavirus type 18
23	35	77.8	154	1	VE6_HPV40	P36812 human papillomavirus type 18
24	35	77.8	285	2	Q98IU4	Q98IU4 rhizobium l
25	35	77.8	327	2	Q6F739	Q6F739 acinetobact
26	35	77.8	462	2	Q7USJ8	Q7USJ8 rhodospirillum rubrum
27	35	77.8	494	2	O85YQ6	O85YQ6 euphorbia i
28	35	77.8	615	2	Q9THK5	Q9THK5 reidia sp
29	35	77.8	675	1	NUSM_ACACA	Q37372 acanthamoeba castellanii
30	35	77.8	1155	2	Q6RJU3	Q6RJU3 homo sapiens
31	35	77.8	1165	2	Q6RJU1	Q6RJU1 homo sapiens

RESULT 1

ID	VE6 HPV18	STANDARD	PRT	158 AA
AC	P06463			
DT	01-JAN-1988	(Rel. 06, Created)		
DT	01-JAN-1988	(Rel. 06, Last sequence update)		
DT	05-JUL-2004	(Rel. 44, Last annotation update)		
DE	E6 protein.			
GN	Name=E6			
OS	Human papillomavirus type 18.			
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;			
OC	Papillomavirus.			
OX	NCBI_TaxID=10582			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87283882; PubMed=3039146;			
RA	Cole S.T., Danos O.;			
RT	"Nucleotide sequence and comparative analysis of the human papillomavirus type 18 genome. Phylogeny of papillomaviruses and repeated structure of the E6 and E7 gene products.";			
RL	J. Mol. Biol. 193:599-608(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86306665; PubMed=3018129;			
RA	Matlahewski G., Banks L., Wu-Liao J., Spence P., Pim D., Crawford L.;			
RT	"The expression of human papillomavirus type 18 E6 protein in bacteria and the production of anti-E6 antibodies.";			
RL	J. Gen. Virol. 67:1909-1916(1986).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88188247; PubMed=2833614;			
RA	Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M., Sugimura T.;			
RT	"Nucleotide sequences of cDNAs for human papillomavirus type 18 transcripts in HeLa cells.";			
RL	J. Virol. 62:1640-1646(1988).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87053870; PubMed=3023067;			
RA	Schneider-Gadick A., Schwarz E.;			
RT	"Different human cervical carcinoma cell lines show similar transcription patterns of human papillomavirus type 18 early genes.";			
RL	EMBO J. 5:2285-2292(1986).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87218459; PubMed=3034571;			
RA	Seedorf K., Oltersdorf T., Kraemer G., Roewekamp W.;			
RT	"Identification of early proteins of the human papilloma virus type 16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells.";			
RL	EMBO J. 6:139-144(1987).			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87218459; PubMed=3034571;			
RA	Seedorf K., Oltersdorf T., Kraemer G., Roewekamp W.;			
RT	"Identification of early proteins of the human papilloma virus type 16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells.";			
RL	EMBO J. 6:139-144(1987).			
RN	[6]			
RP	ZINC-BINDING.			
RX	Q37372 acanthamoeba castellanii			
RA	MEDLINE=89385606; PubMed=2550872;			
RX	Grossman S.R., Laimins L.A.;			

Q6RJU2 homo sapien
Q6RJU5 homo sapien
Q9P2F6 homo sapien
Q7RDA4 plasmodium
Q919C4 human papil
P22158 human papil
Q93309 tachinus lu
O99312 drocephylia
O99314 amphichroum
O99315 proteinus s
O99316 megathrus
O99329 oncholeues
Q85X7 human papil
Q61JH6 drosophila

ALIGNMENTS

RT "E6 protein of human papillomavirus type 18 binds zinc.";

RL Oncogene 4:1089-1093(1989).

RN [7]

RP INTERACTION WITH FBLN1, AND INHIBITION OF E6-MEDIATED TRANSFORMATION.

RX MEDLINE=22189366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;

RA Du M., Fan X., Hong E., Chen J.J.;

RL "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";

RL Biochem. Biophys. Res. Commun. 296:962-969(2002).

CC -!- FUNCTION: This protein has transforming activity in vitro.

CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double stranded DNA (in vitro).

CC -!- SUBUNIT: Interacts with FBLN1.

CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.

CC -----

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CC -----

DR EMBL; X04354; CAA27879.1; -

DR EMBL; X05015; CAA28664.1; -

DR EMBL; M20325; AAA99514.1; -

DR EMBL; M26798; AAA46946.1; -

DR EMBL; X04773; CAA28466.1; -

DR EMBL; A06324; CAA00539.1; -

DR EMBL; A06328; CAA00542.1; -

DR PIR; A26165; W6WL18.

DR InterPro: IPR001334; E6.

DR Pfam; PF00518; E6; 1.

KW DNA-binding; Early protein; Nuclear protein; Oncogene; Zinc-finger.

FT ZN FING 32 68

FT ZN FING 105 141

FT ZN FING 105 141

FT CONFLICT 22 22 N -> S (in Ref. 4).

SQ SEQUENCE 158 AA; 18871 MW; 5BCF13CF43D157FA CRC64;

Query Match 100.0%; Score 45; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.25;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9

Db 47 FAFKDLFVV 55

RESULT 2

Q9QNP8 PRELIMINARY; PRT; 158 AA.

AC Q9QNP8;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE E6 protein.

OS Human papillomavirus type 18.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10582;

RN [1]

RP SEQUENCE FROM N.A.

RA Laesri M., Gul'ko L., Vinokurova S., Kisseljeva N., Veiko V.,

RA Kisseljev F.;

RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and

RT Transformation Potential of E7 Gene and its Mutants.";

RL Virus Genes 182:139-149(1999).

RN [2]

RP SEQUENCE FROM N.A.

RA Veiko V.P.;

RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; Y18491; CAB53096.1; -

DR GO; GO:0042025; C:host cell nucleus; IEA.

DR GO; GO:0003677; F:DNA binding; IEA.

DR InterPro: IPR001334; E6.

DR Pfam; PF00518; E6; 1.

SQ SEQUENCE 158 AA; 18886 MW; 5BCF13CF43D407AF CRC64;

Query Match 100.0%; Score 45; DB 2; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.25;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9

Db 47 FAFKDLFVV 55

RESULT 3

Q9Y4Y4 PRELIMINARY; PRT; 158 AA.

AC Q9Y4Y4;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE E6 protein.

GN Name=HPV45 E6;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Carnivora; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Sastre-Garau X., Favre M., Couturier J., Orth G.;

RT "Distinct patterns of alteration of myc genes associated with

RT integration of human papillomavirus type 16 oe type 45 in two genital

RT tumors.";

RL J. Gen. Virol. 81:198-199(2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Favre M.G.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ242956; CAB44706.1; -

DR GO; GO:0042025; C:host cell nucleus; IEA.

DR GO; GO:0003677; F:DNA binding; IEA.

DR InterPro: IPR001334; E6.

DR Pfam; PF00518; E6; 1.

SQ SEQUENCE 158 AA; 18914 MW; A61AEF98390AEEB3 CRC64;

Query Match 97.8%; Score 44; DB 2; Length 158;

Best Local Similarity 88.9%; Pred. No. 0.41;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9

Db 47 FAFKDLFVV 55

RESULT 4

O10608 PRELIMINARY; PRT; 158 AA.

AC O10608;

DT 01-JUL-1997 (TrEMBLrel. 04, Created)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Oncoprotein E6.

OS Human papillomavirus type 45.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10593;

RN [1]

RP SEQUENCE FROM N.A.

RA Sastre-Garau X., Favre M., Couturier J., Orth G.;

RT "Distinct patterns of alteration of myc genes associated with

RT integration of HPV16 or HPV45 DNA in two genital tumors.";

RL J. Gen. Virol. 0:0-0(0).

RN [2]

RP SEQUENCE FROM N.A.

```

RA Favre M.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y13218; CAA73660.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 18914 MW; A61AEF98390AE8B3 CRC64;

Query Match
Best Local Similarity 97.8%; Score 44; DB 2; Length 158;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9
DB 47 FAFKDLFIV 55

RESULT 5
Q9WHG0 PRELIMINARY; PRT; 157 AA.
AC Q9WHG0;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative transforming protein E6.
OS Human papillomavirus candHPV85.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus; Human papillomavirus unidentified type.
OX NCBI_TaxID=151757;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20047972; PubMed=10580054;
RX Chow V.T., Leong P.W.;
RT "Complete nucleotide sequence, genomic organization and phylogenetic
analysis of a novel genital human papillomavirus type, HLT7474-S.";
RL J. Gen. Virol. 80:2923-2929 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Chow V.T.K., Leong W.F.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF131950; AAD24181.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 157 AA; 18450 MW; 1B154BA2C49EED7 CRC64;

Query Match
Best Local Similarity 86.7%; Score 39; DB 2; Length 157;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9
DB 47 FAFADLFVV 55

RESULT 6
VB6_HPV70 STANDARD; PRT; 158 AA.
AC P50804;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 70.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=39457;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96249586; PubMed=8815087;

Forslund O., Hansson B.G.;
RT "Human papillomavirus type 70 genome cloned from overlapping PCR
products: complete nucleotide sequence and genomic organization.";
RL J. Clin. Microbiol. 34:802-809 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97060129; PubMed=8904450;
RA Longuet M., Beaudenon S., Orth G.;
RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70,
related to the potentially oncogenic HPV39.";
RL J. Clin. Microbiol. 34:738-744 (1996).
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double
stranded DNA (in vitro).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
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CC -----
DR EMBL; U21941; AAC54850.1; -.
DR EMBL; U22461; AAC54880.1; -.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW DNA-binding; Early protein; Nuclear protein; Zinc-finger.
FT ZN FING 32 68
FT ZN FING 105 141
FT ZN FING 100 100 N -> D (in Ref. 2).
FT CONFLICT 100 100 68610800D923D6DE CRC64;
SQ SEQUENCE 158 AA; 18617 MW; 68610800D923D6DE CRC64;

Query Match
Best Local Similarity 86.7%; Score 39; DB 1; Length 158;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9
DB 47 FAFSDLFIV 55

RESULT 7
Q81964 PRELIMINARY; PRT; 160 AA.
AC Q81964;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ORF putative E6 protein.
GN Name=ORF putative E6;
OS Human papillomavirus type 59.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=37115;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94303229; PubMed=8030272;
RA Rho J., Roy-Burman A., Kim H., de Villiers E.M., Matsukura T.,
RA Choe J.;
RT "Nucleotide sequence and phylogenetic classification of human
papillomavirus type 59.";
RL Virology 203:158-161 (1994).
DR EMBL; X77858; CAA54849.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 160 AA; 19042 MW; B060020AFD530A16 CRC64;

Query Match
Best Local Similarity 86.7%; Score 39; DB 2; Length 160;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 FAFKDLFV 9
|||:|||||
Db 47 FAFNDLFV 55

RESULT 8
QYX21 PRELIMINARY; PRT; 1192 AA.
AC Q7XE21
DT 01-OCT-2003 (TREMELrel. 25, Created)
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Putative receptor-like protein kinase.
GN ORFNames=QJNBA0046P18.9;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Wang R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
DR EMBL; AE017098; AAP53969.1; -.
DR HSP; F35278; IHUQ.
DR Gramene; Q7XE21; -.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0015031; P:protein transport; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p...); IEA.
DR InterPro; IPR008985; ConA_like_lect_g1.
DR InterPro; IPR003579; GTPase Rab.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000985; Lectin_legA.
DR InterPro; IPR001220; Lectin_legB.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001806; Ras_trnsfrmg.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002078; Sig54_interact.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00138; Lectin_legA; 1.
DR Pfam; PF00139; Lectin_legB; 1.
DR Pfam; PF00071; Ras; 1.
DR ProDom; PD000671; Lectin_legA; 1.
DR ProDom; PD000711; Lectin_legB; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00175; RAB; 1.
DR TIGRfams; TIGR00231; small_GTP; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00675; SIGMA54_INTERACT_1; 1.
KW ATP-binding; GTP-binding; Kinase; Receptor; Transferase.
SQ SEQUENCE 1192 AA; 12283 MW; 198812108358ABDD CRC64;

Query Match 84.4%; Score 38; DB 2; Length 1192;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAFKDLFV 8
|||:|||||
Db 850 FAFKDLFV 857

RESULT 9
QYX21 STANDARD; PRT; 144 AA.
AC Q81018;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 54.
OS Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=37113;
RN [1]
RP SEQUENCE FROM N.A.
RA Delius H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double stranded DNA (in vitro).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC EMBL; U37488; AAA79187.1; -.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW DNA-binding; Early protein; Nuclear protein; Zinc-finger.
FT ZN_FING 32 68
FT ZN_FING 105 141
SQ SEQUENCE 144 AA; 17132 MW; BD6F4F0BD1D0F83C CRC64;

Query Match 82.2%; Score 37; DB 1; Length 144;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFKDLFV 9
|||:|||||
Db 47 FOYKDLFV 55

RESULT 10
QYX21 STANDARD; PRT; 158 AA.
AC P24835;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 39.
OS Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10588;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91135017; PubMed=1847266;
RA Volpers C., Strebeck R.E.;
RT "Genome organization and nucleotide sequence of human papillomavirus type 39.";
RL Virology 181:419-423(1991).
CC -!- FUNCTION: This protein may be involved in the oncogenic potential of this virus (cervical neoplasia-associated virus).
```

Qy 1 FAFKDLFV 9
| : | | | |
Db 284 FSEKDLFFV 292

```
ID VE6 HPV45 STANDARD; PRT; 158 AA.
AC P21735;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 45.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10593;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94265501; PubMed=8205938;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
[2]
RP SEQUENCE FROM N.A.
RA Kaplan J.B., Burk R.D.;
RL Submitted (AUG-1990) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This protein has transforming activity in vitro.
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double
CC stranded DNA (in vitro).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X74479; CAA52573.1; -.
DR EMBL; M38198; AAA46973.1; -.
DR PIR; S36561; S36561.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR DNA-binding; Early protein; Nuclear protein; Oncogene; Zinc-finger.
FT ZN_FING 32 68
FT ZN_FING 105 141
FT ZN_FING 105 141
FT CONFLICT 10 10 R -> P (in Ref. 2).
FT CONFLICT 30 30 I -> N (in Ref. 2).
FT CONFLICT 118 118 R -> A (in Ref. 2).
SQ SEQUENCE 158 AA; 18997 MW; FICF10DD33AA4C3E CRC64;

Query Match 80.0%; Score 36; DB 1; Length 158;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9
Db 47 FAFKDLCLIV 55

RESULT 15
Q815N4 PRELIMINARY; PRT; 225 AA.
AC Q815N4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Two-component response regulator.
GN OrderedLocusNames=Bc5107;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
```

```
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyripides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
CC -!- SIMILARITY: Contains 1 response regulatory domain.
DR EMBL; AE017014; AAP11976.1; -.
DR HSPF; Q9WXY0; 1P2F.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. .; IEA.
DR InterPro; IPR009059; bi_resp_regltr_C.
DR InterPro; IPR011006; CheY_like.
DR InterPro; IPR001789; Response_reg.
DR InterPro; IPR001867; Trans_reg_C.
DR Pfam; PF00072; Response_reg; 1.
DR Pfam; PF00486; Trans_reg_C; 1.
DR ProDom; PD000039; Response_reg; 1.
DR ProDom; PD000329; Trans_reg_C; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS01110; RESPONSE REGULATORY; 1.
DR Complete proteome; DNA-binding; Phosphorylation; Sensory transduction;
KW Transcription; Transcription regulation.
SQ SEQUENCE 225 AA; 25960 MW; A427FC9EC803BE51 CRC64;

Query Match 80.0%; Score 36; DB 2; Length 225;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFKDLFV 8
Db 130 FQFKDLFV 137

Search completed: June 28, 2005, 21:23:56
Job time : 56.1 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-27

Perfect score: 45

Sequence: 1 FAFKDLFVV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	158	1 W6WL18	E6 protein - human
2	37	82.2	158	1 W6WL39	E6 protein - human
3	36	80.0	158	2 S36561	E6 protein - human
4	36	80.0	953	2 A11972	hypothetical prote
5	35	77.8	154	2 S36555	E6 protein - human
6	35	77.8	154	2 S36584	E6 protein - human
7	35	77.8	159	1 S15614	E6 protein - human
8	35	77.8	675	2 S3831	NADH2 dehydrogenas
9	35	77.8	1194	2 C39436	KIAA1391 protein (
10	34	75.6	153	1 S15621	E6 protein - human
11	34	75.6	353	2 T83337	genitaisate 1,2-diox
12	34	75.6	669	2 T08960	serine/threonine-s
13	33	73.3	150	1 W6WL44	E6 protein - human
14	33	73.3	155	1 W6WL43	E6 protein - human
15	33	73.3	158	1 W6WL43	protein E6 - human
16	33	73.3	656	2 A96724	hypothetical prote
17	33	73.3	666	2 H96723	hypothetical prote
18	32	71.1	153	2 A71893	hypothetical prote
19	32	71.1	185	2 C96808	protein P28K19.4 (
20	32	71.1	301	2 S11132	ADP,ATP carrier pr
21	32	71.1	313	2 T32685	hypothetical prote
22	32	71.1	317	2 T32857	hypothetical prote
23	32	71.1	342	2 F91007	probable genitaisate
24	32	71.1	342	2 H5851	probable 1,2-dioxy
25	32	71.1	347	2 T02669	hypothetical prote
26	32	71.1	379	2 T04608	ADP,ATP carrier pr
27	32	71.1	379	2 S21313	ADP,ATP carrier pr
28	32	71.1	382	2 S33630	ADP,ATP carrier pr
29	32	71.1	385	1 S29852	ADP,ATP carrier pr

30 32 71.1 386 2 S17917 ADP,ATP carrier pr
31 32 71.1 386 2 S21974 ADP,ATP carrier pr
32 32 71.1 386 2 S14874 ADP,ATP carrier pr
33 32 71.1 386 2 T09709 ADP,ATP carrier pr
34 32 71.1 387 2 S16568 ADP,ATP carrier pr
35 32 71.1 387 2 S14876 ADP,ATP carrier pr
36 32 71.1 571 1 H65169 probable transport
37 32 71.1 571 2 D91206 probable cotranspo
38 32 71.1 571 2 F86052 probable cotranspo
39 32 71.1 2406 2 A54148 odz protein - fru
40 32 71.1 2515 2 S47008 tenascin-like prot
41 31 68.9 113 2 T14976 hypothetical prote
42 31 68.9 126 2 B59104 hypothetical prote
43 31 68.9 149 1 W6WL33 E6 protein - human
44 31 68.9 263 2 A70244 hypothetical prote
45 31 68.9 275 2 A56641 probable membrane

ALIGNMENTS

RESULT 1

W6WL18

E6 protein - human papillomavirus type 18

C:Species: human papillomavirus type 18

C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004

C:Accession: A26165; G26251

R:Seedorf, K.; Olteradorf, T.; Kraemmer, G.; Roewekamp, W.

EMBO J. 6, 139-144, 1987

A:Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)

A:Reference number: A91068; MUID:87218459; PMID:3034571

A:Accession: A26165

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P06463; GB:X04773; NID:G60876; PIDN:CAA28466.1; PID:G60877

R:Colte, S.T.; Danos, O.

J. Mol. Biol. 193, 599-608, 1987

A:Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 18

A:Reference number: A92937; MUID:87283882; PMID:3039146

A:Accession: G26251

A:Molecule type: DNA

A:Residues: 1-158 <COL>

A:Cross-references: GB:X05015; NID:G60975; PIDN:CAA28664.1; PID:G60976

R:Matlashewski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pim, D.; Crawford, L.

J. Gen. Virol. 67, 1909-1916, 1986

A:Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the p

A:Reference number: A92791; MUID:86306665; PMID:3018129

A:Contents: annotation; identification of the protein

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; transforming protein; zinc finger

F:32-68/Region: zinc finger CCCC motif

F:105-141/Region: zinc finger CCCC motif

Query Match 100.0%; Score 45; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.053;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFKDLFVV 9

Db 47 FAFKDLFVV 55

RESULT 2

W6WL39

E6 protein - human papillomavirus type 39

C:Species: human papillomavirus type 39

C:Date: host Homo sapiens (man)

A:Note: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C:Accession: A38502

R:Volpers, C.; Strebeck, R.E.

Virology 181, 419-423, 1991

A:Title: Genome organization and nucleotide sequence of human papillomavirus type 39.

A:Reference number: A38502; MUID:91135017; PMID:1847266

A;Accession: A38502
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-158 <VOL>

C;Cross-references: UNIPROT:P24935; GB:M62849; EMBL:M38185; NID:g333245; PIDN:AAA47050.1
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;32-68/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif

Query Match 82.2%; Score 37; DB 1; Length 158;
Best Local Similarity 77.8%; Pred. No. 2.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FAFKDLFVY 9
Db 47 FAFSDLYVY 55
|||||:|

RESULT 3

E6 protein - human papillomavirus type 45
C;Species: human papillomavirus type 45
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36561

R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.

A;Reference number: S36469
A;Accession: S36561
A;Molecule type: DNA
A;Residues: 1-158

C;Cross-references: UNIPROT:P21735; EMBL:X74479; NID:g397022; PIDN:CAAS2573.1; PID:g3970
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 80.0%; Score 36; DB 2; Length 158;
Best Local Similarity 77.8%; Pred. No. 4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FAFKDLFVY 9
Db 47 FAFKDLCLIV 55
|||||:|

RESULT 4

AH1972
hypothetical protein alr1331 [Imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH1972

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AH1972
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-953 <KUR>

C;Cross-references: UNIPROT:Q8YX84; GB:BA000019; PIDN:BA073288.1; PID:gl7130678; GSPDB:C
A;Experimental source: strain PCC 7120

C;Genetics:
A;Gene: alr1331

Query Match 80.0%; Score 36; DB 2; Length 953;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFKDLFV 8
Db 256 FAFKDLIVY 263
|||||:|

RESULT 5

S36555

E6 protein - human papillomavirus type 40
C;Species: human papillomavirus type 40

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36555

R;Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A;Description: Primer-directed sequencing of human papillomavirus types.

A;Reference number: S36469

A;Accession: S36555

A;Molecule type: DNA

A;Residues: 1-154

A;Cross-references: UNIPROT:P36812; EMBL:X74478; NID:g397014; PIDN:CAAS2567.1; PID:g6718

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 77.8%; Score 35; DB 2; Length 154;
Best Local Similarity 66.7%; Pred. No. 6.2;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFKDLFVY 9
Db 45 FAFRELYVY 53
|||||:|

RESULT 6

S36584

E6 protein - human papillomavirus type 7
C;Species: human papillomavirus type 7

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36584

R;Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A;Description: Primer-directed sequencing of human papillomavirus types.

A;Reference number: S36469

A;Accession: S36584

A;Molecule type: DNA

A;Residues: 1-154

A;Cross-references: UNIPROT:P36800; EMBL:X74463; NID:g397060; PIDN:CAAS2476.1; PID:g3970

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 77.8%; Score 35; DB 2; Length 154;
Best Local Similarity 66.7%; Pred. No. 6.2;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFKDLFVY 9
Db 45 FAFRELYVY 53
|||||:|

RESULT 7

S15614

E6 protein - human papillomavirus type 2a
C;Species: human papillomavirus type 2a

A;Note: host Homo sapiens (man)

C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004

C;Accession: S15614

R;Hirsch-Behnman, A.; Delius, H.; de Villiers, E.M.

Virus Res. 18, 81-98, 1990

A;Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and 1

A;Reference number: S15614; MUID:9118699; PMID:1964523

A;Accession: S15614

A;Molecule type: DNA

A;Residues: 1-159 <HIR>

A;Cross-references: UNIPROT:P25484; EMBL:X55964

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; transforming protein; zinc finger

F;35-71/Region: zinc finger CCCC motif

F;108-144/Region: zinc finger CCCC motif


```
Query Match      77.8%; Score 35; DB 1; Length 159;
Best Local Similarity 77.8%; Pred. No. 6.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9
Db 50 FAFKDLFVV 58

RESULT 8
S53831
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Acanthamoeba castellanii mitocho
C:Species: mitochondrion Acanthamoeba castellanii
C>Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S53831
R:Burger, G.; Plante, I.; Lonergan, K.M.; Gray, M.W.
J. Mol. Biol. 245, 522-537, 1995
A:Title: The mitochondrial DNA of the amoeboid protozoan, Acanthamoeba castellanii: comp
A:Reference number: S53825; MUID:95147275; PMID:7844823
A:Accession: S53831
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-675 <SUR>
A:Cross-references: UNIPROT:Q37372; GB:U12386; NID:G562028; PIDN:AAD11823.1; PID:G562035
A:Experimental source: strain Neff; ATCC 30010
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C:Genetics:
A:Genome: mitochondrion
A:Genetic code: SGC6
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match      77.8%; Score 35; DB 2; Length 675;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 8
Db 480 FIFKDLFI 487

RESULT 9
CS9436
KIAA1391 protein [imported] - human
C:Species: Homo sapiens [man]
C>Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004
C:Accession: CS9436; D59436
R:Nagase, T.; Kikuno, R.; Ishikawa, K.I.; Hirose, M.; Ohara, O.
DNA Res. 7, 65-73, 2000
A:Title: Prediction of the coding sequences of unidentified human genes. XVI. The comple
A:Reference number: CS9436
A:Accession: CS9436
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1194 <NAG>
A:Cross-references: UNIPROT:Q92P26; GB:BAA92629; PID:g7243163; PIDN:BAA92629.1
R:Ohara, O.; Nagase, T.; Kikuno, R.
submitted to GenBank, January 2000
A:Reference number: D59436
A:Accession: D59436
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1194 <OHA>
A:Cross-references: GB:BAA92629; PID:g7243163; PIDN:BAA92629.1

Query Match      77.8%; Score 35; DB 2; Length 1194;
Best Local Similarity 77.8%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9
Db 109 FLFNDLFVV 117
```

RESULT 10

E6 protein - human papillomavirus type 57
C:Species: human papillomavirus type 57

A>Note: host Homo sapiens (man)
C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C:Accession: S15621
R:Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990

A:Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and 5
A:Reference number: S15614; MUID:91188699; PMID:1964523
A:Accession: S15621
A:Molecule type: DNA

A:Residues: 1-153 <HIR>
A:Cross-references: UNIPROT:P22158; EMBL:X55965; NID:G60882; PIDN:CAA39430.1; PID:G60883

C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:29-65/Region: zinc finger CCCC motif
F:102-138/Region: zinc finger CCCC motif

Query Match 75.6%; Score 34; DB 1; Length 153;
Best Local Similarity 77.8%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9
Db 44 FAFKDLFVV 52

RESULT 11

H83337
gentisate 1,2-dioxygenase PA2470 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: H83337

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bri
adman, S.; Kuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H83337

A>Status: preliminary
A:Molecule type: DNA

A:Residues: 1-353 <STO>

A:Cross-references: UNIPROT:Q91112; GB:AE004674; GB:AE004091; NID:G9948512; PIDN:AAG05851

A:Experimental source: strain PAO1

C:Genetics:

A:Gene: gtdA; PA2470

Query Match 75.6%; Score 34; DB 2; Length 353;
Best Local Similarity 81.8%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 FAF--KDLFVV 9
Db 302 FAFKDLFVV 312

RESULT 12

T08960
serine/threonine-specific protein kinase (EC 2.7.1.1) F19B15.80 - Arabidopsis thaliana

N:Alternate names: protein F19B15.80

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 16-Aug-2004

C:Accession: T08960

R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,

submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16519

A:Accession: T08960

A:Molecule type: DNA

A;Residues: 1-669 <BEV>
A;Cross-references: UNIPROT:Q9SZD5; EMBL:AL078470; GSPDB:GN00062; ATSP:F19B15.80
A;Experimental source: cultivar Columbia; BAC clone F19B15

C;Genetics:

A;Map position: 4
A;Gene: ATSP:F19B15.80
C;Superfamily: protein kinase homology
C;Keywords: phosphotransferase; protein kinase
F;342-623/Domain: protein kinase homology <KIN>

Query Match 75.6%; Score 34; DB 2; Length 669;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 8
DB 332 FAYKOLYI 339

RESULT 13

W6WL44

E6 protein - human papillomavirus type 44
C;Species: human papillomavirus type 44
A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Accession: B34144
R;Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; Schmidt, B.J.; Temple, G.F.
J. Virol. 63, 2829-2834, 1989
A;Title: Cloning and partial DNA sequencing of two new human papillomavirus types associated with cervical intraepithelial neoplasia
A;Reference number: A34144; MUID:89259065; PMID:2542593
A;Accession: B34144
A;Molecule type: DNA
A;Residues: 1-150 <LOE>

A;Cross-references: UNIPROT:P19710; GB:M27023; NID:G341597; PIDN:AAA63454.1; PID:G703248
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;31-67/Region: zinc finger CCCC motif
F;104-140/Region: zinc finger CCCC motif

Query Match 73.3%; Score 33; DB 1; Length 150;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9
DB 46 FAYKOLYV 54

RESULT 14

W6WL43

E6 protein - human papillomavirus type 43
C;Species: human papillomavirus type 43
A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Accession: A34144
R;Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; Schmidt, B.J.; Temple, G.F.
J. Virol. 63, 2829-2834, 1989
A;Title: Cloning and partial DNA sequencing of two new human papillomavirus types associated with cervical intraepithelial neoplasia
A;Reference number: A34144; MUID:89259065; PMID:2542593
A;Accession: A34144
A;Molecule type: DNA
A;Residues: 1-155 <LOE>

A;Cross-references: UNIPROT:P19709; GB:M27022; NID:G341596; PIDN:AAA63453.1; PID:G703247
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;31-67/Region: zinc finger CCCC motif
F;104-140/Region: zinc finger CCCC motif

Query Match 73.3%; Score 33; DB 1; Length 155;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9

DB 46 FAFRDLRVV 54

RESULT 15

W6WLHS

protein E6 - human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03682; T10427
R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099

A;Accession: A03682
A;Molecule type: DNA

A;Residues: 1-158 <SEE>

A;Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
R;Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A;Title: A negative element in the human poapillomavirus type 16 genome acts at the level of transcriptional activation

A;Reference number: Z17014; MUID:91162763; PMID:1848319

A;Accession: T10427

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-158 <KEN>

A;Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C;Genetics:

A;Gene: E6

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

F;37-73/Region: zinc finger CCCC motif

F;110-146/Region: zinc finger CCCC motif

Query Match 73.3%; Score 33; DB 1; Length 158;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9
DB 52 FAFRDLCLIV 60

Search completed: June 28, 2005, 21:27:42
Job time : 12.15 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-26
Perfect score: 44
Sequence: 1 ELTEVFBEFA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trenli.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	159	1 V86 HPV18	P06463 human papil
2	44	100.0	158	2 Q9GNP8	Q9GNP8 human papil
3	37	84.1	85	2 Q6LDE7	Q6LDE7 rattus sp.
4	37	84.1	322	1 D1DH RAT	P23457 rattus norv
5	36	81.8	235	2 Q8RCR5	Q8RCR5 thermoanaer
6	36	81.8	452	2 Q8RZM4	Q8RZM4 anabaena sp
7	35	79.5	241	2 Q62JJO	Q62JJO burkholderi
8	35	79.5	241	2 Q63T75	Q63T75 burkholderi
9	35	79.5	287	2 Q737R2	Q737R2 bacillus ce
10	34	77.3	302	2 Q9A5W1	Q9A5W1 caulobacter
11	34	77.3	336	1 ADHP_ECOLI	P39451 escherichia
12	34	77.3	336	2 Q8XG17	Q8XG17 salmonella
13	34	77.3	336	2 Q7CQ19	Q7CQ19 salmonella
14	34	77.3	336	2 Q83R96	Q83R96 shigella fl
15	34	77.3	346	2 Q7AE27	Q7AE27 escherichia
16	34	77.3	346	2 Q8XEF9	Q8XEF9 escherichia
17	34	77.3	346	2 Q8FHH2	Q8FHH2 escherichia
18	34	77.3	533	2 Q8S8S2	Q8S8S2 lactobacill
19	34	77.3	1408	2 Q8MQF4	Q8MQF4 caenorhabdi
20	34	77.3	1409	1 AEX3 CAEEL	Q02626 caenorhabdi
21	33	75.0	185	2 Q96Z95	Q96Z95 sulfolobus
22	33	75.0	305	2 Q64YS9	Q64YS9 bacteroides
23	33	75.0	305	2 Q8A531	Q8A531 bacteroides
24	33	75.0	410	1 Y845 PYRAB	Q9U3K1 pyrococcus
25	33	75.0	785	2 Q94070	Q94070 candida alb
26	33	75.0	861	2 Q9N5I9	Q9N5I9 caenorhabdi
27	33	75.0	1138	2 Q757T4	Q757T4 aeshbva goss
28	33	75.0	1307	2 Q6C8M8	Q6C8M8 yarrowia li
29	32	72.7	76	2 Q7MZJ3	Q7MZJ3 photorhabdu
30	32	72.7	157	2 Q9WHG0	Q9WHG0 human papil
31	32	72.7	158	1 V86 HPV39	P24835 human papil

RESULT 1

ID	VE6 HPV18	STANDARD;	PRT;	158 AA.
AC	P06463;			
DT	01-JAN-1988	(Rel. 06, Created)		
DT	01-JAN-1988	(Rel. 06, Last sequence update)		
DT	05-JUL-2004	(Rel. 44, Last annotation update)		
DE	E6 protein.			
GN	Name=E6;			
OS	Human papillomavirus type 18.			
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;			
OC	Papillomavirus.			
OX	NCBI_TaxID=10582;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87283882; PubMed=3039146;			
RT	Cole S.T., Danos O.;			
RT	"Nucleotide sequence and comparative analysis of the human papillomavirus type 18 genome. Phylogeny of papillomaviruses and repeated structure of the E6 and E7 gene products.";			
RL	J. Mol. Biol. 193:599-608(1987).			
[2]				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86306665; PubMed=3018129;			
RA	Matlahewski G., Banks L., Wu-Liao J., Spence P., Pim D., Crawford L.;			
RT	"The expression of human papillomavirus type 18 E6 protein in bacteria and the production of anti-E6 antibodies.";			
RL	J. Gen. Virol. 67:1909-1916(1986).			
[3]				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88188247; PubMed=2833614;			
RA	Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M.,			
RA	Sugimura T.;			
RT	"Nucleotide sequences of cDNAs for human papillomavirus type 18 transcripts in HeLa cells.";			
RL	J. Virol. 62:1640-1646(1988).			
[4]				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87053870; PubMed=3023067;			
RA	Schneider-Gaedcke A., Schwarz E.;			
RT	"Different human cervical carcinoma cell lines show similar transcription patterns of human papillomavirus type 18 early genes.";			
RL	EMBO J. 5:2285-2292(1986).			
[5]				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87218459; PubMed=3034571;			
RA	Seedorf K., Oltersdorf T., Kraemer G., Roewekamp W.;			
RT	"Identification of early proteins of the human papilloma viruses type 16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells.";			
RL	EMBO J. 6:139-144(1987).			
[6]				
RP	ZINC-BINDING.			
RX	MEDLINE=89385606; PubMed=2550872;			
RA	Grossman S.R., Laimins L.A.;			

32	32	72.7	158	1	VE6 HPV45	P21735 human papil
33	32	72.7	158	1	VE6 HPV68	P54667 human papil
34	32	72.7	158	1	VE6 HPV70	P50804 human papil
35	32	72.7	158	1	VE6 HPVME	P27962 human papil
36	32	72.7	158	2	Q94Y4	Q94Y4 homo sapien
37	32	72.7	158	2	O10608	O10608 human papil
38	32	72.7	158	2	Q7KYR8	Q7KYR8 human papil
39	32	72.7	162	2	Q9UI29	Q9UI29 human papil
40	32	72.7	303	2	Q6BYE2	Q6BYE2 debaromyce
41	32	72.7	311	1	PYDA_ENTFA	P59626 enterococcu
42	32	72.7	322	2	Q841I8	Q841I8 enterococcu
43	32	72.7	332	2	Q6D5T7	Q6D5T7 erwinia car
44	32	72.7	411	2	Q6AIWI	Q6AIWI desulfotale
45	32	72.7	464	2	Q8YST7	Q8YST7 anabaena sp

ALIGNMENTS

RT "E6 protein of human papillomavirus type 18 binds zinc."; [7]
RL Oncogene 4:1089-1093(1989).
RN
RP INTERACTION WITH FBLN1, AND INHIBITION OF E6-MEDIATED TRANSFORMATION.
RX MEDLINE=2218366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;
RA Du M., Fan X., Hong E., Chen J.J.;
RT "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1."; Biochem. Biophys. Res. Commun. 296:962-969(2002).
RL
CC -!- FUNCTION: This protein has transforming activity in vitro.
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double stranded DNA (in vitro).
CC
CC -!- SUBUNIT: Interacts with FBLN1.
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC
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CC
DR EMBL; X04354; CAA27879.1; -
DR EMBL; X05015; CAA28664.1; -
DR EMBL; M20325; AAA99514.1; -
DR EMBL; M26798; AAA46946.1; -
DR EMBL; X04773; CAA28466.1; -
DR EMBL; A06324; CAA00539.1; -
DR EMBL; A06328; CAA00542.1; -
DR PIR; A26165; W6WL18.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW DNA-binding; Early protein; Nuclear protein; Oncogene; Zinc-finger.
FT ZN FING 32 68
FT ZN FING 105 141
FT ZN FING 105 141
FT CONFLICT 22 22 N -> S (in Ref. 4).
SQ SEQUENCE 158 AA; 18871 MW; 5BCF13CF43D157FA CRC64;
Query Match 100.0%; Score 44; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELTEVFPEFA 9
Db 40 ELTEVFPEFA 48
RESULT 2
Q9QNP8 PRELIMINARY; PRT; 158 AA.
ID Q9QNP8
AC Q9QNP8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RA Laasri M., Gul'ko L., Vinokurova S., Kisseljeva N., Veiko V., Kisseljev F.;
RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and Transformation Potential of E7 Gene and its Mutants."; Virus Genes 182:139-149(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Veiko V.P.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DDJ databases.
DR EMBL; Y18491; CAB53096.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.

DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 18886 MW; 5BCF13CF43D407AF CRC64;
Query Match 100.0%; Score 44; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELTEVFPEFA 9
Db 40 ELTEVFPEFA 48
RESULT 3
Q6LDE7 PRELIMINARY; PRT; 85 AA.
ID Q6LDE7
AC Q6LDE7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE 3 alpha-hydroxysteroid dehydrogenase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92170599; PubMed=1793046;
RA Pawlowski J., Huizinga M., Penning T.M.;
RT "Isolation and partial characterization of a full-length cDNA clone for 3 alpha-hydroxysteroid dehydrogenase: a potential target enzyme for nonsteroidal anti-inflammatory drugs."; Agents Actions 34:289-293(1991).
RL Agents Actions 34:289-293(1991).
DR EMBL; S35751; AAB21512.1; -
DR HSSP; P23457; 1AFS.
DR InterPro; IPR001395; Aldo/ket red.
DR ProDom; PD000288; Aldo/ket red; 1.
DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
FT NON-TER 85 85
SQ SEQUENCE 85 AA; 9928 MW; 8AC2E592E8D2463A CRC64;
Query Match 84.1%; Score 37; DB 2; Length 85;
Best Local Similarity 87.5%; Pred. No. 9.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELTEVFPEFA 8
Db 42 ELTQVFEF 49
RESULT 4
DIDH_RAT STANDARD; PRT; 322 AA.
ID DIDH_RAT
AC P23457;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 3-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.50) (3-alpha-HSD) (Hydroxyprostaglandin dehydrogenase).
GN Name=Akr1c9;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver.
RX MEDLINE=91224978; PubMed=1840601;
RA Pawlowski J.E., Huizinga M., Penning T.M.;
RT "Cloning and sequencing of the cDNA for rat liver 3 alpha-hydroxysteroid/dihydrodiol dehydrogenase."; J. Biol. Chem. 266:8820-8825(1991).
RN [2]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=91332047; PubMed=1714456;
RA Stoiz A., Rahimi-Kiani M., Ameis D., Chan E., Ronk M., Shively J.E.;
RT "Molecular structure of rat hepatic 3 alpha-hydroxysteroid
RL dehydrogenase. A member of the oxidoreductase gene family.";
RN J. Biol. Chem. 266:15253-15257(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92017888; PubMed=1922097;
RA Cheng K.-C., White P.C., Qin K.-N.;
RT "Molecular cloning and expression of rat liver 3 alpha-hydroxysteroid
RL dehydrogenase.";
RN Mol. Endocrinol. 5:823-828(1991).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=94266748; PubMed=7515872;
RA Usui E., Okuda K., Kato Y., Noshiro M.;
RT "rat hepatic 3 alpha-hydroxysteroid dehydrogenase: expression of cDNA
RL and physiological function in bile acid biosynthetic pathway.";
RN J. Biochem. 115:230-237(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=20084373; PubMed=10619355; DOI=10.1016/S0960-0760(99)00122-3;
RA Lin H.K., Hung C.F., Moore M., Penning T.M.;
RT "Genomic structure of rat 3alpha-hydroxysteroid/dihydrodiol
RL dehydrogenase (3alpha-HSD/DP, AKR1C9).";
RN J. Steroid Biochem. Mol. Biol. 71:29-39(1999).
RN [6]
RP SEQUENCE OF 162-171; 208-223 AND 232-246.
RX MEDLINE=91224979; PubMed=2026597;
RA Penning T.M., Abrams W.R., Pawlowski J.E.;
RT "Affinity labeling of 3 alpha-hydroxysteroid dehydrogenase with 3
RL alpha-bromoacetoxyandrostene and 11 alpha-bromoacetoxyprogesterone.
RT Isolation and sequence of active site peptides containing reactive
RT cysteines; sequence confirmation using nucleotide sequence from a cDNA
RL clone.";
RN J. Biol. Chem. 266:8826-8834(1991).
RN [7]
RP DISTRIBUTION IN BRAIN.
RC TISSUE=Brain;
RX MEDLINE=95352485; PubMed=7626489; DOI=10.1016/0960-0760(95)00019-V;
RA Khanna M., Qin K.N., Cheng K.C.;
RT "Distribution of 3 alpha-hydroxysteroid dehydrogenase in rat brain and
RL molecular cloning of multiple cDNAs encoding structurally related
RN proteins in humans.";
RN J. Steroid Biochem. Mol. Biol. 53:41-46(1995).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RC TISSUE=Liver;
RX MEDLINE=94195773; PubMed=8146147;
RA Hoog S.S., Pawlowski J.E., Alzari P.M., Penning T.M., Lewis M.;
RT "Three-dimensional structure of rat liver 3 alpha-
RL hydroxysteroid/dihydrodiol dehydrogenase: a member of the aldo-keto
RN reductase superfamily.";
RN Proc. Natl. Acad. Sci. U.S.A. 91:2517-2521(1994).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=96346063; PubMed=8718859; DOI=10.1021/bi9604688;
RA Bennett M.J., Schlegel B.P., Jez J.M., Penning T.M., Lewis M.;
RT "Structure of 3 alpha-hydroxysteroid/dihydrodiol dehydrogenase
RL complexed with NADP+.";
RN Biochemistry 35:10702-10711(1996).
CC -!- FUNCTION: Besides being a 3-alpha-hydroxysteroid dehydrogenase,
CC the enzyme can accomplish diverse functions: as quinone reductase,
CC as an aromatic alcohol dehydrogenase, as dihydrodiol
CC dehydrogenase, and as 9-, 11-, and 15-hydroxyprostaglandin
CC dehydrogenase.
CC
CC -!- CATALYTIC ACTIVITY: Androstene + NAD(P)(+) = 5-alpha-androstane-
CC 3,17-dione + NAD(P)H.
CC
CC -!- ENZYME REGULATION: Potently inhibited by the nonsteroidal anti-

inflammatory drugs (NSAID).
-!- SUBUNIT: Monomer.
-!- TISSUE SPECIFICITY: In brain, highest levels found in olfactory
bulb. Moderate levels present in cerebellum, cerebral cortex,
hypothalamus and pituitary. Low levels present in amygdala, brain
stem, caudate putamen, cingulate cortex, hippocampus, midbrain,
and thalamus.
-!- SIMILARITY: Belongs to the aldo/keto reductase family.

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or send an email to license@isb-sib.ch).

EMBL; M64393; AAA0605.1; -
DR EMBL; M61937; AAA41077.1; -
DR EMBL; D17310; BAA04132.1; -
DR EMBL; S57790; BAB19918.1; -
DR EMBL; AF180334; AAF25813.1; -
DR EMBL; AF180326; AAF25813.1; JOINED.
DR EMBL; AF180327; AAF25813.1; JOINED.
DR EMBL; AF180328; AAF25813.1; JOINED.
DR EMBL; AF180329; AAF25813.1; JOINED.
DR EMBL; AF180330; AAF25813.1; JOINED.
DR EMBL; AF180331; AAF25813.1; JOINED.
DR EMBL; AF180332; AAF25813.1; JOINED.
DR EMBL; AF180333; AAF25813.1; JOINED.
DR PIR; A39350; A39350.
DR PDB; 1AFS; X-ray; A/B=1-322.
DR PDB; 1LWI; X-ray; A/B=1-322.
DR PDB; 1RAL; X-ray; @=1-308.
DR InterPro; IPR001395; Aldo/ket_red.
DR Pfam; PF00248; Aldo_ket_red; 1.
DR PRINTS; PR00069; ALDKETREDTASE.
DR ProDom; PD000288; Aldo/ket_red; 1.
DR PROSITE; PS00798; ALDOKETO_REDUCTASE_1; 1.
DR PROSITE; PS00062; ALDOKETO_REDUCTASE_2; 1.
DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; 1.
KW 3D-structure; Direct protein sequencing; NAD; Oxidoreductase.
FT MOD_RES 1
FT N_BIND 217 280
FT ACT_SITE 55 55
FT BINDING 117 117
FT CONFLICT 108 108
FT CONFLICT 273 274
FT CONFLICT 280 280
FT HELIX 3 5
FT STRAND 7 9
FT TURN 11 12
FT STRAND 15 17
FT STRAND 20 22
FT TURN 27 28
FT TURN 31 32
FT TURN 33 43
FT TURN 44 45
FT STRAND 48 50
FT TURN 53 56
FT HELIX 58 70
FT TURN 71 72
FT HELIX 76 78
FT STRAND 80 85
FT TURN 87 89
FT TURN 92 94
FT HELIX 95 106
FT STRAND 111 116
FT STRAND 121 122
FT STRAND 131 131
FT TURN 133 134
FT STRAND 137 137

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FT STRAND 139 140
FT HELIX 144 156
FT TURN 157 158
FT STRAND 160 166
FT TURN 170 177
FT HELIX 178 178
FT TURN 180 181
FT STRAND 188 192
FT STRAND 194 194
FT TURN 195 196
FT STRAND 197 197
FT HELIX 200 209
FT TURN 210 210
FT STRAND 212 216
FT TURN 218 219
FT TURN 225 227
FT TURN 230 231
FT HELIX 235 237
FT TURN 239 247
FT TURN 248 249
FT HELIX 252 262
FT TURN 263 264
FT STRAND 266 269
FT HELIX 274 280
FT TURN 281 284
FT HELIX 290 297
FT TURN 298 299
FT HELIX 309 311
FT TURN 312 313
FT TURN 315 316
SQ SEQUENCE 322 AA; 37027 MW; 592EFC584726A4F6 CRC64;

Query Match 84.1%; Score 37; DB 1; Length 322;
Best Local Similarity 87.5%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELTEVFEEF 8
|||:||||
DB 279 ELTQVFEF 286

RESULT 5
Q8RCR5 PRELIMINARY; PRT; 235 AA.
AC Q8RCR5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypothetical protein TTR0348.
GN OrderedLocusNames=TT0348;
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4 / JCM 11007;
RX MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013007; AAM23640.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 235 AA; 27937 MW; A64C69A613429E7B CRC64;

Query Match 81.8%; Score 36; DB 2; Length 235;
Best Local Similarity 77.8%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELTEVFEEFA 9
| |||||:|

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Db 225 EYTEVFEEFA 233

RESULT 6
Q8YZN4 PRELIMINARY; PRT; 452 AA.
AC Q8YZN4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE All0423 protein.
GN OrderedLocusNames=all0423;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003582; BAB72381.1; -.
DR FIR; AF1859; AF1859.
KW Complete proteome.
SQ SEQUENCE 452 AA; 47469 MW; D6FCB84EA6FF6CA2 CRC64;

Query Match 81.8%; Score 36; DB 2; Length 452;
Best Local Similarity 75.0%; Pred. No. 78;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELTEVFEEF 8
|||:|:|
DB 184 ELTIFDF 191

RESULT 7
Q62JU0 PRELIMINARY; PRT; 241 AA.
AC Q62JU0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE DNA-binding response regulator Risa.
GN Name=risa; ORFNames=BMA1485;
OS Burkholderia mallei ATCC 23344.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=243160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 23344;
RA Nieman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T., Ulrich R.L., Rinning C.M., Brinkac L.M., Daugherty S.C.,
RA Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
RA Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
RA Mohammad Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,
RA Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
RA Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
DR EMBL; CP000010; AAU47660.1; -.
KW DNA-binding.
SQ SEQUENCE 241 AA; 27335 MW; 523E1D2AC58D99AE CRC64;

Query Match 79.5%; Score 35; DB 2; Length 241;
Best Local Similarity 87.5%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 ELTEVEFEF 8
Db 136 ETTEVEFEF 143

RESULT 8
Q63775 PRELIMINARY; PRT; 241 AA.
AC Q63775;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Oxidative stress related two component system, transcriptional
DE regulator.
GN Name=ompR; ORFNames=BFS12094;
OS Burkholderia pseudomallei K96243.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=272560;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=K96243;
RX PubMed=15377794;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdano-Tarraga A.M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabbington E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).
DR EMBL; BX571965; CHA36097.1; -.
SQ SEQUENCE 241 AA; 27335 MW; 523E1D2AC58D99AE CRC64;

Query Match 79.5%; Score 35; DB 2; Length 241;
Best Local Similarity 87.5%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ELTEVEFEF 8
Db 136 ETTEVEFEF 143

RESULT 9
Q737R2 PRELIMINARY; PRT; 287 AA.
AC Q737R2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BCE2584;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
SEQUENCE FROM N.A.
RP PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angluoi S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pX01.";
RL Nucleic Acids Res. 32:977-988 (2004).
DR EMBL; AE017272; AAS41500.1; -.
DR TIGR; BCE2584; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.

DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot Kinase.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Complete proteome.
SQ SEQUENCE 287 AA; 33789 MW; 15654F3FB23C89C5 CRC64;

Query Match 79.5%; Score 35; DB 2; Length 287;
Best Local Similarity 75.0%; Pred. No. 80;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LTEVEFEFA 9
Db 149 LTKIFEFA 156

RESULT 10
Q9A5W1 PRELIMINARY; PRT; 302 AA.
AC Q9A5W1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE MotA/TolQ/ExbB proton channel family protein.
GN MotA/TolQ/ExbB proton channel family protein.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141 (2001).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the exbB / tolQ family.
DR EMBL; AE005903; AAK24307.1; -.
DR PIR; G87538; G87538.
DR TIGR; CC2336; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008565; F:protein transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002898; MotA_ExbB.
DR Pfam; PF01618; MotA_ExbB; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 302 AA; 30850 MW; 19F0051868F948CB CRC64;

Query Match 77.3%; Score 34; DB 2; Length 302;
Best Local Similarity 75.0%; Pred. No. 14e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LTEVEFEFA 9
Db 109 LTKIFEFA 116

RESULT 11
ADHP_ECOLI STANDARD; PRT; 336 AA.
AC P39451; P76126; P78157; P78268;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Alcohol dehydrogenase, propanol-preferring (EC 1.1.1.1).

```

GN Name=adhp; OrderedLocusNames=bl478;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 EX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251357; PubMed=9097039;
 RA Aiba H., Baba T., Fujita K., Hayaashi K., Inada T., Isono K., Itoh T.,
 RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
 RA Sampei G., Seki Y., Sivasubramanian S., Tagami H., Takeda J.,
 RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).
 RN [3]
 RP SEQUENCE OF 1-35, AND CHARACTERIZATION.
 RA Harayama S.;
 RL Submitted (OCT-1994) to Swiss-Prot.
 RN [4]
 RP SEQUENCE OF 87-118 FROM N.A.
 RX MEDLINE=90236945; PubMed=2158980;
 RA Kubo K.M., Craig N.L.;
 RT "Bacterial transposon Tn7 utilizes two different classes of target
 sites.";
 RL J. Bacteriol. 172:2774-2778(1990).
 CC -!- FUNCTION: Preferred specificity is towards 1-propanol.
 CC -!- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
 NADH.
 CC -!- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
 CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U00096; AAC74551.1; ALT_INIT.
 DR EMBL; D90788; BAAL5126.1; -.
 DR EMBL; D90789; BAAL5135.1; -.
 DR EMBL; D90790; BAAL5145.1; -.
 DR EMBL; M31532; -; NOT_ANNOTATED_CDS.
 DR HSSP; P39462; 1JVB.
 DR ECHOBASE; EB2506; -.
 DR ECGene; EG12622; adhp.
 DR InterPro; IPR002328; ADH_zinc.
 DR InterPro; IPR002085; Adh zn family.
 DR InterPro; IPR011032; GroES like.
 DR InterPro; IPR000051; SAM bind.
 DR Pfam; PF00107; ADH_zinc_N; 1.
 DR PROSITE; PS00059; ADH_ZINC; 1.
 KW Complete proteome; Direct protein sequencing; Metal-binding; NAD;
 Oxidoreductase; Zinc.
 DR METAL 37 37 Zinc 1 (catalytic) (By similarity).
 FT METAL 58 58 Zinc 1 (catalytic) (By similarity).
 FT METAL 89 89 Zinc 2 (By similarity).

FT METAL 92 92 Zinc 2 (By similarity).
 FT METAL 95 95 Zinc 2 (By similarity).
 FT METAL 103 103 Zinc 2 (By similarity).
 FT METAL 145 145 Zinc 1 (catalytic) (By similarity).
 FT CONFLICT 34 34 C -> P (in Ref. 3).
 FT CONFLICT 90 90 G -> R (in Ref. 4).
 FT CONFLICT 104 104 R -> P (in Ref. 4).
 FT CONFLICT 108 108 N -> K (in Ref. 4).
 FT CONFLICT 112 112 S -> G (in Ref. 4).
 FT CONFLICT 117 118 MA -> RV (in Ref. 4).
 SQ SEQUENCE 336 AA; 35379 MW; 8A9080F273866947 CRC64;

Query Match 77.3%; Score 34; DB 1; Length 336;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELTEVFPEPA 9
 :||| |||
 Db 289 DLTEAFQFA 297

RESULT 12

Q8XGI7 PRELIMINARY; PRT; 336 AA.
 ID Q8XGI7; O7AM29;
 DT 01-MAR-2002 (TRENBLrel. 20, Created)
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE Alcohol dehydrogenase.
 GN Name=adhp; OrderedLocusNames=STY1493, t1482;
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ty2 / ATCC 700931;
 RX MEDLINE=22531367; PubMed=12644504;
 EX DOI=10.1128/JB.185.7.2330-2337.2003;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
 and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Conerton P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jajels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 CC -!- COFACTOR: Zinc (By similarity).
 CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 family.

CC EMBL; AE016839; AA069120.1; -.
 DR EMBL; AL627270; CAD01753.1; -.
 DR HSSP; P39462; 1JVB.
 DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
 DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. .; IEA.
 DR GO; GO:0008270; F;zinc ion binding; IEA.
 DR Pfam; PF00107; ADH_zinc_N; 1.
 DR PROSITE; PS00059; ADH_ZINC; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 KW Complete proteome; Metal-binding; Oxidoreductase; Zinc.
 SQ SEQUENCE 336 AA; 35541 MW; 39E7F48AB54EDB66 CRC64;


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Query Match      77.3%; Score 34; DB 2; Length 336;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 ELTEVFPEFA 9
DB      289 DUTEAFQFA 297

RESULT 13
Q7CQ19          PRELIMINARY; PRT; 336 AA.
AC Q7CQ19;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Alcohol dehydrogenase (EC 1.1.1.1).
GN Name=adhP; OrderedLocusNames=STM1567;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856 (2001).
CC -!- SIMILARITY: Zinc (By similarity).
CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
CC family.
DR EMBL; AEO08768; AAL20485.1; -.
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. .; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR002328; ADH_zinc.
DR InterPro; IPR002085; Adh zn family.
DR InterPro; IPR00345; CytC heme BS.
DR InterPro; IPR011032; GroES like.
DR InterPro; IPR000051; SAM bind.
DR Pfam; PF0107; ADH_zinc_N; 1.
DR PROSITE; PS00059; ADH_ZINC; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Complete proteome; Metal-binding; Oxidoreductase; Zinc.
SQ SEQUENCE 336 AA; 35541 MW; 39E7F48AB54EDB66 CRC64;

Query Match      77.3%; Score 34; DB 2; Length 336;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 ELTEVFPEFA 9
DB      289 DUTEAFQFA 297

RESULT 14
Q83R96          PRELIMINARY; PRT; 336 AA.
AC Q83R96; Q7C1C9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Alcohol dehydrogenase.
GN Name=adhP; OrderedLocusNames=S1880, SF1747;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

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OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=2227406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157."
RL Nucleic Acids Res. 30:4432-4441 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=2457T;
RX MEDLINE=22590274; PubMed=12704152;
RX DOI=10.1128/IAI.71.5.2775-2786.2003;
RA Wei J., Goldberg M.B., Butland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T."
RL Infect. Immun. 71:2775-2786 (2003).
CC -!- COFACTOR: Zinc (By similarity).
CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
CC family.
DR EMBL; AEO15195; AAN43319.1; -.
DR EMBL; AEO16984; AAP17205.1; -.
DR HSSP; Q59096; 1F8F.
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. .; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR002328; ADH_zinc.
DR InterPro; IPR002085; Adh zn family.
DR InterPro; IPR00345; CytC heme BS.
DR InterPro; IPR011032; GroES like.
DR InterPro; IPR000051; SAM bind.
DR Pfam; PF0107; ADH_zinc_N; 1.
DR PROSITE; PS00059; ADH_ZINC; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Metal-binding; Oxidoreductase; Zinc.
SQ SEQUENCE 336 AA; 35522 MW; AA782C1072144E5E CRC64;

Query Match      77.3%; Score 34; DB 2; Length 336;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 ELTEVFPEFA 9
DB      289 DUTEAFQFA 297

RESULT 15
Q7AE27          PRELIMINARY; PRT; 346 AA.
AC Q7AE27;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Alcohol dehydrogenase.
GN OrderedLocusNames=EC92082;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

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RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohemorrhagic Escherichia coli
 O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001).
 CC -!- COFACTOR: Zinc (By similarity).
 CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 CC family.
 DR EMBL; AP002557; BAB35505.1; -.
 DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. . .; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR InterPro; IPR002328; ADH_zinc.
 DR InterPro; IPR002085; Adh_zn_family.
 DR InterPro; IPR00345; CytC_heme_BS.
 DR InterPro; IPR011032; GROES_like.
 DR InterPro; IPR000051; SAM_bind.
 DR Pfam; PF00107; ADH_zinc_N; 1.
 DR PROSITE; PS00059; ADH_ZINC; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 KW Metal-binding; Oxidoreductase; Zinc.
 SQ SEQUENCE 346 AA; 36496 MW; AFDD1E0D0037F267 CRC64;

Query Match 77.3%; Score 34; DB 2; Length 346;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELTEVFEEPA 9
 :||| |:|
 Db 299 DLTEAFQFA 307

Search completed: June 28, 2005, 21:23:55
 Job time : 58.1 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-26

Perfect score: 44

Sequence: 1 ELTEVFPEFA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	158	1 W6WL18	E6 protein - human
2	37	84.1	322	1 A39350	3alpha-hydroxyster
3	36	81.8	452	2 A1859	hypothetical prote
4	34	77.3	302	2 G87538	MoTA/ToIQ/ExdB pro
5	34	77.3	336	2 A40672	alcohol dehydrogen
6	34	77.3	346	1 A64901	alcohol dehydrogen
7	34	77.3	346	2 B90889	alcohol dehydrogen
8	34	77.3	346	2 G85728	alcohol dehydrogen
9	34	77.3	1409	2 T37188	presynaptic activi
10	33	75.0	410	2 C75094	probable RNA methy
11	33	75.0	785	2 T18252	conserved hypothet
12	32	72.7	158	1 W6WL39	E6 protein - human
13	32	72.7	158	1 W6WLPR	E6 protein - human
14	32	72.7	158	2 S36561	E6 protein - human
15	32	72.7	464	2 A21800	diaminopimelate de
16	32	72.7	496	2 B72398	L-arabinose isomer
17	32	72.7	539	2 F75497	probable arginine
18	32	72.7	566	1 F64329	arginine-tRNA liga
19	31	70.5	34	2 J4218	phosphofructokinase
20	31	70.5	111	2 S69593	hypothetical prote
21	31	70.5	137	2 A92558	conserved hypothet
22	31	70.5	269	2 S59316	hypothetical prote
23	31	70.5	288	1 BVECR4	rePA protein - Esc
24	31	70.5	295	2 S23585	carboxyphosphonoe
25	31	70.5	336	2 G98829	alcohol dehydrogen
26	31	70.5	463	2 G30657	hypothetical prote
27	31	70.5	463	2 G85508	hypothetical prote
28	31	70.5	492	2 G82498	conserved hypothet
29	31	70.5	512	2 B84501	probable cytochrom

30 31 70.5 526 1 P5XR15 outer capsid prote
31 31 70.5 1473 2 T38791 probable ferredoxi
32 31 70.5 4151 2 T13734 groovin gene prote
33 30 68.2 68 2 G89975 conserved hypothet
34 30 68.2 105 2 H69949 transcription regu
35 30 68.2 119 2 T44790 probable glucose-f
36 30 68.2 141 1 JDBOB glia maturation fa
37 30 68.2 141 1 S22149 glia maturation fa
38 30 68.2 142 1 PT0410 glia maturation fa
39 30 68.2 142 2 JC7218 glia maturation fa
40 30 68.2 173 2 A75512 hypothetical prote
41 30 68.2 218 2 T27678 hypothetical prote
42 30 68.2 247 2 D97445 transcription acti
43 30 68.2 253 2 H83238 probable peptidyl-
44 30 68.2 267 2 D64351 nitrate transport
45 30 68.2 284 2 JC8053 deoxyribonuclease

ALIGNMENTS

RESULT 1

W6WL18

E6 protein - human papillomavirus type 18

C:Species: human papillomavirus type 18

C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004

C:Accession: A26165; G26251

R:Seedorf, K.; Olteradof, T.; Kraemmer, G.; Roewekamp, W.

EMBO J. 6, 139-144, 1987

A:Title: Identification of early proteins of the human papilloma viruses type 16. (HPV 16)

A:Reference number: A91068; MUID:87218459; PMID:3034571

A:Accession: A26165

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P06463; GB:X04773; NID:G60876; PIDN:CAA28466.1; PID:G60877

R:Coile, S.T.; Danos, O.

J. Mol. Biol. 193, 599-608, 1987

A:Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 18

A:Reference number: A92937; MUID:87283882; PMID:3039146

A:Accession: G26251

A:Molecule type: DNA

A:Residues: 1-158 <COL>

A:Cross-references: GB:X05015; NID:G60975; PIDN:CAA28664.1; PID:G60976

R:Matlashewski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pim, D.; Crawford, L.

J. Gen. Virol. 67, 1909-1916, 1986

A:Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the p

A:Reference number: A92791; MUID:86306665; PMID:3018129

A:Contents: annotation; identification of the protein

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; transforming protein; zinc finger

F:32-68/Region: zinc finger CCCC motif

F:105-141/Region: zinc finger CCCC motif

Query Match 100.0%; Score 44; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELTEVFPEFA 9

Db 40 ELTEVFPEFA 48

RESULT 2

A39350

3alpha-hydroxysteroid dehydrogenase (B-specific) (EC 1.1.1.50) - rat

N:Alternate names: dehydroascorbate reductase; dihydrodiol dehydrogenase

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 16-Aug-2004

C:Accession: A39350; A39839; A61163; A23730; S53338

R:Stolz, A.; Rahimi-Kiani, M.; Ameis, D.; Chan, E.; Ronk, M.; Shively, J.E.

J. Biol. Chem. 266, 15253-15257, 1991

A:Title: Molecular structure of rat hepatic 3alpha-hydroxysteroid dehydrogenase. A member

A:Reference number: A39350; MUID:91332047; PMID:1714456

A;Accession: A39350
A;Molecule type: mRNA
A;Residues: 1-322 <STO>
A;Cross-references: UNIPROT:P23457; GB:M64393; NID:g202528; PIDN:AAA40605.1; PID:g202529
A;Note: parts of this sequence were confirmed by peptide sequencing
R;Pawlowski, J.E.; Huizinga, M.; Penning, T.M.
J. Biol. Chem. 266, 8820-8825, 1991
A;Title: Cloning and sequencing of the cDNA for rat liver 3alpha-hydroxysteroid/dihydrod
A;Reference number: A39839; MUID:91224978; PMID:1840601
A;Accession: A39839
A;Molecule type: mRNA
A;Residues: 1-322 <PAW>
A;Cross-references: GB:M61937; NID:g203917; PIDN:AAA41077.1; PID:g203918
A;Note: parts of this sequence were confirmed by peptide sequencing
R;Pawlowski, J.; Huizinga, M.; Penning, T.M.
Agents Actions 34, 289-293, 1991
A;Title: Isolation and partial characterization of a full-length cDNA clone for 3alpha-h
A;Reference number: A61163; MUID:92170599; PMID:1793046
A;Accession: A61163
A;Molecule type: mRNA
A;Residues: 112-169; 238-322 <PA2>
A;Cross-references: GB:S35751; GB:S35752
R;Cheng, K.C.; White, P.C.; Qin, K.N.
Mol. Endocrinol. 5, 823-828, 1991
A;Title: Molecular cloning and expression of rat liver 3alpha-hydroxysteroid dehydrogena
A;Reference number: A23730; MUID:92017888; PMID:1922097
A;Accession: A23730
A;Molecule type: mRNA
A;Residues: 1-107, 'Q', 109-272, 'KP', 275-279, 'P', 281-322 <CHE>
A;Cross-references: GB:S57790; NID:g236057; PIDN:AA819918.1; PID:g236058
A;Note: it is unclear whether the differences in this report indicate the presence of mu
R;Del Bello, B.; Maellaro, E.; Sutherland, L.; Santucci, A.; Comperti, M.; Casini, A.F.
Biochem. J. 304, 385-390, 1994
A;Title: Purification of NADPH-dependent dehydroascorbate reductase from rat liver and i
A;Reference number: S53338; MUID:95091669; PMID:7998972
A;Accession: S53338
A;Molecule type: protein
A;Residues: 2-16; 121-135; 152-166; 203-217
A;Experimental source: liver
A;Comment: This enzyme also has 9-, 11-, and 15-hydroxyprostaglandin dehydrogenase activ
C;Comment: This enzyme is inhibited by nonsteroidal anti-inflammatory drugs.
C;Superfamily: Aldehyde reductase
C;Keywords: monomer; NADP; oxidoreductase

Query Match 84.1%; Score 37; DB 1; Length 322;
Best Local Similarity 87.5%; Pred. No. 7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELTEVFEF 8
|||:|||||
DB 279 ELTQVFEF 286

RESULT 3
AF1859
Hypothetical protein all0423 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AF1859
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yanada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF1859
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-452 <KUR>
A;Cross-references: UNIPROT:Q8Y2N4; GB:BA000019; PIDN:BA872381.1; PID:g17129768; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all0423

Query Match 81.8%; Score 36; DB 2; Length 452;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELTEVFEF 8
|||:|||||
DB 184 ELTEIFDF 191

RESULT 4

G87538
Mota/ToIQ/ExbB proton channel family protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: G87538
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87538
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-302 <STO>
A;Cross-references: UNIPROT:Q9A5W1; GB:AE005673; NID:gl3423861; PIDN:AAK24307.1; GSPDB:G
C;Genetics:
A;Gene: CC2336

Query Match 77.3%; Score 34; DB 2; Length 302;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTEVFEFA 9
|||:|||||
DB 109 LTKIFEFA 116

RESULT 5

AH0672
alcohol dehydrogenase (EC 1.-.-.-) [similarity] - Salmonella enterica subsp. enterica ser
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella Typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AH0672
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0672
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-336 <PAR>
A;Cross-references: GB:ALU13382; PIDN:CAD01753.1; PID:gl6502601; GSPDB:GN00176
C;Genetics:
A;Gene: STY1493
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: oxidoreductase; zinc
F;37,58,145/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted

Query Match 77.3%; Score 34; DB 2; Length 336;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELTEVFEFA 9
|||:|||||
DB 289 DLTEAFQFA 297

```

RESULT 6
A:Gene: Ec4901
A:Title: alcohol dehydrogenase (EC 1.1.1.1) b1478 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: A64901
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen,
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: A64901
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-346 <BLAT>
A:Cross-references: GB:AE000245; GB:U00096; NID:g1787752; PIDN:AAC74551.1; PID:g1787753;
A:Experimental source: strain K-12, substrain MG1655
C:Function:
A:Description: catalyzes the reversible oxidation of primary and secondary alcohols to a
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: alcohol metabolism; metalloprotein; NAD; oxidoreductase; zinc
F:32-334/Domain: long-chain alcohol dehydrogenase homology <LADH>
F:47.68.155/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted
F:99.102.105.113/Binding site: zinc, noncatalytic (Cys) #status predicted

Query Match 77.3%; Score 34; DB 1; Length 346;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELTEVFPEFA 9
DB 299 DLTEAFQFA 307

RESULT 7
A:Gene: Ec5089
A:Title: alcohol dehydrogenase (EC 1.1.1.-) [similarity] - Escherichia coli (strain O157:H7, subs
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: B90889
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: B90889
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-346 <HAY>
A:Cross-references: UNIPROT:Q8XEF9; GB:BA000007; PIDN:BA035505.1; PID:g13361548; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: Ec52082
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: oxidoreductase; zinc
F:47.68.155/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted

Query Match 77.3%; Score 34; DB 2; Length 346;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELTEVFPEFA 9
DB 299 DLTEAFQFA 307

RESULT 8
A:Gene: G85728
A:Title: alcohol dehydrogenase (EC 1.1.1.-) [similarity] - Escherichia coli (strain O157:H7, subs
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: G85728
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

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iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85728
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-346 <STO>
A:Cross-references: UNIPROT:Q8XEF9; GB:AE005174; NID:g12515203; PIDN:AAG56291.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: adhP
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: oxidoreductase; zinc
F:47.68.155/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted

Query Match 77.3%; Score 34; DB 2; Length 346;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELTEVFPEFA 9
DB 299 DLTEAFQFA 307

RESULT 9
T37188
A:Title: presynaptic activity regulator aex-3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37188
R:Leimbac, D.; Minx, M.
submitted to the EMBL Data Library, February 1996
A:Description: The sequence of C. elegans coamid C02H7.
A:Reference number: Z20523
A:Accession: T37188
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1409 <LEI>
A:Cross-references: UNIPROT:O03626; EMBL:U49945; PIDN:AAC47926.1; GSPDB:GN00029
A:Experimental source: strain Bristol N2; clone C02H7
C:Genetics:
A:Gene: aex-3; CESP:C02H7.3
A:Map position: X
A:Introns: 77/1; 136/2; 183/2; 232/3; 283/3; 386/3; 427/3; 527/3; 577/1; 699/3; 782/2; 84/

Query Match 77.3%; Score 34; DB 2; Length 1409;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELTEVFPEFA 9
DB 237 DLQVFEFA 245

RESULT 10
C75094
A:Title: probable RNA methyltransferase PAB0760 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: C75094
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A:Reference number: A75001
A:Accession: C75094
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-410 <KAW>
A:Cross-references: UNIPROT:Q9UZX1; GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB5005
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB0760

```

C:Superfamily: hypothetical protein HI0333

Query Match 75.0%; Score 33; DB 2; Length 410;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ELTEVFEEFA 9
| | | | |
Db 199 ELTEAFGEFA 207

RESULT 11

T18252

conserved hypothetical protein - yeast (Candida albicans)

C:Species: Candida albicans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T18252

R:Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, November 1998

A:Reference number: Z18831

A:Accession: T18252

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-785 <BAR>

A:Cross-references: UNIPROT:O94070; EMBL:AL033503; PIDN:CAA22026.1

C:Genetics:

A:Note: Ca49C4.16

C:Superfamily: Saccharomyces cerevisiae hypothetical protein YNL126w

Query Match 75.0%; Score 33; DB 2; Length 785;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LTEVFEEFA 9
| | | | |
Db 189 LREVFEEFA 196

RESULT 12

W6WL39

E6 protein - human papillomavirus type 39

C:Species: human papillomavirus type 39

A:Note: host Homo sapiens (man)

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C:Accession: A38502

R:Volpers, C.; Strebeck, R.E.

Virology 181, 419-423, 1991

A:Title: Genome organization and nucleotide sequence of human papillomavirus type 39.

A:Reference number: A38502; MUID:91135017; PMID:1847266

A:Accession: A38502

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-158 <VOL>

A:Cross-references: UNIPROT:P24835; GB:M62849; EMBL:M38185; NID:G333245; PIDN:AAA47050.1

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; transforming protein; zinc finger

F:32-68/Region: zinc finger CCCC motif

F:105-141/Region: zinc finger CCCC motif

Query Match 72.7%; Score 32; DB 1; Length 158;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TEVFEEFA 9
| | | | |
Db 42 TEVFEEFA 48

RESULT 13

W6WLPR

E6 protein - human papillomavirus type ME180 (provirus)

C:Species: human papillomavirus type ME180

A:Note: host Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: C40509
R:Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5568, 1991
A:Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma (C40509)
A:Reference number: A40509; MUID:91374616; PMID:1716694
A:Accession: C40509
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-158 <REU>
A:Cross-references: UNIPROT:P27962; GB:M73258
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:32-68/Region: zinc finger CCCC motif
F:105-141/Region: zinc finger CCCC motif

Query Match 72.7%; Score 32; DB 1; Length 158;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TEVFEEFA 9
| | | | |
Db 42 TEVFEEFA 48

RESULT 14

S36561

E6 protein - human papillomavirus type 45

C:Species: human papillomavirus type 45

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S36561

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36561

A:Molecule type: DNA

A:Residues: 1-158

A:Cross-references: UNIPROT:P21735; EMBL:X74479; NID:G397022; PIDN:CAA52573.1; PID:G39702

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 72.7%; Score 32; DB 2; Length 158;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ELTEVFEEFA 9
| | | | |
Db 40 ERTEVYQFA 48

RESULT 15

AF2180

diaminopimelate decarboxylase [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AF2180

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AF2180

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-464 <KUR>

A:Cross-references: UNIPROT:Q8YST7; GB:BA000019; PIDN:BA074696.1; PID:gi7132091; GSPDB:G

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all2997

C:Superfamily: diaminopimelate decarboxylase

Query Match 72.7%; Score 32; DB 2; Length 464;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ELTEVFEEF 8
: |||||
Db 213 DLAEVFEEF 220

Search completed: June 28, 2005, 21:27:41
Job time : 12.15 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-25

Perfect score: 41

Sequence: 1 KTVLELTV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	57	2 I56705	E6 protein - human
2	41	100.0	158	1 W6WL18	E6 protein - human
3	36	87.8	1483	2 T19751	hypothetical prote
4	33	80.5	123	2 B71350	probable ribosomal
5	33	80.5	451	2 A13623	acridinyl resistat
6	33	80.5	481	2 AE1207	two-component sens
7	33	80.5	500	1 ITHUC1	complement C1 inh
8	32	78.0	298	2 T34259	hypothetical prote
9	32	78.0	380	2 T48953	hypothetical prote
10	32	78.0	446	2 AC0617	integrase (impor
11	32	78.0	576	2 G72277	NH(3)-dependent NA
12	32	78.0	603	2 T39866	hypothetical prote
13	31	75.6	287	2 JQ1743	hypothetical 33.6K
14	31	75.6	343	2 T20529	hypothetical prote
15	31	75.6	350	2 G89445	hypothetical prote
16	31	75.6	362	2 C90674	hypothetical prote
17	31	75.6	362	2 C64758	yaba protein - Esc
18	31	75.6	365	2 F85524	hypothetical prote
19	31	75.6	492	2 G97858	hypothetical prote
20	31	75.6	492	2 F71643	hypothetical prote
21	31	75.6	644	2 T46211	hypothetical prote
22	31	75.6	993	2 S49461	synaptonemal compl
23	30	73.2	120	2 JN0432	ribosomal protein
24	30	73.2	132	2 C97738	hypothetical prote
25	30	73.2	236	2 D86778	acetylactate decar
26	30	73.2	236	2 D67116	hypothetical prote
27	30	73.2	242	2 D97229	probable pseudouri
28	30	73.2	254	1 WMBECT	major early 30K pr
29	30	73.2	254	2 B81293	hypothetical prote

30 30 73.2 269 2 F96506
31 30 73.2 305 2 D69822
32 30 73.2 326 2 AF2082
33 30 73.2 408 2 A70594
34 30 73.2 456 2 S31125
35 30 73.2 461 2 G70379
36 30 73.2 481 2 S47441
37 30 73.2 497 2 G81598
38 30 73.2 519 2 E86555
39 30 73.2 519 2 H72067
40 30 73.2 535 1 A69771
41 30 73.2 636 2 A84903
42 30 73.2 742 1 VGBEHT
43 30 73.2 743 1 VGBEHC
44 30 73.2 1262 1 B48758
45 30 73.2 1363 2 T47492

ALIGNMENTS

RESULT 1

I56705

E6 protein - human papillomavirus type 18

C:Species: human papillomavirus type 18

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I56705

R:Inagaki, Y.; Tsunokawa, Y.; Takebe, N.; Nawa, H.; Nakanishi, S.; Terada, M.; Sugimura,

J. Virol. 62, 1640-1646, 1988

A:Title: Nucleotide sequences of cDNAs for human papillomavirus type 18 transcripts in He

A:Reference number: I56705; MUID:88188247; PMID:2833614

A:Accession: I56705

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-57 <RES>

A:Cross-references: UNIPROT:Q90133; GB:M20324; NID:gl83933; PIDN:AAA99512.1; PID:G306834

C:Superfamily: papillomavirus E6 protein

Query Match 100.0%; Score 41; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 0.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9

Db 36 KTVLELTV 44

RESULT 2

W6WL18

E6 protein - human papillomavirus type 18

C:Species: human papillomavirus type 18

C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004

C:Accession: A26185; G26251

R:Seedorf, K.; Oltersdorf, T.; Kraemmer, G.; Roewekamp, W.

EMBO J. 6, 139-144, 1987

A:Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)

A:Reference number: A91068; MUID:87218459; PMID:3034571

A:Accession: A26185

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P06463; GB:X04773; NID:G60876; PIDN:CAA28466.1; PID:G60877

R:Cole, S.T.; Danos, O.

J. Mol. Biol. 193, 599-608, 1987

A:Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 18

A:Reference number: A92937; MUID:87283882; PMID:3039146

A:Accession: G26251

A:Molecule type: DNA

A:Residues: 1-158 <COL>

A:Cross-references: GB:X05015; NID:G60975; PIDN:CAA28664.1; PID:G60976

R:Matlashewski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pim, D.; Crawford, L.

J. Gen. Virol. 67, 1909-1916, 1986

A:Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the p

A:Reference number: A92791; MUID:86306665; PMID:3018129

A;Contents: annotation; identification of the protein
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;32-68/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif

Query Match 100.0%; Score 41; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELDEV 9
| | | | |
Db 36 KTVLELDEV 44

RESULT 3
Tl9751
hypothetical protein C35CS.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: Tl9751
R;White, S.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z19173
A;Accession: Tl9751
A;Status: preliminary; translated from GB/EMBL/DDBB
A:Molecule type: DNA
A;Residues: 1-1483 <WIL>
A;Cross-references: UNIPROT:Q93332; EMBL:Z78417; PIDN:CAB01688.1; GSPDB:GN00028; CESP:C35CS
A;Experimental source: clone C35CS
C;Genetics:
A;Gene: CESP:C35CS.2
A;Map position: X
A;Introns: 61/1; 203/3; 248/1; 293/3; 331/1; 437/1; 485/2; 523/2; 556/1; 595/3; 620/2; 620/2;

Query Match 87.8%; Score 36; DB 2; Length 1483;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELDEV 9
| | | | |
Db 665 KTVLELSEI 673

RESULT 4
B71350
Probable ribosomal protein L7/l12 (rplL) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: B71350
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin-ther, J.; Khaliq, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDowell, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: B71350
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A;Residues: 1-129 <COL>
A;Cross-references: UNIPROT:O83268; GB:A8001205; NID:G3322501; PIDN:AAC6522
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: IP0240
C;Superfamily: Escherichia coli ribosomal protein L12

Query Match 80.5%; Score 33; DB 2; Length 129;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELDEV 9
| | | | |
Db 16 KTVLELSEL 24

RESULT 5

Ai3623
acriflavin resistance protein a precursor [imported] - Brucella melitensis (strain 16M)
. C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AI3623
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, J.; Kaper, A.B.; Wilson, D.A.; U.S.A. 99, 443-448, 2002
Proc. Natl. Acad. Sci. U.S.A.
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AI3623
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-451 <KUR>
A:Cross-references: UNIPROT:Q8YBI6; GB:AE008918; PIDN:AAL54156.1; PID:g17985121; GSPDB:GN
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEII0914
A:Map position: II

Query Match 80.5%; Score 33; DB 2; Length 451;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTE 8
|||:|||
Db 284 KTIIDLTE 291

RESULT 6

AE1207
two-component sensor histidine kinase homolog lmo1061 [imported] - Listeria monocytogenes
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AE1207
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Faihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schluter, T.; Smoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of Listeria species.
A:Reference number: AE1077; MUID:21537279; PMID:11679669
A:Accession: AE1207
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-481 <GLA>
A:Cross-references: UNIPROT:Q8Y857; GB:NC_003210; PIDN:CAC99139.1; PID:g16410463; GSPDB:G
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1061

```

Query Match      80.5%;   Score 33;   DB 2;   Length 481;
Best Local Similarity 77.8%;
Pred. No. 50;
Matches 7;   Conservative 1;   Mismatches 1;   Indels 0;   Gaps 0;

Oy      1 KTVLELTEV 9
      ||:|||||
Db      238 KTMLELNEV 246

RESULT 7
IRHUCI
complement C1 inhibitor precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S15386; S00403; A38781; B38781; A24161; A38782; S03370; A34847; S15084; A24;
R:Cartier, P.E.; Duponchel, C.; Tosi, M.; Fothergill, J.E.
Eur. J. Biochem. 197, 301-308, 1991
A:Title: Complete nucleotide sequence of the gene for human C1 inhibitor with an unusual

```

A:Reference number: S15385; MUID:91224119; PMID:2026152
 A:Accession: S15386
 A:Molecule type: DNA
 A:Residues: 1-500 <CA2>
 A:Cross-references: UNIPROT:P05155; EMBL:X54486; NID:g29534; PIDN:CAA38358.1; PID:g29535
 R:Carter, P.E.; Dunbar, B.; Fothergill, J.E.
 Eur. J. Biochem. 173, 163-169, 1988
 A:Title: Genomic and cDNA cloning of the human C1 inhibitor. Intron-exon junctions and cDNA sequence
 A:Reference number: S00403; MUID:88185313; PMID:3267220
 A:Accession: S00403
 A:Molecule type: DNA
 A:Residues: 1-500 <CA3>
 A:Cross-references: EMBL:X07427; NID:g29520; PIDN:CAA30314.1; PID:g1197499
 A:Accession: A38781
 A:Molecule type: mRNA
 A:Residues: 178-500 <CA3>
 A:Cross-references: GB:X07577; NID:g29536; PIDN:CAA30469.1; PID:g1340170
 A:Accession: B38781
 A:Molecule type: protein
 A:Residues: 173-237, 'X', 239-252, 'X', 254, 'X', 256-264, 'X', 266-268; 277-286; 330-333; 335-340; 342-343; 345-346; 348-349; 351-352; 354-355; 357-358; 360-361; 363-364; 366-367; 369-370; 372-373; 375-376; 378-379; 381-382; 384-385; 387-388; 390-391; 393-394; 396-397; 399-400; 402-403; 405-406; 408-409; 411-412; 414-415; 417-418; 420-421; 423-424; 426-427; 429-430; 432-433; 435-436; 438-439; 441-442; 444-445; 447-448; 450-451; 453-454; 456-457; 459-460; 462-463; 465-466; 468-469; 471-472; 474-475; 477-478; 480-481; 483-484; 486-487; 489-490; 492-493; 495-496; 498-499; 501-502; 504-505; 507-508; 510-511; 513-514; 516-517; 519-520; 522-523; 525-526; 528-529; 531-532; 534-535; 537-538; 540-541; 543-544; 546-547; 549-550; 552-553; 555-556; 558-559; 561-562; 564-565; 567-568; 570-571; 573-574; 576-577; 579-580; 582-583; 585-586; 588-589; 591-592; 594-595; 597-598; 600-601; 603-604; 606-607; 609-610; 612-613; 615-616; 618-619; 621-622; 624-625; 627-628; 630-631; 633-634; 636-637; 639-640; 642-643; 645-646; 648-649; 651-652; 654-655; 657-658; 660-661; 663-664; 666-667; 669-670; 672-673; 675-676; 678-679; 681-682; 684-685; 687-688; 690-691; 693-694; 696-697; 699-700; 702-703; 705-706; 708-709; 711-712; 714-715; 717-718; 720-721; 723-724; 726-727; 729-730; 732-733; 735-736; 738-739; 741-742; 744-745; 747-748; 750-751; 753-754; 756-757; 759-760; 762-763; 765-766; 768-769; 771-772; 774-775; 777-778; 780-781; 783-784; 786-787; 789-790; 792-793; 795-796; 798-799; 801-802; 804-805; 807-808; 810-811; 813-814; 816-817; 819-820; 822-823; 825-826; 828-829; 831-832; 834-835; 837-838; 840-841; 843-844; 846-847; 849-850; 852-853; 855-856; 858-859; 861-862; 864-865; 867-868; 870-871; 873-874; 876-877; 879-880; 882-883; 885-886; 888-889; 891-892; 894-895; 897-898; 899-900; 902-903; 905-906; 908-909; 911-912; 914-915; 917-918; 920-921; 923-924; 926-927; 929-930; 932-933; 935-936; 938-939; 941-942; 944-945; 947-948; 950-951; 953-954; 956-957; 959-960; 962-963; 965-966; 968-969; 971-972; 974-975; 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R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseid, M.; Mewes, H.W.; Rudd, S.;
submitted to the Protein Sequence Database, April 2000
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R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moul, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
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Db 99 TVLELTE 105

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R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
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Query Match 78.0%; Score 32; DB 2; Length 576;
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Db 530 KTVLDTVTEM 538

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C;Accession: T39866
R;Volckaert, G.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, February 1998
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C;Genetics:
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Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9
||| |||||
Db 24 KTVLELTV 32

RESULT 13
JQ1743
hypothetical 33.6K protein - rabbit fibroma virus
N;Alternate names: H2R protein; protein kinase homolog
C;Species: rabbit fibroma virus, Shope fibroma virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JQ1743
R;Massung, R.F.; McFadden, G.; Moyer, R.W.
J. Gen. Virol. 73, 2903-2911, 1992

Search completed: June 28, 2005, 21:27:40
Job time : 13.15 secs

A>Title: Nucleotide sequence analysis of a unique near-terminal region of the tumorigen
A:Reference number: JQ1741; MUID:93057362; PMID:1331293
A:Accession: JQ1743
A:Molecule type: DNA
A:Residues: 1-287 <MAS>
A:Cross-references: UNIPROT:Q9Q8T6

Query Match 75.6%; Score 31; DB 2; Length 287;
Best Local Similarity 75.0%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTVLELTE 8
||:||||
DB 53 KAILELTE 60

RESULT 14
T20529
hypothetical protein F07A11.5 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T20529
R:Palmer, S.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z19287
A:Accession: T20529
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-343 <WIL>
A:Cross-references: UNIPROT:Q19133; EMBL:Z66511; PIDN:CAA91318.1; GSPDB:GN000020; CESP:FO
A:Experimental source: clone F07A11
C:Genetics:
A:Gene: CESP:F07A11.5
A:Map position: 2
A:Introns: 19/1; 49/2; 136/1; 221/3; 259/1; 284/3
C:Superfamily: ribokinase

Query Match 75.6%; Score 31; DB 2; Length 343;
Best Local Similarity 55.6%; Pred. No. 92;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTVLELTEV 9
||:||||:
DB 206 KTIELVDI 214

RESULT 15
G69445
hypothetical protein AF1568 - *Archaeoglobus fulgidus*
C:Species: *Archaeoglobus fulgidus*
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: G69445
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiaich, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: G69445
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-350 <KLE>
A:Cross-references: UNIPROT:O28704; GB:AE0000994; GB:AE000782; NID:G2689317; PIDN:AAB8968

Query Match 75.6%; Score 31; DB 2; Length 350;
Best Local Similarity 55.6%; Pred. No. 94;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTVLELTEV 9
||:||||:
DB 57 KTIENVTEI 65

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-24

Perfect score: 53

Sequence: 1 EITCVYCKT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	53	100.0	57	2 Q90133	Q90133 human papil
2	53	100.0	158	1 V56 HPV18	P06463 human papil
3	53	100.0	158	2 Q9NPN8	Q9NPN8 human papil
4	45	84.9	157	2 Q9WHG0	Q9WHG0 human papil
5	45	84.9	470	2 Q9Y4Z3	Q9Y4Z3 homo sapien
6	45	84.9	617	2 Q9Y4Z4	Q9Y4Z4 homo sapien
7	45	84.9	734	2 Q75112	Q75112 homo sapien
8	42	79.2	62	2 Q8F6V1	Q8F6V1 leptospira
9	42	79.2	158	1 V56 HPV70	P50804 human papil
10	42	79.2	304	2 Q75F40	Q75F40 ashbya goss
11	41	77.4	148	2 Q676V2	Q676V2 human papil
12	41	77.4	158	2 Q8MWF0	Q8MWF0 drosophila
13	41	77.4	336	2 Q16329	Q16329 caenorhabdi
14	41	77.4	863	2 Q7PPY6	Q7PPY6 anopheles g
15	41	77.4	863	2 Q7Q9N5	Q7Q9N5 anopheles g
16	40	75.5	154	1 V56 HPV40	P36812 human papil
17	40	75.5	336	2 Q16330	Q16330 caenorhabdi
18	40	75.5	421	2 Q6INU3	Q6INU3 xenopus lae
19	40	75.5	489	2 Q7R8G3	Q7R8G3 plasmodium
20	40	75.5	543	2 Q6BGX1	Q6BGX1 debaryomyce
21	40	75.5	622	2 Q811P2	Q811P2 mus musculu
22	40	75.5	649	2 Q6ZN20	Q6ZN20 homo sapien
23	40	75.5	661	2 Q811P4	Q811P4 mus musculu
24	40	75.5	661	2 Q9UKS3	Q9UKS3 mus musculu
25	40	75.5	679	2 Q811P3	Q811P3 mus musculu
26	40	75.5	723	2 Q3UKS4	Q3UKS4 mus musculu
27	40	75.5	723	2 Q9VWH2	Q9VWH2 mus musculu
28	40	75.5	730	2 Q6A038	Q6A038 mus musculu
29	40	75.5	1521	2 Q7RNB0	Q7RNB0 plasmodium
30	40	75.5	3550	2 Q9JUN2	Q9JUN2 mus musculu
31	40	75.5	3567	2 Q86UP3	Q86UP3 homo sapien

32 39 73.6 151 1 V56 HPV51 P25554 human papil
33 39 73.6 290 1 HSLO_STRPN P64403 streptococc
34 39 73.6 290 1 HSLO_STRPN P64404 streptococc
35 39 73.6 430 2 Q67RH9 Q67rh9 symbiobacte
36 39 73.6 497 2 Q7Q2N5 Q7Q2n5 anopheles g
37 39 73.6 670 2 Q8FAC1 Q8fac1 escherichia
38 38 71.7 141 2 Q9VIR2 Q9virk2 pyrococcus
39 38 71.7 148 2 Q81997 Q81997 human papil
40 38 71.7 150 1 V56 HPV26 P36807 human papil
41 38 71.7 151 2 Q994A0 Q994a0 human papil
42 38 71.7 151 2 Q9IR59 Q9ir59 human papil
43 38 71.7 151 2 Q9JH51 Q9jhs1 human papil
44 38 71.7 154 2 Q705E9 Q705e9 human papil
45 38 71.7 158 1 V56 HPV45 P21735 human papil

ALIGNMENTS

RESULT 1
Q90133 PRELIMINARY; PRT; 57 AA.
AC Q90133;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Protein E6.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8918247; PubMed=2833614;
RA Inagaki Y., Tsunokawa Y., Takebe N., Nakanishi S., Terada M.,
RA Sugimura T.;
RT "Nucleotide sequences of cDNAs for human papillomavirus type 18
RT transcripts in HeLa cells.";
RL J. Virol. 62:1640-1646(1988).
DR EMBL; M20324; AAA99512.1; .
DR PIR; I56705; I56705.
SQ SEQUENCE 57 AA; 6531 MW; 31CF1A65B3740D2C CRC64;

Query Match 100.0%; Score 53; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9
|||
Db 29 EITCVYCKT 37

RESULT 2
V56 HPV18 STANDARD; PRT; 158 AA.
ID V56 HPV18
AC P06463;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87283882; PubMed=3039146;
RA Cole S.T., Danos O.;
RT "Nucleotide sequence and comparative analysis of the human
RT papillomavirus type 18 genome. Phylogeny of papillomaviruses and
RT repeated structure of the E6 and E7 gene products.";
RL J. Mol. Biol. 193:599-608(1987).

RP SEQUENCE FROM N.A.
RX MEDLINE=86306665; PubMed=3018129;
RA Matlashewski G., Banks L., Wu-Liao J., Spence P., Pim D., Crawford L.;
RT "The expression of human papillomavirus type 18 E6 protein in bacteria
and the production of anti-E6 antibodies.";
RL J. Gen. Virol. 67:1909-1916(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88188247; PubMed=2833614;
RA Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M.,
RA Sugimura T.;
RT Nucleotide sequences of cDNAs for human papillomavirus type 18
transcripts in HeLa cells.;
RL J. Virol. 62:1640-1646(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=87053870; PubMed=3023067;
RA Schneider-Gaedcke A., Schwarz E.;
RT "Different human cervical carcinoma cell lines show similar
transcription patterns of human papillomavirus type 18 early genes.";
RL EMBO J. 5:2285-2292(1986).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=87218459; PubMed=3034571;
RA Seedorf K., Oltersdorf T., Kraemer G., Roewekamp W.;
RT "Identification of early proteins of the human papilloma viruses type
16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells.";
RL EMBO J. 6:139-144(1987).
RN [6]
RP ZINC-BINDING.
RX MEDLINE=89385606; PubMed=2550872;
RA Groisman S.R., Laimins L.A.;
RT "E6 protein of human papillomavirus type 18 binds zinc.";
RL Oncogene 4:1089-1093(1989).
RN [7]
RP INTERACTION WITH FBLN1, AND INHIBITION OF E6-MEDIATED TRANSFORMATION.
RX MEDLINE=22189366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;
RA Du M., Fan X., Hong E., Chen J.J.;
RT "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";
RL Biochem. Biophys. Res. Commun. 296:962-969(2002).
CC -!- FUNCTION: This protein has transforming activity in vitro.
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double
stranded DNA (in vitro). FBLN1.
CC -!- SUBUNIT: Interacts with FBLN1.
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; X04354; CAA27879.1; -;
DR EMBL; X05015; CAA28664.1; -;
DR EMBL; M20325; AAA99514.1; -;
DR EMBL; M26798; AAA46946.1; -;
DR EMBL; X04773; CAA28466.1; -;
DR EMBL; A06324; CAA00539.1; -;
DR EMBL; A06328; CAA00542.1; -;
DR F01; A26165; W6WU18.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR DNA-binding; Early protein; Nuclear protein; Oncogene; Zinc-finger.
FT ZN_FING 32 68
FT ZN_FING 105 141
FT ZN_FING 22 22
FT CONFLICT 22 22 N -> S (in Ref. 4).
SQ SEQUENCE 158 AA; 18871 MW; 5BCF13CF43D157FA CRC64;
Query Match 100.0%; Score 53; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EITCVYCKT 9
Db 29 EITCVYCKT 37
| | | | | | | | | |
| | | | | | | | | |
RESULT 3
Q9QNP8 PRELIMINARY; PRT; 158 AA.
ID Q9QNP8
AC Q9QNP8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RA Laassri M., Gul'ko L., Vinokurova S., Kissel'ova N., Veiko V.,
RA Kissel'ev F.;
RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
Transformation Potential of E7 Gene and its Mutants.";
RL Virus Genes 182:139-149(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Veiko V.P.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y18491; CAB53096.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 18886 MW; 5BCF13CF43D407AF CRC64;
Query Match 100.0%; Score 53; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EITCVYCKT 9
Db 29 EITCVYCKT 37
| | | | | | | | | |
| | | | | | | | | |
RESULT 4
Q9WHG0 PRELIMINARY; PRT; 157 AA.
ID Q9WHG0
AC Q9WHG0
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative transforming protein E6.
OS Human papillomavirus candHPV8.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus; Human papillomavirus unidentified type.
OX NCBI_TaxID=151757;
RN [1]
RP SEQUENCE FROM N.A.
RA Chow V.T., Leong P.W.;
RT "Complete nucleotide sequence, genomic organization and phylogenetic
analysis of a novel genital human papillomavirus type, HLT7474-S.";
RL J. Gen. Virol. 80:2923-2929(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Chow V.T.K., Leong W.F.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF131950; AAD24181.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.


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DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 157 AA; 18450 MW; 1B154BA2C49EED7 CRC64;

Query Match      84.9%; Score 45; DB 2; Length 157;
Best Local Similarity 77.8%; Pred. No. 3.8;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9
Db 29 EISCYCKS 37

RESULT 5
ID Q9Y4Z3 PRELIMINARY; PRT; 470 AA.
AC Q9Y4Z3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE ZASP protein (Fragment).
GN Name=ZASP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle and heart;
RX MEDLINE=93357848; PubMed=10427098; DOI=10.1083/jcb.146.2.465;
RA Faulkner G., Pallavicini A., Formentin E., Comelli A., Levoletta C.,
RA Trevisan S., Bortoletto G., Scannapieco P., Salamon M., Mouly G.,
RA Valle G., Lanfranchi G.;
RT "ZASP: a new Z-band alternatively spliced PDZ-motif protein.";
RL J. Cell Biol. 146:465-475(1999).
CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC -!- SIMILARITY: Contains 3 LIM zinc-binding domains.
DR EMBL: AJ133768; CAB46729.1; -.
DR GO: GO:0005515; F:protein binding; IEA.
DR HSSP: Q05158; IQLI.
DR InterPro: IPR000345; CytC_heme_BS.
DR InterPro: IPR001781; LIM.
DR InterPro: IPR001478; PDZ.
DR Pfam: PF00412; LIM; 3.
DR Pfam: PF00595; PDZ; 1.
DR ProDom: PD000094; LIM; 3.
DR SMART: SM00132; LIM; 3.
DR SMART: SM00228; PDZ; 1.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE: PS00478; LIM_DOMAIN_1; 2.
DR PROSITE: PS50023; LIM_DOMAIN_2; 3.
DR PROSITE: PS50106; PDZ; 1.
DR LIM domain; Metal-binding; Zinc.
FT NON TER 1
SQ SEQUENCE 470 AA; 50661 MW; AE787648FALA2BCF CRC64;

Query Match      84.9%; Score 45; DB 2; Length 470;
Best Local Similarity 77.8%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9
Db 317 EFTCAYCKT 325

RESULT 6
ID Q9Y4Z4 PRELIMINARY; PRT; 617 AA.
AC Q9Y4Z4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE ZASP protein (Fragment).
GN Name=ZASP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC -!- SIMILARITY: Contains 3 LIM zinc-binding domains.

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DE ZASP protein (Fragment).
GN Name=ZASP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle and heart;
RX MEDLINE=93357848; PubMed=10427098; DOI=10.1083/jcb.146.2.465;
RA Faulkner G., Pallavicini A., Formentin E., Comelli A., Levoletta C.,
RA Trevisan S., Bortoletto G., Scannapieco P., Salamon M., Mouly G.,
RA Valle G., Lanfranchi G.;
RT "ZASP: a new Z-band alternatively spliced PDZ-motif protein.";
RL J. Cell Biol. 146:465-475(1999).
CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC -!- SIMILARITY: Contains 3 LIM zinc-binding domains.
DR EMBL: AJ133767; CAB46728.1; -.
DR GO: GO:0005515; F:protein binding; IEA.
DR HSSP: P48059; INYP.
DR InterPro: IPR000345; CytC_heme_BS.
DR InterPro: IPR001781; LIM.
DR InterPro: IPR001478; PDZ.
DR InterPro: IPR008916; Retrov_capsid_C.
DR InterPro: IPR006643; ZASP.
DR Pfam: PF00412; LIM; 3.
DR Pfam: PF00595; PDZ; 1.
DR ProDom: PD000094; LIM; 3.
DR SMART: SM00132; LIM; 3.
DR SMART: SM00228; PDZ; 1.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE: PS00478; LIM_DOMAIN_1; 2.
DR PROSITE: PS50023; LIM_DOMAIN_2; 3.
DR PROSITE: PS50106; PDZ; 1.
DR LIM domain; Metal-binding; Zinc.
FT NON TER 1
SQ SEQUENCE 617 AA; 66518 MW; 22FC77402352A340 CRC64;

Query Match      84.9%; Score 45; DB 2; Length 617;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9
Db 464 EFTCAYCKT 472

RESULT 7
ID Q75112 PRELIMINARY; PRT; 734 AA.
AC Q75112;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE KIAA0613 protein (Fragment).
GN Name=KIAA0613;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC -!- SIMILARITY: Contains 3 LIM zinc-binding domains.

```

```

DR EMBL; AB014513; BAA31588.1; -.
DR HSP; Q05158; 1QLI.
DR Genew; HGNC:15710; LDB3.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR000345; Cyt c heme_BS.
DR InterPro; IPR000306; Ig MHC.
DR InterPro; IPR001781; LIM.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR008916; Retrov_capsid_C.
DR InterPro; IPR006643; ZASP.
DR Pfam; PF00412; LIM; 3.
DR Pfam; PF00595; PDZ; 1.
DR ProDom; PD000094; LIM; 3.
DR SMART; SM00132; LIM; 3.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00735; ZW; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
DR PROSITE; PS00478; LIM DOMAIN 1; 2.
DR PROSITE; PS00023; LIM DOMAIN_2; 3.
DR PROSITE; PS0106; PDZ; 1.
DR LIM domain; Metal-binding; Zinc.
FT NON TER 1
SQ SEQUENCE 734 AA; 77738 MW; 5CB9AC39CC690FB8 CRC64;

Query Match 84.9%; Score 45; DB 2; Length 734;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EITCVYCKT 9
DB 581 EFTCAYCKT 589

RESULT 8
ID Q8F6V1 PRELIMINARY; PRT; 62 AA.
AC Q8F6V1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypothetical protein.
GN OrderedLocusNames=LAI199;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AE011302; AAN48398.1; -.
KW Complete proteome.
SQ SEQUENCE 62 AA; 7513 MW; 4E4A58229E970672 CRC64;

Query Match 79.2%; Score 42; DB 2; Length 62;
Best Local Similarity 66.7%; Pred. No. 5.4;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EITCVYCKT 9
DB 42 ELTCVWCKS 50

RESULT 9
ID_VE6_HPV70 STANDARD; PRT; 158 AA.
AC PS0804;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 70.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=39457;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96249586; PubMed=8815087;
RA Forslund O., Hansson B.G.;
RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70,
RT related to the potentially oncogenic HPV39.";
RL J. Clin. Microbiol. 34:738-744(1996).
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double
CC stranded DNA (in vitro).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U21941; AAC54850.1; -.
DR EMBL; U22461; AAC54880.1; -.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW DNA-binding; Early protein; Nuclear protein; Zinc-finger.
FT ZN_FING 32 68
FT ZN_FING 105 141
FT ZN_FING 100 100 N -> D (in Ref. 2).
FT CONFLICT 100 100
SQ SEQUENCE 158 AA; 18617 MW; 6B610800D923D6DE CRC64;

Query Match 79.2%; Score 42; DB 1; Length 158;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ITCVYCKT 9
DB 30 IDCYVYCKT 37

RESULT 10
ID Q75F40 PRELIMINARY; PRT; 304 AA.
AC Q75F40;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AAL112cp.
GN ORFNames=AAL112C;
OS Ashbya gossypii (Yeast) (Bremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-ATCC 10895;
RA Dietrich F.S., Voegeli S.E., Brachet S., Lerch A., Gaffney T.,
RA Philippsen P.;
RL EMBL: A016814; to the EMBL/GenBank/DBJ databases.
DR EMBL: A016814; AAS0254.1; -
DR AGD: AAL112C; -
SQ SEQUENCE 304 AA; 36190 MW; EF90DD2FF9C0DAD8 CRC64;

Query Match      79.2%; Score 42; DB 2; Length 304;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EITCVYCK 8
Db 271 ELTCTYCK 278

RESULT 11
Q576V2 PRELIMINARY; PRT; 148 AA.
AC Q676V2;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Putative transforming protein E6.
OS Human papillomavirus type 62.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=37117;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15346342;
RA Fu L., Terai M., Matsukura T., Herrero R., Burk R.D.;
RT "Codetection of a Mixed Population of candHPV62 Containing Wild-Type
RT and Disrupted E1 Open-Reading Frame in a 45-Year-Old Woman with Normal
RT Cytology.";
RL J. Infect. Dis. 190:1303-1309(2004).
DR EMBL: AY395706; AAR32246.1; -
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 148 AA; 17061 MW; C0BF71566CD02689 CRC64;

Query Match      77.4%; Score 41; DB 2; Length 148;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ITCVYCKT 9
Db 27 LTCIFCKT 34

RESULT 12
Q8MMF0 PRELIMINARY; PRT; 158 AA.
AC Q8MMF0;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE CG30219-PA.
GN ORFNames=CG30219;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

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Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Bianknoch C., Baldwin D.,
RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Benson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celnikier S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnikier S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Mirra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.B., Whittier E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celnikier S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.

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RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE003458; AAM71110.1; -.
DR FlyBase; FBN0050219; CG30219.
SQ SEQUENCE 158 AA; 18193 MW; C22E8AD7819359A7 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 158;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9
Db 115 DITCPYCRT 123

RESULT 13
O16329 PRELIMINARY; PRT; 336 AA.
AC O16329;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Seven tm receptor protein 143.
GN Caenorhabditis elegans.
OS Caenorhabditis elegans; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RL investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "The sequence of C. elegans cosmid C09H5.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Wilson R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF016433; AAB65389.1; -.
DR PIR: T31761; T31761.
DR WormBase; WBGene00006190; C09H5.4.
DR WormPep; C09H5.4; C808046.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003002; 7TM_chemreceptl.
DR InterPro; IPR000168; Nm7TM_chemrecept.
DR Pfam; PF01461; 7tm_4; 1.
DR Receptor.
KW SEQUENCE 336 AA; 38603 MW; E07C248876CACC24 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 336;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9
Db 91 EITCLYCSS 99

us-08-170-344-24.rup Page 6
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Qy 1 BITCVYCKT 9
Db :||| |
830 QISCVYCS 838

Search completed: June 28, 2005, 21:23:50
Job time : 57.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-24

Perfect score: 53

Sequence: 1 BITCVYCKT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	57	2 I56705	E6 protein - human
2	53	100.0	158	1 W6WL18	E6 protein - human
3	41	77.4	336	2 T31761	hypothetical prote
4	40	75.5	154	2 S36555	E6 protein - human
5	40	75.5	336	2 T31762	hypothetical prote
6	39	73.6	151	1 W6WL51	E6 protein - human
7	39	73.6	290	2 F98120	chaperonin (heat s
8	39	73.6	290	2 F95255	chaperonin, 33 kDa
9	38	71.7	141	2 D75158	hypothetical prote
10	38	71.7	150	2 S36544	E6 protein - human
11	38	71.7	158	2 S36561	E6 protein - human
12	38	71.7	2408	2 T24483	hypothetical prote
13	37	69.8	84	2 AH3402	hypothetical cytos
14	37	69.8	152	2 AE1812	hypothetical prote
15	37	69.8	153	1 S15621	E6 protein - human
16	37	69.8	153	2 S36503	E6 protein - human
17	37	69.8	155	1 W6WL56	E6 protein - human
18	37	69.8	155	2 A44890	E6 protein - human
19	37	69.8	212	2 I40603	hypothetical prote
20	37	69.8	328	2 E71863	phenylalanine-tRNA
21	37	69.8	328	2 C64570	phenylalanine-tRNA
22	37	69.8	330	2 A81363	phenylalanine-tRNA
23	37	69.8	633	2 F96652	protein F23N19.13
24	36	67.9	94	2 B82847	hypothetical prote
25	36	67.9	133	2 S77067	hypothetical prote
26	36	67.9	148	2 S36515	E6 protein - human
27	36	67.9	149	1 W6WL31	E6 protein - human
28	36	67.9	149	1 W6WL35	E6 protein - human
29	36	67.9	150	1 W6WL6	E6 protein - human

30	36	67.9	155	2 T35626	probable membrane
31	36	67.9	649	2 S58064	hdc protein - frui
32	36	67.9	688	2 T33708	hypothetical prote
33	36	67.9	930	2 T34334	hypothetical prote
34	36	67.9	1406	2 T17429	gag-pol polyprotei
35	36	67.9	3085	2 T00327	polyprotein - infe
36	35	66.0	135	1 W6WL5P	E6 protein - Euro
37	35	66.0	150	1 W6WL42	E6 protein - human
38	35	66.0	158	1 W6WL39	E6 protein - human
39	35	66.0	158	1 W6WLHS	protein E6 - human
40	35	66.0	204	2 T10275	late expression fa
41	35	66.0	238	2 AD0109	thiol disulfide in
42	35	66.0	351	2 T23625	probable alcohol d
43	35	66.0	367	2 H88035	protein M01D1.1 [i
44	35	66.0	411	2 JC1482	TYA protein - yeas
45	35	66.0	413	2 S52610	TYA protein - yeas

ALIGNMENTS

RESULT 1

I56705

E6 protein - human papillomavirus type 18

C:Species: human papillomavirus type 18

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I56705

R: Inagaki, Y.; Tsunokawa, Y.; Takebe, N.; Nawa, H.; Nakanishi, S.; Terada, M.; Sugimura,

J. Virol. 62, 1640-1646, 1988

A:Title: Nucleotide sequences of cDNAs for human papillomavirus type 18 transcripts in He

A:Reference number: I56705; MUID:88188247; PMID:2833614

A:Accession: I56705

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-57 <RES>

A:Cross-references: UNIPROT:Q90133; GB:M20324; NID:g183933; PIDN:AAA99512.1; PID:g306834

C:Superfamily: papillomavirus E6 protein

Query Match 100.0%; Score 53; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 0.065;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BITCVYCKT 9

Db 29 BITCVYCKT 37

RESULT 2

W6WL18

E6 protein - human papillomavirus type 18

C:Species: human papillomavirus type 18

C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004

C:Accession: A26185; G26251

R:Seedorf, K.; Oltersdorf, T.; Kraemmer, G.; Roewekamp, W.

EMBO J. 6, 139-144, 1987

A:Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)

A:Reference number: A91068; MUID:87218459; PMID:3034571

A:Accession: A26185

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P06463; GB:X04773; NID:g60876; PIDN:CAA28466.1; PID:g60877

R: Cole, S.T.; Danos, O.

J. Mol. Biol. 193, 599-608, 1987

A:Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 1

A:Reference number: A92937; MUID:87283882; PMID:3039146

A:Accession: G36251

A:Molecule type: DNA

A:Residues: 1-158 <COL>

A:Cross-references: GB:X05015; NID:g60975; PIDN:CAA28664.1; PID:g60976

R: Matlashewski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pim, D.; Crawford, L.

J. Gen. Virol. 67, 1909-1916, 1986

A:Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the p

A:Reference number: A92791; MUID:86306665; PMID:3018129

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A;Contents: annotation; identification of the protein
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;32-68/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif

Query Match      100.0%; Score 53; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9
Db 29 EITCVYCKT 37

RESULT 3
T31761
hypothetical protein C09H5.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31761
R;Le, T.T.; Waterston, R.
A;Description: The sequence of C. elegans cosmid C09H5.
A;Reference number: Z21081
A;Accession: T31761
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-336 <LET>
A;Cross-references: UNIPROT:O16329; EMBL:AF016433; PIDN:AAB65389.1; GSPDB:GN00023; CESP:
A;Experimental source: strain Bristol N2; clone C09H5
C;Genetics:
A;Gene: CESP:C09H5.4
A;Map position: 5
A;Introns: 65/3; 120/2; 165/2; 212/3; 255/3; 315/1

Query Match      77.4%; Score 41; DB 2; Length 336;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9
Db 91 EITCLYCSS 99

RESULT 4
S36555
E6 protein - human papillomavirus type 40
C;Species: human papillomavirus type 40
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36555
R;Deilius, H.; Hofmann, B.
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36555
A;Molecule type: DNA
A;Residues: 1-154 <DEL>
A;Cross-references: UNIPROT:P36812; EMBL:X74478; NID:G397014; PIDN:CAAS2567.1; PID:G6718
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match      75.5%; Score 40; DB 2; Length 154;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9
Db 27 QIDCVFCKT 35

RESULT 5
T31762
```

```
hypothetical protein C09H5.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31762
R;Le, T.T.; Waterston, R.
A;Description: The sequence of C. elegans cosmid C09H5.
A;Reference number: Z21081
A;Accession: T31762
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-336 <LET>
A;Cross-references: UNIPROT:O16330; EMBL:AF016433; PIDN:AAB65390.1; GSPDB:GN00023; CESP:
A;Experimental source: strain Bristol N2; clone C09H5
C;Genetics:
A;Gene: CESP:C09H5.5
A;Map position: 5
A;Introns: 65/3; 120/2; 165/2; 212/3; 255/3; 315/1

Query Match      75.5%; Score 40; DB 2; Length 336;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EITCVYCK 7
Db 91 EITCLYC 97

RESULT 6
W6WL51
E6 protein - human papillomavirus type 51
C;Species: human papillomavirus type 51
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: E40415
R;Lungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991
A;Title: Biologic properties and nucleotide sequence analysis of human papillomavirus type
A;Reference number: A40415; MUID:91303675; PMID:1649326
A;Accession: E40415
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-151 <LUN>
A;Cross-references: UNIPROT:P26554; GB:M62877
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match      73.6%; Score 39; DB 1; Length 151;
Best Local Similarity 62.5%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EITCVYCK 8
Db 27 QVVCVYCK 34

RESULT 7
F98120
chaperonin (heat shock protein 33) [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: F98120
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: F98120
A;Status: preliminary
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A:Molecule type: DNA
A:Residues: 1-290 <KUR>
A:Cross-references: UNIPROT:Q97N76; GB:AE007317; PIDN:AA00795.1; PID:g15459697; GSPDB:G
C:Genetics:
C:Gene: hep33
C:Superfamily: conserved hypothetical protein s111988

Query Match 73.6%; Score 39; DB 2; Length 290;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EITCVYCKT 9
|||||:|:
265 EITCQFCQT 273

Db

RESULT 8
F95255
chaperonin, 33 kDa [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: F95255
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: F95255
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-290 <KUR>
A:Cross-references: UNIPROT:Q97N76; GB:AE005672; PIDN:AAK76239.1; PID:g14973699; GSPDB:G
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP2188
C:Superfamily: conserved hypothetical protein s111988

Query Match 73.6%; Score 39; DB 2; Length 290;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EITCVYCKT 9
|||||:|:
265 EITCQFCQT 273

Db

RESULT 9
D75158
hypothetical protein PAB2064 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: D75158
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: D75158
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-141 <KAW>
A:Cross-references: UNIPROT:Q9V1K2; GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB4934
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2064
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH1854

Query Match 71.7%; Score 38; DB 2; Length 141;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ITCVYCKT 9

Db 34 ITCPYCKS 41
|||||:
RESULT 10
S36544
E6 protein - human papillomavirus type 26
C:Species: human papillomavirus type 26
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36544
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36544
A:Molecule type: DNA
A:Residues: 1-150
A:Cross-references: UNIPROT:P36807; EMBL:X74472; NID:g396956; PIDN:CAAS2530.1; PID:g396956
C:Superfamily: papillomavirus E6 protein
C:Keywords: early protein; zinc finger

Query Match 71.7%; Score 38; DB 2; Length 150;
Best Local Similarity 62.5%; Pred. No. 31;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EITCVYCK 8
|||||:
27 QVQCVCYCK 34

Db

RESULT 11
S36561
E6 protein - human papillomavirus type 45
C:Species: human papillomavirus type 45
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36561
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36561
A:Molecule type: DNA
A:Residues: 1-158
A:Cross-references: UNIPROT:P21735; EMBL:X44479; NID:g397022; PIDN:CAAS2573.1; PID:g39702
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 71.7%; Score 38; DB 2; Length 158;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ITCVYCK 8
|||||:
30 IACVYCK 36

Db

RESULT 12
T24483
hypothetical protein T05A1.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24483
R:Lloyd, C.
submitted to the EMBL Data Library, December 1995
A:Reference number: Z19897
A:Accession: T24483
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2408 <WIL>
A:Cross-references: UNIPROT:Q22184; EMBL:Z68219; PIDN:CAAS2477.1; GSPDB:GN00022; CESP:T0
A:Experimental source: clone T05A1
C:Genetics:
A:Gene: CESP:T05A1.4

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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-23
Perfect score: 46
Sequence: 1 LQDIEITCV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	57	2 Q90133	Q90133 human papil
2	46	100.0	158	1 V86 HPV18	P06463 human papil
3	46	100.0	158	2 Q90NP8	Q90NP8 human papil
4	42	91.3	157	2 Q9WHG0	Q9WHG0 human papil
5	40	87.0	99	2 Q9HWP0	Q9HWP0 pseudomonas
6	40	87.0	481	2 Q9VWK3	Q9VWK3 drosophila
7	39	84.8	148	2 Q8JNA1	Q8JNA1 human papil
8	37	80.4	285	2 Q17327	Q17327 caenorhabdi
9	36	78.3	135	2 Q6SKS2	Q6SKS2 human immun
10	36	78.3	156	2 Q6EGP5	Q6EGP5 human papil
11	36	78.3	156	2 Q6EQ02	Q6EQ02 human papil
12	36	78.3	156	2 Q6EGR6	Q6EGR6 human papil
13	36	78.3	274	1 GLO2 YEAST	Q05584 saccharomyc
14	36	78.3	274	2 Q6Q5S8	Q6Q5S8 saccharomyc
15	36	78.3	454	2 Q9SNM0	Q9SNM0 oryza sativ
16	36	78.3	1085	2 Q7Q193	Q7Q193 anopheles g
17	36	78.3	1834	2 Q6FJK7	Q6FJK7 candida gla
18	36	78.3	3347	2 Q8MMJ9	Q8MMJ9 bombyx mori
19	36	78.3	3354	2 Q8T101	Q8T101 bombyx mori
20	35	76.1	108	2 Q55903	Q55903 human immun
21	35	76.1	128	2 Q8FV49	Q8FV49 brucella su
22	35	76.1	148	2 Q81977	Q81977 human papil
23	35	76.1	158	1 V86 HPV39	P24835 human papil
24	35	76.1	158	1 V86 HPV45	P21735 human papil
25	35	76.1	158	2 Q9Y4Y4	Q9Y4Y4 homo sapien
26	35	76.1	158	2 Q10608	Q10608 human papil
27	35	76.1	160	2 Q8BE09	Q8BE09 foot-and-mo
28	35	76.1	160	2 Q8BE10	Q8BE10 foot-and-mo
29	35	76.1	160	2 Q8BE12	Q8BE12 foot-and-mo
30	35	76.1	160	2 Q8BE16	Q8BE16 foot-and-mo
31	35	76.1	160	2 Q8BE18	Q8BE18 foot-and-mo

ALIGNMENTS

RESULT 1

Q90133 PRELIMINARY; PRT; 57 AA.
AC Q90133;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Protein E6.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8818247; PubMed=2833614;
RA Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M., Sugimura T.;
RT "Nucleotide sequences of cDNAs for human papillomavirus type 18 transcripts in HeLa cells.";
RL J. Virol. 62:1640-1646(1988).
DR EMBL; M20324; AAA9512.1; -.
DR PIR; I56705; I56705.
SQ SEQUENCE 57 AA; 6531 MW; 31CF1A5B3740D2C CRC64;

Query Match 100.0%; Score 46; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
Db 25 LQDIEITCV 33

RESULT 2

V86 HPV18 STANDARD; PRT; 158 AA.
ID V86 HPV18
AC P06463;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87283882; PubMed=3039146;
RA Cole S.T., Danos O.;
RT "Nucleotide sequence and comparative analysis of the human papillomavirus type 18 genome. Phylogeny of papillomaviruses and repeated structure of the E6 and E7 gene products.";
RL J. Mol. Biol. 193:599-608(1987).

```
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=8630665; PubMed=3018129;
RA Matlashewski G., Banks L., Wu-Liao J., Spence P., Pim D., Crawford L.;
RT "The expression of human papillomavirus type 18 E6 protein in bacteria
RL and the production of anti-E6 antibodies.";
RL J. Gen. Virol. 67:1909-1916(1986).
RN
RP
[3]
RN SEQUENCE FROM N.A.
RX MEDLINE=8818247; PubMed=2833614;
RA Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M.,
RA Sugimura T.;
RT "Nucleotide sequences of cDNAs for human papillomavirus type 18
RL transcripts in HeLa cells.";
RL J. Virol. 62:1640-1646(1988).
RN
RP
[4]
RN SEQUENCE FROM N.A.
RX MEDLINE=87218459; PubMed=3023067;
RA Schneider-Gaedcke A., Schwarz E.;
RT "Different human cervical carcinoma cell lines show similar
RL transcription patterns of human papillomavirus type 18 early genes.";
RL EMBO J. 5:2285-2292(1986).
RN
RP
[5]
RN SEQUENCE FROM N.A.
RX MEDLINE=87218459; PubMed=3034571;
RA Seedorf K., Oltersdorf T., Kraemer G., Roewekamp W.;
RT "Identification of early proteins of the human papilloma viruses type
RL 16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells.";
RL EMBO J. 6:139-144(1987).
RN
RP
[6]
RN ZINC-BINDING.
RX MEDLINE=89385606; PubMed=2550872;
RA Grossman S.R., Laimins L.A.;
RT "E6 protein of human papillomavirus type 18 binds zinc.";
RL Oncogene 4:1089-1093(1989).
RN
RP
[7]
RN INTERACTION WITH FBIN1, AND INHIBITION OF E6-MEDIATED TRANSFORMATION.
RX MEDLINE=22189366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;
RA Du M., Fan X., Hong E., Chen J.J.;
RT "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";
RL Biochem. Biophys. Res. Commun. 296:962-969(2002).
CC
CC -!- FUNCTION: This protein has transforming activity in vitro.
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double
CC stranded DNA (in vitro). FBIN1.
CC -!- SUBUNIT: Interacts with FBIN1.
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL; X04354; CAA27879.1; -
DR EMBL; X05015; CAA28664.1; -
DR EMBL; M20325; AAA99514.1; -
DR EMBL; M26798; AAA46946.1; -
DR EMBL; X04773; CAA28466.1; -
DR EMBL; A06324; CAA00539.1; -
DR EMBL; A06328; CAA00542.1; -
DR F01; A26165; W6WLI8.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW DNA-binding; Early protein; Nuclear protein; Oncogene; Zinc-finger.
FT ZN_FING 32 68
FT ZN_FING 105 141
FT ZN_FING 22 22
FT CONFLICT 22 22 N -> S (in Ref. 4).
SQ SEQUENCE 158 AA; 18871 MW; 5BCF13CF43D157FA CRC64;
Query Match 100.0%; Score 46; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LQDIEITCV 9
Db 25 LQDIEITCV 33
RESULT 3
Q9QNP8 PRELIMINARY; PRT; 158 AA.
AC Q9QNP8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RN SEQUENCE FROM N.A.
RA Laassri M., Gul'ko L., Vinokurova S., Kissel'jova N., Veiko V.,
RA Kissel'jev F.;
RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
RL Transformation Potential of E7 Gene and its Mutants.";
RL Virus Genes 182:139-149(1999).
RN [2]
RN SEQUENCE FROM N.A.
RA Veiko V.P.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y18491; CAB53096.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 18886 MW; 5BCF13CF43D407AF CRC64;
Query Match 100.0%; Score 46; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LQDIEITCV 9
Db 25 LQDIEITCV 33
RESULT 4
Q9WHG0 PRELIMINARY; PRT; 157 AA.
AC Q9WHG0;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative transforming protein E6.
OS Human papillomavirus candHPV85.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus; Human papillomavirus unidentified type.
OX NCBI_TaxID=151757;
RN [1]
RN SEQUENCE FROM N.A.
RA Chow V.T., Leong P.W.;
RT "Complete nucleotide sequence, genomic organization and phylogenetic
RL analysis of a novel genital human papillomavirus type, HLT7474-S.";
RL J. Gen. Virol. 80:2923-2929(1999).
RN [2]
RN SEQUENCE FROM N.A.
RA Chow V.T.K., Leong W.F.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF131950; AAD24181.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
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DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 157 AA; 18450 MW; 1B154BA2C49EBDE7 CRC64;

Query Match
Best Local Similarity 91.3%; Score 42; DB 2; Length 157;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
Db 25 LQDIEISCV 33

RESULT 5
Q9HWFO PRELIMINARY; PRT; 99 AA.
AC Q9HWFO;
DT 01-MAR-2001 (TREMELrel. 16, Created) (
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=PA4141;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.B., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RL Nature 406:959-964 (2000).
DR EMBL; AE004830; AAG07528.1; -
RA PIR; D83129; D83129.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 99 AA; 9656 MW; CEC469A7938A2BFF CRC64;

Query Match
Best Local Similarity 87.0%; Score 40; DB 2; Length 99;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
Db 4 LNDIEVTCV 12

RESULT 6
Q9VWK3 PRELIMINARY; PRT; 481 AA.
AC Q9VWK3;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 25-OCT-2004 (TREMELrel. 28, Last annotation update)
DE CG8784-PA (GHI3361p).
GN ORFNames=CG8784;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

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```

Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA April J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
RA Easler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodagef, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC FlyBase;
RG Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RL [6]

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RP SEQUENCE FROM N.A.
RC FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brockstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003511; AAF48935.1; -.
DR EMBL; BT004882; AAC45238.1; -.
DR FlyBase; FBgn0030999; CG7874.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_PeRA.
DR Pfam; PF01607; CBW_14; 1.
DR SMART; SM00494; ChEBD2; 1.
DR PROSITE; PS00940; CHIT_BIND II; 1.
SQ SEQUENCE 481 AA; 50912 MW; 4E3F0A7C6241AC4E CRC64;

Query Match 87.0%; Score 40; DB 2; Length 481;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDIETCV 8
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Db 308 LQDIETLC 315

RESULT 7
Q8JNA1 PRELIMINARY; PRT; 148 AA.
AC Q8JNA1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Putative transforming protein E6.
OS Human papillomavirus type 90.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=202251;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2207981; PubMed=12085327;
RA Terai M., Burk R.D.;
RT "Identification and characterization of 3 novel genital human
RT papillomaviruses by overlapping polymerase chain reaction: candHPV89,
RT candHPV90, and candHPV91."
RT J. Infect. Dis. 185:1794-1797(2002).
DR EMBL; AY057438; AALJ4204.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001334; E6.
DR InterPro; IPR002345; Lipocalin.
DR Pfam; PF00518; E6; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
SQ SEQUENCE 148 AA; 17173 MW; 374D44C7D05C95DA CRC64;

Query Match 84.8%; Score 39; DB 2; Length 148;
Best Local Similarity 77.8%; Pred. No. 9.1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQDIETCV 9
|||||
Db 22 LQDLNITCV 30
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RESULT 8
OL7327 PRELIMINARY; PRT; 285 AA.
AC OL7327;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein C10E2.1.
GN ORFNames=C10E2.1, C10E2.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wohldmann P., Sansone J.;
RT "The sequence of C. elegans cosmid C10E2."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026202; AAB71241.2; -.
DR PIR; T32429; T32429.
DR WormBase; WBGene00015672; C10E2.1.
DR WormPep; C10E2.1; CE35393.
DR InterPro; IPR011038; Calycin.
KW Hypothetical protein.
SQ SEQUENCE 285 AA; 33628 MW; 2B1A3072391B2396 CRC64;

Query Match 80.4%; Score 37; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DIEITCV 9
|||||
Db 63 DIEITCV 69

RESULT 9
Q6SKS2 PRELIMINARY; PRT; 135 AA.
AC Q6SKS2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
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RP SEQUENCE FROM N.A.
 RA Bartolo I., Gama A., Epalanga M., Bartolomeu J., Fonseca M.,
 RA Mendes A., Taveira N.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY456307; AAS16877.1; --
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 FT NON_TER 135 135
 FT NON_TER 135 135
 SQ SEQUENCE 135 AA; 15019 MW; 881FC5CF0C22C687 CRC64;

Query Match 78.3%; Score 36; DB 2; Length 135;
 Best Local Similarity 87.5%; Pred. No. 34;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QDIETVCV 9
 |||||
 Db 45 QSIETVCV 52

RESULT 10
 Q6EGP5 PRELIMINARY; PRT; 156 AA.
 AC Q6EGP5;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DE Putative transforming protein E6.
 OS Human papillomavirus type 71.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=120686;
 [1]
 RN SEQUENCE FROM N.A.
 RA Fu L., Burk R.D.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY330623; AAQ95198.1; --
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR001334; E6.
 DR InterPro; IPR002345; Lipocalin.
 DR Pfam; PF00518; E6; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
 SQ SEQUENCE 156 AA; 17876 MW; 7E88A7CEC653E5E5 CRC64;

Query Match 78.3%; Score 36; DB 2; Length 156;
 Best Local Similarity 55.6%; Pred. No. 39;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQDIEITCV 9
 |||||
 Db 30 LQDLNLTCI 38

RESULT 11
 Q6EGQ2 PRELIMINARY; PRT; 156 AA.
 AC Q6EGQ2;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DE Putative transforming protein E6.
 OS Human papillomavirus type 71.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=120686;

RN SEQUENCE FROM N.A.
 RP Fu L., Burk R.D.;
 RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY330622; AAQ95191.1; --
 DR EMBL; AY330621; AAQ95184.1; --
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR001334; E6.
 DR InterPro; IPR002345; Lipocalin.
 DR Pfam; PF00518; E6; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
 SQ SEQUENCE 156 AA; 17906 MW; 0BFFA7BEC306E0B5 CRC64;

Query Match 78.3%; Score 36; DB 2; Length 156;
 Best Local Similarity 55.6%; Pred. No. 39;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQDIEITCV 9
 |||||
 Db 30 LQDLNLTCI 38

RESULT 12
 Q6EGR6 PRELIMINARY; PRT; 156 AA.
 AC Q6EGR6;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DE Putative transforming protein E6.
 OS Human papillomavirus type 71.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=120686;
 [1]
 RN SEQUENCE FROM N.A.
 RA Fu L., Burk R.D.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY330620; AAQ95177.1; --
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR001334; E6.
 DR InterPro; IPR002345; Lipocalin.
 DR Pfam; PF00518; E6; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
 SQ SEQUENCE 156 AA; 17890 MW; 1FBABF7A16873CB5 CRC64;

Query Match 78.3%; Score 36; DB 2; Length 156;
 Best Local Similarity 55.6%; Pred. No. 39;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQDIEITCV 9
 |||||
 Db 30 LQDLNLTCI 38

RESULT 13
 GLO2 YEAST STANDARD; PRT; 274 AA.
 ID GLO2 YEAST
 AC Q05584;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Hydroxycylglutathione hydrolase, cytoplasmic isozyme (EC 3.1.2.6)
 DE (Glyoxalase II) (Glx II).
 GN Name=GLO2; OrderedLocusNames=YDR272W; ORFNames=D9954.5;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 ON NCBI_TaxID=4932;
 OP [1]
 PP SEQUENCE FROM N.A.
 RQ STRAIN=W303.
 RX MEDLINE=97407946; PubMed=9261170; DOI=10.1074/jbc.272.34.21509;
 RY Bito A., Haidler M., Hadler I., Breitenbach M.;
 RT "Identification and phenotypic analysis of two glyoxalase II encoding
 RT genes from Saccharomyces cerevisiae, GLO2 and GLO4, and intracellular
 RT localization of the corresponding proteins.";
 RL J. Biol. Chem. 272:21509-21519(1997).
 RP [2]
 RQ SEQUENCE FROM N.A.
 RQ STRAIN=S288C / AB972;
 RC MEDLINE=97313263; PubMed=9169867;
 RD Jacq C., Ali-Moerbe J., Andre B., Arnold W., Bahr A., Ballesta J.P.G.,
 RE Bagues M., Baron L., Becker A., Biteau N., Bloecker H., Blugeon C.,
 RF Bobkovic J., Brandt P., Bruckner M., Butrago M.J., Cosser F.,
 RG Delleave T., del Rey F., Dujon B., Eide L.G., Garcia-Cantalejo J.M.,
 RH Goffeau A., Gomez-Peris A., Granotier C., Hanemann V., Hankeln T.,
 RI Hoheisel J.D., Jaeger W., Jimenez A., Jonniaux J.-L., Kraemer C.,
 RJ Kueter H., Laamanen P., Legros Y., Louis E.J., Moeller-Riekter S.,
 RK Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Paricio N.,
 RL Paulin L., Perera J., Perez-Alonso M., Perez-Ortin J.E., Pohl T.M.,
 RM Prydz H., Purnelle B., Rasmussen S.W., Remacha M., Revuelta J.L.,
 RN Rieger M., Salom D., Saluz H.P., Saiz J.E., Saten A.-M., Schaefer M.,
 RO Schaefer M., Schmidt E.R., Schneider C., Scholler P., Schwarz S.,
 RP Urrestarazu L.A., Verhasselt P., Vissers S., Voet M., Volckaert G.,
 RQ Wagner G., Wambutt R., Wedler E., Wedler H., Woelfl S., Harris D.E.,
 RA Bowman S., Brown D., Churcher C.M., Connor R., Dedman K., Gentles S.,
 RH Hamilton N., Hunt S., Jones L., McDonald S., Murphy L., Niblett D.,
 RO Odell C., Oliver K., Rajandream M.A., Richards C., Shore L.,
 RI Walsh S.V., Barrell B.G., Dietrich F.S., Mulligan J.T., Allen E.,
 RJ Araujo R., Aviles E., Berno A., Carpenter J., Chen E., Cherry J.M.,
 RK Chung E., Duncan M., Hunnicke-Smith S., Hyman R.W., Komp C.,
 RL Lashkari D., Lew H., Lin D., Mosedale D., Nakanara K., Namath A.,
 RM Oefner P., Oh C., Petel F.X., Roberts D., Schramm S., Schroeder M.,
 RN Shogren T., Shroff N., Winant A., Yelton M.A., Botstein D.,
 RO Davis R.W., Johnston M., Andrews S., Brinkman R., Cooper J., Ding H.,
 RI Du Z., Favello A., Fulton L., Gattung S., Greco T., Hallsworth K.,
 RJ Hawkins J., Hillier L.W., Jier M., Johnson D., Johnson L.,
 RK Kirsten J., Kucaba T., Langston Y., Latreille P., Le T., Mardis E.,
 RM Meneses S., Miller N., Nhan M., Pauley A., Peluso D., Rifkin L.,
 RN Riles L., Taich A., Trevasakis E., Vignati D., Wilcox L., Wohlman P.,
 RO Vaudin M., Wilson R., Waterston R., Albermann K., Hani J., Heumann K.,
 RI Kleine K., Mewes H.-W., Zollner A., Zaccaria P.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome IV.";
 RL Nature 387:75-78(1997).
 RQ CC -1- FUNCTION: Thiolesterase that catalyzes the hydrolysis of S-D-
 CC lactoyl-glutathione to form glutathione and D-lactic acid.
 CC CC -1- CATALYTIC ACTIVITY: (S)-(2-hydroxyacyl)glutathione + H(2)O =
 CC glutathione + a 2-hydroxy acid anion.
 CC CC -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
 CC CC -1- PATHWAY: Glyoxal pathway.
 CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC CC -1- SIMILARITY: Belongs to the glyoxalase II family.
 CC -----
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 CC -----
 DR EMBL; Y10292; CAA71335.1; -;
 DR EMBL; U51030; AAB64450.1; -;
 DR PIR; S70130; S70130.
 DR HSP; Q16775; 1QH5.
 DR GeneOnline; 140764; -;
 DR SGD; S000002680; GLO2.
 DR DR GO; GO:0005737; C:cytoplasm; IDA.
 DR DR GO; GO:0004416; F:hydroxyacylglutathione hydrolase activity; IMP.

RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ma J., SanMiguel P.J., Dubcovsky J., Shiloff B.A., Rostoks N.,
 RA Jiang Z., Busso C.S., Kleinhofs A., Devos K.M., Ramakrishna W.,
 RA Bennetzen J.L.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP000559; BAA84809.1; -;
 DR EMBL; AF488413; AAO33145.1; -;
 DR EMBL; AP002542; BAB19371.1; -;
 DR Gramene; Q84Z20; -;
 DR Gramene; Q98NM0; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR InterPro; IPR009637; Lung_7TM_recept.
 DR Pfam; PF06814; Lung_7-TM_R; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 454 AA; 50120 MW; 0ADBA567F016CA21 CRC64;

Query Match 78.3%; Score 36; DB 2; Length 454;
 Best Local Similarity 62.5%; Pred. NO. 1.1e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITC 8
 Db 94 LQDLDTVC 101

Search completed: June 28, 2005, 21:23:48
 Job time : 56.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11:15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-23

Perfect score: 46

Sequence: 1 LQDIEITCV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	57	2	I56705
2	46	100.0	158	1	W6WL18
3	40	87.0	99	2	D83129
4	37	80.4	391	2	T32429
5	36	78.3	274	2	S70130
6	35	76.1	158	1	W6WL39
7	35	76.1	158	2	S36561
8	35	76.1	170	2	AE3546
9	35	76.1	445	2	B81289
10	35	76.1	776	2	F81289
11	34	73.9	3135	2	A48584
12	33	71.7	154	2	T17580
13	33	71.7	198	2	T19797
14	33	71.7	223	2	T19793
15	33	71.7	391	2	T34284
16	33	71.7	402	2	A10323
17	33	71.7	402	2	AB0193
18	33	71.7	402	2	T14710
19	33	71.7	402	2	AE0267
20	33	71.7	402	2	A10256
21	33	71.7	402	2	AH0298
22	33	71.7	402	2	AG0264
23	33	71.7	402	2	AB0472
24	33	71.7	402	2	AE0197
25	33	71.7	402	2	AE0190
26	33	71.7	402	2	AG0210
27	33	71.7	402	2	AG0339
28	33	71.7	402	2	AB0358
29	33	71.7	402	2	A10181

30 33 71.7 402 2 AH0193
31 33 71.7 402 2 AE0242
32 33 71.7 402 2 AG0260
33 33 71.7 402 2 AC0341
34 33 71.7 402 2 AD0002
35 33 71.7 402 2 AI0313
36 33 71.7 402 2 AF0348
37 33 71.7 820 2 B83739
38 32 69.6 156 1 W6WL41
39 32 69.6 222 2 A97148
40 32 69.6 264 2 A55487
41 32 69.6 266 2 H82839
42 32 69.6 405 2 A28009
43 32 69.6 691 2 S41008
44 32 69.6 808 2 D88564
45 32 69.6 971 2 A70179

ALIGNMENTS

RESULT 1

I56705

E6 protein - human papillomavirus type 18

C:Species: human papillomavirus type 18

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I56705

R:Inagaki, Y.; Tsunokawa, Y.; Takebe, N.; Nawa, H.; Nakanishi, S.; Terada, M.; Sugimura, J. Virol. 62, 1640-1646, 1988

A:Title: Nucleotide sequences of cDNAs for human papillomavirus type 18 transcripts in He

A:Reference number: I56705; PMID:88188247; PMID:2833614

A:Accession: I56705

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-57 <RES>

A:Cross-references: UNIPROT:Q90133; GB:M20324; NID:gl83933; PIDN:AAA99512.1; PID:G306834

C:Superfamily: papillomavirus E6 protein

Query Match 100.0%; Score 46; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 0.036;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9

Db 25 LQDIEITCV 33

RESULT 2

W6WL18

E6 protein - human papillomavirus type 18

C:Species: human papillomavirus type 18

C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004

C:Accession: A26185; G26251

R:Seedorf, K.; Oltersdorf, T.; Kraemmer, G.; Roewekamp, W.

EMBO J. 6, 139-144, 1987

A:Title: Identification of early proteins of the human papilloma

A:Reference number: A91068; PMID:87218459; PMID:3034571

A:Accession: A26185

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P06463; GB:X04773; NID:g60876; PIDN:CAA28466.1; PID:g60877

R:Cole, S.T.; Danos, O.

J. Mol. Biol. 193, 599-608, 1987

A:Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 18

A:Reference number: A92917; PMID:87283882; PMID:3039146

A:Accession: G26251

A:Molecule type: DNA

A:Residues: 1-158 <COL>

A:Cross-references: GB:X05015; NID:g60975; PIDN:CAA28664.1; PID:g60976

R:MacIashewski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pim, D.; Crawford, L.

J. Gen. Virol. 67, 1909-1916, 1986

A:Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the p

A:Reference number: A92791; PMID:86306665; PMID:3018129

A;Contents: annotation; identification of the protein
 C;Superfamily: papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; transforming protein; zinc finger
 F;32-68/Region: zinc finger CCCC motif
 F;105-141/Region: zinc finger CCCC motif

Query Match 100.0%; Score 46; DB 1; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.091;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
 |||||
 Db 25 LQDIEITCV 33

RESULT 3
 DB3129
 hypothetical protein PA4141 [imported] - Pseudomonas aeruginosa (strain PA01)
 C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C;Accession: DB3129
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A;Reference number: AB2950; MUID:20437337; PMID:10984043
 A;Accession: DB3129
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-99 <STO>
 A;Cross-references: UNIPROT:Q9HWP0; GB:AE004830; GB:AE004091; NID:g9950337; PIDN:AAG0752
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: PA4141

Query Match 87.0%; Score 40; DB 2; Length 99;
 Best Local Similarity 77.8%; Pred. No. 0.93;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
 |||||
 Db 4 LNDIEITCV 12

RESULT 4
 T32429
 hypothetical protein C10E2.1 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 R;Wohlmann, P.; Sansone, J.
 submitted to the EMBL Data Library, September 1997
 A;Description: The sequence of C. elegans cosmid C10E2.
 A;Reference number: Z21165
 A;Accession: T32429
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-391 <WOH>
 A;Cross-references: UNIPROT:O17327; EMBL:AF026202; PIDN:AAB71241.1; GSPDB:GN000028; CESP:
 A;Experimental source: strain Bristol N2; clone C10E2
 C;Genetics:
 A;Gene: CESP:C10E2.1
 A;Map position: X
 A;Introns: 25/2; 103/2; 215/3
 C;Superfamily: Caenorhabditis elegans hypothetical protein C10E2.1

Query Match 80.4%; Score 37; DB 2; Length 391;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DIEITCV 9
 |||||

Db 63 DIEITCV 69

RESULT 5
 S70130
 hypothetical protein YDR272w - yeast (Saccharomyces cerevisiae)
 N;Alternate names: hypothetical protein D9954.5
 C;Species: Saccharomyces cerevisiae
 C;Date: 24-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 C;Accession: S70130
 R;Le, T.
 submitted to the EMBL Data Library, May 1996
 A;Description: The sequence of S. cerevisiae cosmid 9954.
 A;Reference number: S70124
 A;Accession: S70130
 A;Molecule type: DNA
 A;Residues: 1-274 <LET>
 A;Cross-references: UNIPROT:Q05584; EMBL:U51030; NID:gl332633; PIDN:AAB64450.1; PID:gl2130
 C;Genetics:
 A;Gene: SGD:GLO2
 A;Cross-references: SGD:S0002680; MIPS:YDR272w
 A;Map position: 4R
 C;Superfamily: glyoxalase

Query Match 78.3%; Score 36; DB 2; Length 274;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
 |||||
 Db 108 LGDLEITCI 116

RESULT 6
 W6WL39
 E6 protein - human papillomavirus type 39
 C;Species: human papillomavirus type 39
 A;Note: host Homo sapiens (man)
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C;Accession: A38502
 R;Volpers, C.; Strebeck, R.E.
 Virology 181, 419-423, 1991
 A;Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
 A;Reference number: A38502; MUID:91135017; PMID:1847266
 A;Accession: A38502
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-158 <VOL>
 A;Cross-references: UNIPROT:P24835; GB:M62849; EMBL:M38185; NID:g333245; PIDN:AAA47050.1;
 C;Superfamily: papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; transforming protein; zinc finger
 F;32-68/Region: zinc finger CCCC motif
 F;105-141/Region: zinc finger CCCC motif

Query Match 76.1%; Score 35; DB 1; Length 158;
 Best Local Similarity 77.8%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
 |||||
 Db 25 LQDITIAVC 33

RESULT 7
 S36561
 E6 protein - human papillomavirus type 45
 C;Species: human papillomavirus type 45
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C;Accession: S36561
 R;Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A;Description: Primer-directed sequencing of human papillomavirus types.
 A;Reference number: S36469

```
A:Accession: S36561
A:Molecule type: DNA
A:Residues: 1-158 <DEL>
A:Cross-references: UNIPROT:P21735; EMBL:X74479; NID:g397022; PIDN:CAA52573.1; PID:g3970
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match      76.1%; Score 35; DB 2; Length 158;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
|||:||||
Db 25 LQDVSIACV 33

RESULT 8
AF3546
biphenyl-2,3-diol 1,2-dioxygenase (EC 1.13.11.39) [imported] - Brucella melitensis (stra
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AF3546
R:DelVecchio, V.G.; Kaparal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzev, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A:Reference number: AD3252; PMID:11756688
A:Accession: AF3546
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-170 <KUR>
A:Cross-references: UNIPROT:Q8YD82; GB:AE008918; PIDN:AAL53537.1; PID:gi7984445; GSPDB:G
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI10295
A:Map position: II
C:Keywords: oxidoreductase

Query Match      76.1%; Score 35; DB 2; Length 170;
Best Local Similarity 62.5%; Pred. No. 15;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITC 8
:|||||
Db 55 VQDIDVTC 62

RESULT 9
B81289
probable sugar transferase Cj1434c [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: B81289
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: AB1250; MUID:20150912; PMID:10688204
A:Accession: B81289
A:Status: preliminary
A:Molecule type: DNA
A:Cross-references: UNIPROT:O9PMW3; GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB7385
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj1434c

Query Match      76.1%; Score 35; DB 2; Length 445;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
|:|||||:
```

```
Db 34 LQDIEILCI 42

RESULT 10
F81289
probable sugar transferase Cj1438c [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: F81289
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: AB1250; MUID:20150912; PMID:10688204
A:Accession: F81289
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-776 <PAR>
A:Cross-references: UNIPROT:Q9PML9; GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB7386;
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj1438c

Query Match      76.1%; Score 35; DB 2; Length 776;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
|:|||||:
Db 34 LQDIEILCI 42

RESULT 11
A48584
transmission blocking target antigen Pfs230 PFB0405w - malaria parasite (Plasmodium falci
C:Species: Plasmodium falciparum
C:Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A48584; F71615
R:Williamson, K.C.; Crisio, M.D.; Kaslow, D.C.
Mol. Biochem. Parasitol. 58, 355-358, 1993
A:Title: Cloning and expression of the gene for Plasmodium falciparum transmission-blocki
A:Reference number: A48584; MUID:93241227; PMID:8479460
A:Accession: A48584
A:Status: not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-3135 <WIL>
A:Cross-references: UNIPROT:Q08372; GB:L08135; NID:g294175; PIDN:AA29734.1; PID:g294176
A:Note: sequence extracted from NCBI backbone (NCBIP:130080)
R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743; PMID:9804551
A:Accession: F71615
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-3135 <GAR>
A:Cross-references: GB:AE001393; GB:AE001362; NID:g3845175; PIDN:AACT71870.1; PID:g3845176
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: Pfs230; PFB0405w
C:Superfamily: transmission-blocking target antigen Pfs230

Query Match      73.9%; Score 34; DB 2; Length 3135;
Best Local Similarity 62.5%; Pred. No. 3.5e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITC 8
|:|:|:|:|
Db 1242 LEDVEISC 1249

RESULT 12
```

Tl7580
hypothetical protein A90R - Chlorella virus PBCV-1
C:Species: Chlorella virus PBCV-1
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Superfamily: Ti7580
R:Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18806
A:Accession: Tl7580
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-154 <GRA>
A:Cross-references: UNIPROT:Q84411; EMBL:U42580; NID:G4028896; PIDN:AAC96458.1
A:Experimental source: specific host Chlorella strain NC64A
C:Genetics:
A:Gene: A90R

Query Match 71.7%; Score 33; DB 2; Length 154;
Best Local Similarity 62.5%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQDIEITC 8
| | | | |
Db 141 LSDLELTC 148

RESULT 13
Tl7979
hypothetical protein C36F7.4b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: Tl7979
R:Lightning, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19178
A:Accession: Tl7979
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-198 <WIL>
A:Cross-references: UNIPROT:Q9NAR0; EMBL:Z81045; PIDN:CAB54202.1; GSPDB:GN00019; CESP:C36F7.4b
A:Experimental source: clone C36F7
C:Genetics:
A:Gene: CESP:C36F7.4b
A:Map position: 1
A:Introns: 77/1; 115/3; 162/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C36F7.4b

Query Match 71.7%; Score 33; DB 2; Length 198;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 QDIEITCV 9
| | | | |
Db 100 QDVDFTCI 107

RESULT 14
Tl9793
hypothetical protein C36F7.4a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: Tl9793
R:Lightning, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19178
A:Accession: Tl9793
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-223 <WIL>
A:Cross-references: UNIPROT:Q93350; EMBL:Z81045; PIDN:CAB02817.1; GSPDB:GN00019; CESP:C36F7.4a
A:Experimental source: clone C36F7
C:Genetics:
A:Gene: CESP:C36F7.4a

A:Map position: 1
A:Introns: 71/2; 102/1; 140/3; 187/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C36F7.4b

Query Match 71.7%; Score 33; DB 2; Length 223;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 QDIEITCV 9
| | | | |
Db 125 QDVDFTCI 132

RESULT 15
T34284
hypothetical protein F47C12.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34284
R:Murray, J.; Wohldmann, P.; Sansone, J.
submitted to the EMBL Data Library, June 1996
A:Description: The sequence of C. elegans cosmid F47C12.
A:Reference number: Z21499
A:Accession: T34284
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-391 <MUR>
A:Cross-references: UNIPROT:Q20531; EMBL:U61946; PIDN:AAC24389.1; GSPDB:GN00022; CESP:F47C12
A:Experimental source: strain Bristol N2; clone F47C12
C:Genetics:
A:Gene: CESP:F47C12.2
A:Map position: 4
A:Introns: 27/3; 118/3; 293/1; 336/1; 383/3

Query Match 71.7%; Score 33; DB 2; Length 391;
Best Local Similarity 62.5%; Pred. No. 82;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQDIEITC 8
| | | | |
Db 41 LTDVELTC 48

Search completed: June 28, 2005, 21:27:37
Job time : 11.15 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-22

Perfect score: 46

Sequence: 1 SLQDIEITC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	46	100.0	57	2 Q90133	Q90133 human papil
2	46	100.0	158	1 VEG HPV18	P06463 human papil
3	46	100.0	158	2 Q9QNP8	Q9QNP8 human papil
4	42	91.3	157	2 Q9WHG0	Q9WHG0 human papil
5	40	87.0	481	2 Q9VWK3	Q9VWK3 drosophila
6	38	82.6	509	1 MAPE HUMAN	P78395 homo sapien
7	38	82.6	509	2 Q8IXN8	Q8IXN8 homo sapien
8	38	82.6	530	2 Q9VVF1	Q9VVF1 drosophila
9	38	82.6	581	2 Q7QB87	Q7QB87 anopheles g
10	36	78.3	99	2 Q9HWP0	Q9HWP0 pseudomonas
11	36	78.3	128	2 Q8FV49	Q8FV49 brucella su
12	36	78.3	170	2 Q8YD82	Q8YD82 brucella me
13	36	78.3	405	2 Q9SNM0	Q9SNM0 oryza sativ
14	36	78.3	1085	2 Q7Q193	Q7Q193 anopheles g
15	36	78.3	1471	2 Q7PY72	Q7PY72 anopheles g
16	35	76.1	148	2 Q8JN1	Q8JN1 human papil
17	35	76.1	158	1 VEG HPV45	P21735 human papil
18	35	76.1	158	2 Q9FY44	Q9FY44 homo sapien
19	35	76.1	158	2 Q10608	Q10608 human papil
20	35	76.1	244	2 Q6WG76	Q6WG76 homo sapien
21	35	76.1	411	2 Q7QJ0	Q7QJ0 anopheles g
22	35	76.1	487	2 Q6PJ35	Q6PJ35 homo sapien
23	35	76.1	673	2 Q9LJP4	Q9LJP4 arabidopsis
24	35	76.1	861	2 Q9NKK3	Q9NKK3 bombyx mori
25	35	76.1	1729	1 TABP HUMAN	Q9C0C2 homo sapien
26	35	76.1	2035	1 NIN MOUSE	Q61043 mus musculu
27	35	76.1	2113	2 Q674R4	Q674R4 mus musculu
28	34	73.9	72	2 Q6WL28	Q6WL28 rhizobium s
29	34	73.9	217	2 Q8FAN2	Q8FAN2 escherichia
30	34	73.9	390	2 Q96TSS	Q96TSS phlebia rad
31	34	73.9	390	2 Q70LM3	Q70LM3 phlebia rad

32 34 73.9 422 2 Q9L9K7 Q9L9K7 pasteurella
33 34 73.9 493 1 ATPB_CHAGL Q881Y2 chaetosphae
34 34 73.9 534 2 Q9VY50 Q9VY50 drosophila
35 34 73.9 538 1 BOCT HUMAN Q8WU55 homo sapien
36 34 73.9 574 2 Q6F9X0 Q6F9X0 acinetobact
37 34 73.9 765 2 Q943P0 Q943P0 oryza sativ
38 34 73.9 1005 2 Q7SGC1 Q7SGC1 neurospora
39 34 73.9 1021 2 Q8L4X2 Q8L4X2 hordeum vul
40 34 73.9 1183 2 Q7Q4Q1 Q7Q4Q1 anopheles g
41 34 73.9 1184 2 Q6BQ08 Q6BQ08 debaryomyce
42 34 73.9 1222 2 Q9VY54 Q9VY54 drosophila
43 34 73.9 3134 2 Q25994 Q25994 plasmodium
44 34 73.9 3135 1 S230_PLAFO Q08372 plasmodium
45 34 73.9 3144 2 Q9GTR4 Q9GTR4 plasmodium

ALIGNMENTS

RESULT 1
Q90133 PRELIMINARY; PRT; 57 AA.
AC Q90133;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Protein E6.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8818247; PubMed=2833614;
RA Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M.,
RT Sugimura T.;
RT "Nucleotide sequences of cDNAs for human papillomavirus type 18
RT transcripts in HeLa cells.";
RL J. Virol. 62:1640-1646(1988).
DR EMBL; M20324; AAA99512.1; -;
DR PIR; I56705; I56705;
SQ SEQUENCE 57 AA; 6531 MW; 31CF1A5B3740D2C CRC64;

Query Match 100.0%; Score 46; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLQDIEITC 9
Db 24 SLQDIEITC 32

RESULT 2
VE6 HPV18 STANDARD; PRT; 158 AA.
ID VEG HPV18
AC P06463;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87283882; PubMed=3039146;
RA Cole S. T., Danos O.;
RT "Nucleotide sequence and comparative analysis of the human
RT papillomavirus type 18 genome. Phylogeny of papillomaviruses and
RT repeated structure of the E6 and E7 gene products.";
RL J. Mol. Biol. 193:599-608(1987).

DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 157 AA; 18450 MW; 1B154BA2C49EED7 CRC64;
Query Match 91.3%; Score 42; DB 2; Length 157;
Best Local Similarity 88.9%; Pred. No. 2.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLQDIEITC 9
|||||:|
Db 24 SLQDIEISC 32

RESULT 5
Q9VWK3 PRELIMINARY; PRT; 481 AA.
AC Q9VWK3;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE CG7874-PA (GH13361p).
GN ORFNames=CG7874;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Prannkoc C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fogle C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kimos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=22426065; PubMed=12537568;
RX Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,

RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RN SEQUENCE FROM N.A.
RP MEDLINE=22426070; PubMed=12537573;
RX Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genome perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
RN SEQUENCE FROM N.A.
RP MEDLINE=22426069; PubMed=12537572;
RX Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[5]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[6]
RN SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
[7]
RN SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dreshek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunco J., Pacle J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003511; AAF48935.1; -.
DR EMBL; BT004882; AAO45238.1; -.
DR FlyBase; FBgn0030999; CG7874.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_Pera.
DR Pfam; PF01607; CBM_14; 1.
DR SMART; SM00494; ChtBD2; 1.
DR PROSITE; PS00940; CHIT_BIND_II; 1.
SQ SEQUENCE 481 AA; 50912 MW; 4E3F0A7C6241AC4E CRC64;
Query Match 87.0%; Score 40; DB 2; Length 481;
Best Local Similarity 87.5%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LQDIEITC 9
|||||:|
Db 308 LQDIEITC 315

RESULT 6
MAPE HUMAN
ID _MAPE_HUMAN STANDARD; PRT; 509 AA.
AC P78395; O43481;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

05-JUL-2004 (Rel. 44, Last annotation update)
 Melanoma antigen preferentially expressed in tumors (Preferentially expressed antigen of melanoma) (OPA-interacting protein 4) (OIP4).
 Name=PRAME; Synonyms=MAPE;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9719265; PubMed=9047241; DOI=10.1016/S1074-7613(00)80426-4; Ikeda H., Lethe B., Lehmann F., van Baren N., Baurain J.-F., de Smet C., Chambost H., Vitale M., Moretta A., Boon T., Coulie P.G.; "Characterization of an antigen that is recognized on a melanoma showing partial HLA loss by CTL expressing an NK inhibitory receptor."; Immunity 6:199-208(1997).
 RL [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [3]
 RN [3]
 RP SEQUENCE OF 452-509 FROM N.A.
 RX MEDLINE=98125741; PubMed=9466265; Williams J.M., Chen G.-C., Zhu L., Rest R.F.; "Using the yeast two-hybrid system to identify human epithelial cell proteins that bind gonococcal Opa proteins: intracellular gonococci bind pyruvate kinase via their Opa proteins and require host pyruvate for growth."; Mol. Microbiol. 27:171-186(1998).
 RL Mol. Microbiol. 27:171-186(1998).
 CC -!- TISSUE SPECIFICITY: Tumor antigen recognized by cytolytic T lymphocytes.
 CC -!- SIMILARITY: Belongs to the MAPE family.
 CC -!- SIMILARITY: Contains 7 leucine-rich (LRR) repeats.
 CC -----
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 CC -----
 CC EMBL; U65011; AAC51160.1; -;
 DR EMBL; BC014074; AAH14074.1; -;
 DR EMBL; AF025440; AAC39560.1; -;
 DR IntAct; P78395; -;
 DR Genew; HGNC:9336; PRAME.
 DR H-invDB; HIX0016292; -;
 DR MIM; 606021; -;
 DR InterPro; IPR007089; LRR_cys.
 KW Antigen; Leucine-rich repeat; Repeat.
 DR PRINTS; PR01415; ANKYRN.
 DR REPEAT 32 55 LRR 1.

FT REPEAT 116 138 LRR 2.
 FT REPEAT 259 283 LRR 3.
 FT REPEAT 321 344 LRR 4.
 FT REPEAT 348 371 LRR 5.
 FT REPEAT 405 429 LRR 6.
 FT REPEAT 454 477 LRR 7.
 FT CONFLICT 452 452 H -> D (in Ref. 3).
 SQ SEQUENCE 509 AA; 57889 MW; B5FF3E7F7B82606 CRC64;
 Query Match 82.6%; Score 38; DB 1; Length 509;
 Best Local Similarity 55.6%; Pred. No. 46;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SLQDIEITC 9
 Db 234 SIEDLEVIC 242
 RESULT 7
 Q8IXN8 PRELIMINARY; PRT; 509 AA.
 ID Q8IXN8
 AC Q8IXN8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Preferentially expressed antigen in melanoma (PRAME protein).
 GN Name=PRAME;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RN Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RP SEQUENCE FROM N.A.
 RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A., Cole C.G., Goward M.E., Aguado B., Mallia M., Mokrab Y., Huckle E.J., Beare D.M., Dunham I.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC039731; AAH39731.1; -;
 DR EMBL; CR456549; CAG30435.1; -;
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007089; LRR_cys.
 DR Pfam; PF00560; LRR 1; 2.
 DR PRINTS; PR01415; ANKYRN.

SQ SEQUENCE 509 AA; 57859 MW; 10FFFE37F7E8273A CRC64;

Query Match 82.6%; Score 38; DB 2; Length 509;
 Best Local Similarity 55.6%; Pred. No. 46;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLQDIETC 9
 Db 234 SLEDIEVC 242

RESULT 8
 Q9VFV1 ID Q9VFV1 PRELIMINARY; PRT; 530 AA.

AC Q9VFV1; MEDLINE=22426070; PubMed=12537573;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE CG9792-PA (RE55542p).
 GN Name=yellow-e; ORFNames=CG9792;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA Sutton G.G., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Fodor C.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hoatlin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodrager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao S., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinschenk G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminler J.S., Bergman C.M., Kronmiller B., Carlson J., Svirkas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminler J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX FlyBase; SEQUENCE FROM N.A.
 RG FlyBase; SEQUENCE FROM N.A.
 RN Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase; SEQUENCE FROM N.A.
 RN Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacle J., Paragas V., Park S.,
 RA Patel S., Shouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003700; AAF54948.1;
 DR EMBL; AY071489; AAL49111.1;
 DR FlyBase; FBgn0041711; yellow-e.
 DR InterPro; IPR003534; Royaljelly.
 DR Pfam; PF03022; MRJP; 1.
 DR PRINTS; PR01366; ROYALJELLY.
 SQ SEQUENCE 530 AA; 58672 MW; 1D80BE42A2PBD378 CRC64;

Query Match 82.6%; Score 38; DB 2; Length 530;
 Best Local Similarity 77.8%; Pred. No. 48;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLQDIETC 9
 Db 143 SLEDIEVC 151

RESULT 9
 Q7QB87 ID Q7QB87 PRELIMINARY; PRT; 581 AA.
 AC Q7QB87;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DE AGCP2455 (Fragment).
 GN Name=agCG46908; ORFNames=ENSGG00000008761;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC Submitter: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAAB01008880; EAA08663.1; -.
 DR InterPro; IPR003534; RoyalJelly.
 DR Pfam; PF03022; MRJP; 1.
 DR PRINTS; PR01366; ROYALJELLY.
 FT NON_TER 1 581
 FT NON_TER 581 581
 SQ SEQUENCE 581 AA; 64158 MW; 187085097171PF545 CRC64;
 Query Match 82.6%; Score 38; DB 2; Length 581;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SLQDIEITC 9
 Db ||| |||
 190 SLEDPEVTC 198
 RESULT 10
 ID Q9HWFO PRELIMINARY; PRT; 99 AA.
 AC Q9HWFO;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS OrderedLocNames=PA4141;
 GN Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Golltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen."
 RL Nature 406:959-964 (2000).
 DR EMBL; AE004830; AAG07528.1; -.
 DR PIR; D83129; D83129.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 99 AA; 9656 MW; CBC469A938A2BFF CRC64;
 Query Match 78.3%; Score 36; DB 2; Length 99;
 Best Local Similarity 75.0%; Pred. No. 22;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LQDIEITC 9
 Db ||| |||
 4 LNDIEVTC 11
 RESULT 11
 ID Q8FV49 PRELIMINARY; PRT; 128 AA.
 AC Q8FV49;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Extradiol ring-cleaving dioxygenase, putative.
 GN OrderedLocNames=BRAL001;
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29461;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1330 / Biovar 1;
 RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
 RA Dougherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,
 RA van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
 RA Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
 RA Fraser C.M.;
 RT "The Brucella suis genome reveals fundamental similarities between
 RT animal and plant pathogens and symbionts."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).
 DR EMBL; AE014593; AAN34170.1; -.
 DR TIGR; BRA1001; -.
 DR InterPro; IPR004360; Gly_bleo_diox.
 DR Pfam; PF00903; Glyoxalase; 1.
 KW Complete proteome.
 SQ SEQUENCE 128 AA; 13987 MW; 3B0DE88AF4DEA39B CRC64;
 Query Match 78.3%; Score 36; DB 2; Length 128;
 Best Local Similarity 55.6%; Pred. No. 29;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLQDIEITC 9
 Db ||| |||
 12 TVQDIDVTC 20
 RESULT 12
 ID Q8YD82 PRELIMINARY; PRT; 170 AA.
 AC Q8YD82;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE BIPHENYL-2,3-DIOL 1,2-DIOXYGENASE III (EC 1.13.11.39).
 GN OrderedLocNames=BMEI10295;
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / Biotype 1;
 RX MEDLINE=20020109; PubMed=11756688; DOI=10.1073/pnas.221575398;
 RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mijer C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyrpides N.C., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
 DR EMBL; AE009668; AAL53537.1; -.
 DR PIR; AF3546; AF3546.
 DR GO; GO:0018583; F:biphenyl-2,3-diol 1,2-dioxygenase activity; IEA.
 DR Pfam; PF00903; Glyoxalase; 1.
 KW Complete proteome.
 SQ SEQUENCE 170 AA; 18497 MW; B30F08D00D1623B6 CRC64;
 Query Match 78.3%; Score 36; DB 2; Length 170;
 Best Local Similarity 55.6%; Pred. No. 38;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SLQDIEITC 9
DB 54 TVQDIDVTC 62

RESULT 13
Q9SNM0 PRELIMINARY; PRT; 454 AA.
AC Q9SNM0; Q84ZZO;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE ESTS AU078277(S1084) (Hypochemical protein 134F10.3) (P0679C08.10
DE protein).
GN Name=134P10.3; Synonyms=P0679C08.10;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ethnacoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RN SEQUENCE FROM N.A.
RP Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ma J., SanMiguel P.J., Dubcovsky J., Shiloff B.A., Rostoks N.,
RA Jiang Z., Bussio C.S., Kleinhofs A., Devos K.M., Ramakrishna W.,
RA Bennetzen J.L.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP000559; BAA84809.1; -
DR EMBL; AF488413; AAC33145.1; -
DR EMBL; AP002542; BAB19371.1; -
DR Gramene; Q84ZZO; -
DR Gramene; Q9SNM0; -
DR GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR009637; Lung_7TM_recept.
DR Pfam; PF06814; Lung_7-TM_R; 1.
KW Hypothetical protein.
SQ SEQUENCE 454 AA; 50120 MW; 0ADBA567F016CA21 CRC64;

Query Match 78.3%; Score 36; DB 2; Length 454;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQDIBITC 9
DB 94 LQDLDVTC 101

RESULT 14
Q7QI93 PRELIMINARY; PRT; 1085 AA.
AC Q7QI93;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE AGCP3794 (Fragment).
GN Name=agCG52930; ORFNames=ENSANGG00000017742;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 5 WD repeats.

-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
EMBL; AAA01008807; EAA04725.1; -.
DR InterPro; IPR011048; Cyt_cdl_haem_C.
DR InterPro; IPR011045; N2O_reductase_N.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 5.
KW Repeat; WD repeat.
FT NON TER 1085
SQ SEQUENCE 1085 AA; 123735 MW; 657A8DAB98B83849 CRC64;

Query Match 78.3%; Score 36; DB 2; Length 1085;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQDIEITC 9
DB 683 LEDVELTC 690

RESULT 15
Q7PY72 PRELIMINARY; PRT; 1471 AA.
AC Q7PY72;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE AGCP12494 (Fragment).
GN Name=agCG47127; ORFNames=ENSANGG00000010363;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
EMBL; AAA01008987; EAA01513.1; -.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR003126; Znf_Nrecognin.
DR Pfam; PF02207; zf-UBR1; 1.
FT NON TER 1471
SQ SEQUENCE 1471 AA; 156495 MW; DAEE697AD5729810 CRC64;

Query Match 78.3%; Score 36; DB 2; Length 1471;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLQDIEITC 9
DB 776 SMQDVSLTC 784

Search completed: June 28, 2005, 21:23:47
Job time : 58.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-22
Perfect score: 46
Sequence: 1 SLQDIEITC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	57	2 IS6705	E6 protein - human
2	46	100.0	158	1 W6WL18	E6 protein - human
3	36	78.3	99	2 D83129	hypothetical prote
4	36	78.3	170	2 AF3546	biphenyl-2,3-diol
5	35	76.1	158	2 S36561	E6 protein - human
6	34	73.9	3135	2 A48584	transmission block
7	33	71.7	154	2 T17580	hypothetical prote
8	33	71.7	274	2 S70130	hypothetical prote
9	33	71.7	305	2 E69946	hypothetical prote
10	33	71.7	391	2 T32429	hypothetical prote
11	33	71.7	391	2 T34284	hypothetical prote
12	33	71.7	445	2 B81289	hypothetical prote
13	33	71.7	776	2 F81289	probable sugar tra
14	33	71.7	820	2 B83739	probable sugar tra
15	33	71.7	1021	2 T40928	exonuclease ABC (
16	32	69.6	83	2 B95974	conserved hypothet
17	32	69.6	128	1 NROW2	probable transcrip
18	32	69.6	156	1 W6WL13	pancreatic ribonuc
19	32	69.6	158	1 W6WL39	E6 protein - human
20	32	69.6	264	2 A55487	electron transfer
21	32	69.6	285	2 H86212	hypothetical prote
22	32	69.6	392	2 E81325	probable dihydroor
23	32	69.6	405	2 A28009	43K postsynaptic m
24	32	69.6	691	2 S41008	hypothetical prote
25	32	69.6	808	2 D88564	protein T05G5.8 li
26	32	69.6	1052	2 T37133	hypothetical prote
27	32	69.6	1330	2 H89567	hypothetical prote
28	31	67.4	114	2 AD0785	conserved hypothet
29	31	67.4	114	2 D64987	hypothetical 12.5

ALIGNMENTS

RESULT 1

156705
E6 protein - human papillomavirus type 18
C:Species: human papillomavirus type 18
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 156705
R:Inagaki, Y.; Tsunokawa, Y.; Takebe, N.; Nawa, H.; Nakanishi, S.; Terada, M.; Sugimura, J. Virol. 62, 1640-1646, 1988
A:Title: Nucleotide sequences of cDNAs for human papillomavirus type 18 transcripts in HeLa cells
A:Reference number: 156705; PMID:88188247; PMID:2833614
A:Accession: 156705
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-57 <RES>

A:Cross-references: UNIPROT:Q90133; GB:M20324; NID:gl83933; PIDN:AAA99512.1; PID:G306834
C:Superfamily: papillomavirus E6 protein

Query Match 100.0%; Score 46; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLQDIEITC 9

Db 24 SLQDIEITC 32

RESULT 2

W6WL18
E6 protein - human papillomavirus type 18
C:Species: human papillomavirus type 18
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: A26185; G26251
R:Seedorf, K.; Oltersdorf, T.; Kraemmer, G.; Roewekamp, W. EMBO J. 6, 139-144, 1987
A:Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)
A:Reference number: A91068; PMID:87218459; PMID:3034571
A:Accession: A26185

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P06463; GB:X04773; NID:G60876; PIDN:CAA28466.1; PID:G60877
R:Cole, S.T.; Danos, O.

J. Mol. Biol. 193, 599-608, 1987

A:Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 18

A:Reference number: A92937; PMID:87283882; PMID:3039146

A:Accession: G26251

A:Molecule type: DNA

A:Residues: 1-158 <COL>

A:Cross-references: GB:X05015; NID:G60975; PIDN:CAA28664.1; PID:G60976

R:Matlashewski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pim, D.; Crawford, L.

J. Gen. Virol. 67, 1909-1916, 1986

A:Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the p

A:Reference number: A92791; PMID:8630665; PMID:3018129

A;Contents: annotation; identification of the protein
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;32-68/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif

Query Match 100.0%; Score 46; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLQDIEITC 9
|:|:|:|:|
Db 24 SLQDIEITC 32

RESULT 3
D83129
hypothetical protein PA4141 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: D83129
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
gen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83129
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <STO>
A;Cross-references: UNIPROT:Q9HWP0; GB:AE004830; GB:AE004091; NID:g9950337; PIDN:AAG0752
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA4141

Query Match 78.3%; Score 36; DB 2; Length 99;
Best Local Similarity 75.0%; Pred. No. 5.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LQDIEITC 9
|:|:|:|
Db 4 LNDIEITC 11

RESULT 4
AF3546
biphenyl-2,3-diol 1,2-dioxygenase (EC 1.13.11.39) [imported] - Brucella melitensis (stra
in)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AF3546
R;DeiVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujter, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
is
A;Reference number: AD3252; PMID:11756688
A;Accession: AF3546
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-170 <KUR>
A;Cross-references: UNIPROT:Q8YD82; GB:AE008918; PIDN:AAL53537.1; PID:g17984445; GSPDB:C
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI10295
A;Map position: 11
C;Keywords: oxidoreductase

Query Match 78.3%; Score 36; DB 2; Length 170;
Best Local Similarity 55.6%; Pred. No. 9.6;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLQDIEITC 9
|:|:|:|:|
Db 1242 LEDVEISC 1249

Db 54 TVQDIDVTC 62

RESULT 5
S36561
E6 protein - human papillomavirus type 45
C;Species: human papillomavirus type 45
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36561
R;Deilus, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36561
A;Molecule type: DNA
A;Residues: 1-158
A;Cross-references: UNIPROT:P21735; EMBL:X74479; NID:g397022; PIDN:CAA52573.1; PID:g39970;
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 76.1%; Score 35; DB 2; Length 158;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SLQDIEITC 9
|:|:|:|
Db 24 SLQDVSIAC 32

RESULT 6
A48584
transmission blocking target antigen Pfs230 PFB0405w - malaria parasite (Plasmodium falci
parum)
C;Species: Plasmodium falciparum
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48584; F71615
R;Williamson, K.C.; Criscio, M.D.; Kaslow, D.C.
Mol. Biochem. Parasitol. 58, 355-358, 1993
A;Title: Cloning and expression of the gene for Plasmodium falciparum transmission-blocki
ng
A;Reference number: A48584; MUID:93241227; PMID:8479460
A;Accession: A48584
A;Status: not compared with conceptual translation
A;Molecule type: nucleic acid; protein
A;Residues: 1-3135 <WIL>
A;Cross-references: UNIPROT:Q08372; GB:L08135; NID:g294175; PIDN:AAA29734.1; PID:g294176
A;Note: sequence extracted from NCBI backbone (NCBI:P130080)
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: F71615
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-3135 <GAR>
A;Cross-references: GB:AE001393; GB:AE001362; NID:g3845175; PIDN:AACT1870.1; PID:g3845176
C;Genetics:
A;Gene: Pfs230; PFB0405w
C;Superfamily: transmission-blocking target antigen Pfs230

Query Match 73.9%; Score 34; DB 2; Length 3135;
Best Local Similarity 62.5%; Pred. No. 3.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LQDIEITC 9
|:|:|:|:|
Db 1242 LEDVEISC 1249

RESULT 7
T17580
hypothetical protein A90R - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T17580
 R:Graves, M.V.; Van Etten, J.L.
 Submitted to the EMBL Data Library, May 1999
 A:Reference number: Z18806
 A:Accession: T17580
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-154 <GRA>
 A:Cross-references: UNIPROT:Q84411; EMBL:U42580; NID:G4028896; PIDN:AAC96458.1
 A:Experimental source: specific host *Chlorella* strain NC64A
 C:Genetics:
 A:Gene: A90R

Query Match 71.7%; Score 33; DB 2; Length 154;
 Best Local Similarity 62.5%; Pred. No. 35;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQDIEITC 9
 | : | : | : |
 DB 141 LSDLELTC 148

RESULT 8
 S70130
 hypothetical protein YDR272w - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: hypothetical protein D9954.5
 C:Species: *Saccharomyces cerevisiae*
 C>Date: 24-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 C:Accession: S70130
 R:Le, T.
 submitted to the EMBL Data Library, May 1996
 A:Description: The sequence of *S. cerevisiae* cosmid 9954.
 A:Reference number: S70124
 A:Accession: S70130
 A:Molecule type: DNA
 A:Residues: 1-274 <LET>
 A:Cross-references: UNIPROT:Q05584; EMBL:U51030; NID:G1332633; PIDN:AAB64450.1; PID:G123
 C:Genetics:
 A:Gene: SGD:GLO2
 A:Cross-references: SGD:S0002680; MIPS:YDR272w
 A:Map position: 4R
 C:Superfamily: glyoxalase

Query Match 71.7%; Score 33; DB 2; Length 274;
 Best Local Similarity 75.0%; Pred. No. 59;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LQDIEITC 9
 | : | : | : |
 DB 108 LGDLEITC 115

RESULT 9
 E69946
 hypothetical protein yqb8 - *Bacillus subtilis*
 C:Species: *Bacillus subtilis*
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C:Accession: E69946
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteaux
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hoisappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Segkiguchi, J.; Sekowska, A.; Serot
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: E69946
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-305 <KUN>
 A:Cross-references: UNIPROT:P45918; GB:Z99117; GB:AL009126; NID:G2634966; PIDN:CAB14558.1
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yqB8

Query Match 71.7%; Score 33; DB 2; Length 305;
 Best Local Similarity 75.0%; Pred. No. 65;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLQDIEIT 8
 | : | : | : | : |
 DB 170 SIQDIEIT 177

RESULT 10
 T32429
 hypothetical protein C10E2.1 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T32429
 R:Wohlmann, P.; Sansone, J.
 submitted to the EMBL Data Library, September 1997
 A:Description: The sequence of *C. elegans* cosmid C10E2.
 A:Reference number: Z21165
 A:Accession: T32429
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-391 <WOH>
 A:Cross-references: UNIPROT:O17327; EMBL:AF026202; PIDN:AAB71241.1; GSPDB:GN00028; CESP:
 A:Experimental source: strain Bristol N2; clone C10E2
 C:Genetics:
 A:Gene: CESP:C10E2.1
 A:Map position: X
 A:Introns: 25/2; 103/2; 215/3
 C:Superfamily: *Caenorhabditis elegans* hypothetical protein C10E2.1

Query Match 71.7%; Score 33; DB 2; Length 391;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DIEITC 9
 | : | : | : | : |
 DB 63 DIEITC 68

RESULT 11
 T34284
 hypothetical protein F47C12.2 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T34284
 R:Murray, J.; Wohlmann, P.; Sansone, J.
 submitted to the EMBL Data Library, June 1996
 A:Description: The sequence of *C. elegans* cosmid F47C12.
 A:Reference number: Z21499
 A:Accession: T34284
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-391 <MUR>
 A:Cross-references: UNIPROT:Q20531; EMBL:U61946; PIDN:AAC24389.1; GSPDB:GN00022; CESP:F47
 A:Experimental source: strain Bristol N2; clone F47C12
 C:Genetics:
 A:Gene: CESP:F47C12.2
 A:Map position: 4
 A:Introns: 27/3; 118/3; 293/1; 336/1; 383/3
 Query Match 71.7%; Score 33; DB 2; Length 391;

Best Local Similarity 62.5%; Pred. No. 82;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LQDIEITC 9
| :|:|
Db 41 LTVDELTC 48

RESULT 12
B81289
probable sugar transferase Cj1434c [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: B81289
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: B81289
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-445 <PAR>
A:Cross-references: UNIPROT:Q9PMW3; GB:AL1139078; GB:AL111168; NID:G6968723; PIDN:CAB7385
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj1434c

Query Match 71.7%; Score 33; DB 2; Length 445;
Best Local Similarity 66.7%; Pred. No. 93;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLQDIEITC 9
| :|:|:|
Db 33 TLKDIEILC 41

RESULT 13
B81289
probable sugar transferase Cj1438c [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: B81289
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: B81289
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-776 <PAR>
A:Cross-references: UNIPROT:Q9PML9; GB:AL1139078; GB:AL111168; NID:G6968723; PIDN:CAB7386
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj1438c

Query Match 71.7%; Score 33; DB 2; Length 776;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLQDIEITC 9
| :|:|:|:|
Db 33 TLKDIEILC 41

RESULT 14
B83739
exonuclease ABC (subunit A) BH0714 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: B83739
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: B83739
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-820 <STO>
A:Cross-references: UNIPROT:Q9KEY5; GB:AP001509; GB:BA000004; NID:gi10173176; PIDN:BA80443
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0714

Query Match 71.7%; Score 33; DB 2; Length 820;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LQDIEITC 9
| :|:|:|
Db 638 LPDLEVTC 645

RESULT 15
T40928
conserved hypothetical protein SPCC132.01c [imported] - fission yeast (Schizosaccharomyce
N:Alternate names: conserved hypothetical protein SPCC132.17c
C:Species: Schizosaccharomyces pombe
C:Date: 20-Oct-2000 #sequence_revision 03-Nov-2000 #text_change 09-Jul-2004
C:Accession: T40928; T40948
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Aert, R.; Voickaert, G.
submitted to the EMBL Data Library, October 1999
A:Reference number: Z21958
A:Accession: T40928
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-549 <LYN>
A:Cross-references: UNIPROT:Q9USN8; EMBL:AL121807; PIDN:CAB58128.1; GSPDB:GN000068; SPDB:G
A:Experimental source: strain 972h-; cosmid c132
R:Lucas, M.; Gaillardin, C.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 1999
A:Reference number: Z21959
A:Accession: T40948
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 374-1021 <LUC>
A:Cross-references: EMBL:AL035259; PIDN:CAA2870.1; GSPDB:GN000068; SPDB:SPCC1322.17c
A:Experimental source: strain 972h-; cosmid c1322
C:Genetics:
A:Gene: SPDB:SPCC132.01c; SPDB:SPCC1322.17c
A:Map position: 3

Query Match 71.7%; Score 33; DB 2; Length 1021;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SLQDIEITC 9
| :|:|:|:|
Db 381 SLQDAQATC 389

Search completed: June 28, 2005, 21:27:37
Job time : 13.15 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-21
Perfect score: 49
Sequence: 1 KLPDLCTEL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trenbl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	25	2 Q8V9K8	Q8V9K8 human papil
2	49	100.0	25	2 Q8V9L1	Q8V9L1 human papil
3	49	100.0	25	2 Q8V9L2	Q8V9L2 human papil
4	49	100.0	25	2 Q8V9L3	Q8V9L3 human papil
5	49	100.0	57	2 Q80133	Q80133 human papil
6	49	100.0	151	2 O12335	O12335 human papil
7	49	100.0	151	2 O12336	O12336 human papil
8	49	100.0	151	2 Q76TS0	Q76TS0 human papil
9	49	100.0	151	2 Q77E16	Q77E16 human papil
10	49	100.0	151	2 Q80966	Q80966 human papil
11	49	100.0	151	2 Q89708	Q89708 human papil
12	49	100.0	158	1 V86_HPV18	V86_HPV18 human papil
13	49	100.0	158	1 V86_HPV45	V86_HPV45 human papil
14	49	100.0	158	2 Q9V4Y4	Q9V4Y4 homo sapien
15	49	100.0	158	2 O10608	O10608 human papil
16	49	100.0	158	2 Q8JMU8	Q8JMU8 human papil
17	49	100.0	158	2 Q8QHN0	Q8QHN0 human papil
18	49	100.0	158	2 Q9QNPF8	Q9QNPF8 human papil
19	45	91.8	151	2 Q9WMP2	Q9WMP2 human papil
20	43	87.8	143	2 Q919B6	Q919B6 human papil
21	43	87.8	143	2 Q919C4	Q919C4 human papil
22	43	87.8	151	2 Q778I6	Q778I6 human papil
23	43	87.8	151	2 Q77JC7	Q77JC7 human papil
24	43	87.8	151	2 Q77ZJ5	Q77ZJ5 human papil
25	43	87.8	151	2 Q80963	Q80963 human papil
26	43	87.8	151	2 Q89640	Q89640 human papil
27	43	87.8	151	2 Q89648	Q89648 human papil
28	43	87.8	151	2 Q89755	Q89755 human papil
29	43	87.8	151	2 Q89852	Q89852 human papil
30	43	87.8	151	2 Q8B564	Q8B564 human papil
31	43	87.8	151	2 Q8BB19	Q8BB19 human papil

32	43	87.8	151	2 Q8BB20	Q8BB20 human papil
33	43	87.8	151	2 Q9W8C3	Q9W8C3 human papil
34	43	87.8	151	2 Q9W931	Q9W931 human papil
35	43	87.8	151	2 Q9WMP4	Q9WMP4 human papil
36	43	87.8	151	2 Q9WMP5	Q9WMP5 human papil
37	43	87.8	158	1 V86_HPV16	V86_HPV16 human papil
38	43	87.8	158	1 V86_HPV39	V86_HPV39 human papil
39	43	87.8	158	1 V86_HPV70	V86_HPV70 human papil
40	43	87.8	158	2 Q8QHP5	Q8QHP5 human papil
41	43	87.8	158	2 Q8QHT0	Q8QHT0 human papil
42	43	87.8	158	2 Q8QRD6	Q8QRD6 human papil
43	43	87.8	158	2 Q8QRD7	Q8QRD7 human papil
44	43	87.8	158	2 Q8QRD8	Q8QRD8 human papil
45	43	87.8	158	2 Q8QRD9	Q8QRD9 human papil

ALIGNMENTS

RESULT 1

Q8V9K8 PRELIMINARY; PRT; 25 AA.
AC Q8V9K8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE E6 protein (Fragment).
GN Name=E6;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21568387; PubMed=11711624;
RX DOI=10.1128/JVI.75.24.12339-12346.2001;
RA Shera K.A., Shera C.A., McDougall J.K.;
RT "Small Tumor Virus Genomes Are Integrated near Nuclear Matrix Attachment Regions in Transformed Cells.";
RL J. Virol. 75:12339-12346(2001).
RL EMBL; AF339138; AAL34456.1; -.
FT NON_TER 25
SQ SEQUENCE 25 AA; 2967 MW; FCC9A030A21AE673 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
|||
Db 13 KLPDLCTEL 21

RESULT 2

Q8V9L1 PRELIMINARY; PRT; 25 AA.
AC Q8V9L1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE E6 protein (Fragment).
GN Name=E6;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21568387; PubMed=11711624;
RX DOI=10.1128/JVI.75.24.12339-12346.2001;
RA Shera K.A., Shera C.A., McDougall J.K.;
RT "Small Tumor Virus Genomes Are Integrated near Nuclear Matrix Attachment Regions in Transformed Cells.";
RL J. Virol. 75:12339-12346(2001).

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RL J. Virol. 75:12339-12346(2001).
DR EMBL: AF339136; AAL34453.1; -.
FR NON TER 25 25
SQ SEQUENCE 25 AA; 2967 MW; FCC9A030A21AE673 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
Db 13 KLPDLCTEL 21

RESULT 3
Q8V9L2 PRELIMINARY; PRT; 25 AA.
AC Q8V9L2;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE E6 protein (Fragment).
GN Name=E6;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21568387; PubMed=11711624;
RX DOI=10.1128/JVI.75.24.12339-12346.2001;
RA Shera K.A., Shera C.A., McDougall J.K.;
RT "Small Tumor Virus Genomes Are Integrated near Nuclear Matrix
Attachment Regions in Transformed Cells.";
RL J. Virol. 75:12339-12346(2001).
DR EMBL: AF339135; AAL34452.1; -.
FR NON TER 25 25
SQ SEQUENCE 25 AA; 2967 MW; FCC9A030A21AE673 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
Db 13 KLPDLCTEL 21

RESULT 4
Q8V9L3 PRELIMINARY; PRT; 25 AA.
AC Q8V9L3;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE E6 protein (Fragment).
GN Name=E6;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21568387; PubMed=11711624;
RX DOI=10.1128/JVI.75.24.12339-12346.2001;
RA Shera K.A., Shera C.A., McDougall J.K.;
RT "Small Tumor Virus Genomes Are Integrated near Nuclear Matrix
Attachment Regions in Transformed Cells.";
RL J. Virol. 75:12339-12346(2001).
DR EMBL: AF339133; AAL34451.1; -.
FR NON TER 25 25
SQ SEQUENCE 25 AA; 2967 MW; FCC9A030A21AE673 CRC64;
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Query Match 100.0%; Score 49; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
Db 13 KLPDLCTEL 21

RESULT 5
Q90133 PRELIMINARY; PRT; 57 AA.
AC Q90133;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Protein E6.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88188247; PubMed=2833614;
RX Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M.,
RA Sugimura T.;
RT "Nucleotide sequences of cDNAs for human papillomavirus type 18
transcripts in HeLa cells.";
RL J. Virol. 62:1640-1646(1988).
DR EMBL: M20324; AAA99512.1; -.
DR PIR: I56705; I56705.
SQ SEQUENCE 57 AA; 6531 MW; 31CF1A65B3740D2C CRC64;

Query Match 100.0%; Score 49; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
Db 13 KLPDLCTEL 21

RESULT 6
Q12335 PRELIMINARY; PRT; 151 AA.
AC Q12335;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RX Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL: AF003015; AAB70732.1; -.
DR GO: GO:0042025; C:Host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;

Query Match 100.0%; Score 49; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 KLPDLCTEL 9
DB 11 KLPDLCTEL 19

RESULT 7
O12336
ID O12336 PRELIMINARY; PRT; 151 AA.
AC O12336;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003016; AAB70733.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C5D8A CRC64;

Query Match 100.0%; Score 49; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLPDLCTEL 9
DB 11 KLPDLCTEL 19

RESULT 8
Q76TS0
ID Q76TS0 PRELIMINARY; PRT; 151 AA.
AC Q76TS0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
DR EMBL; U34114; AAA91661.1; -.
DR EMBL; U34125; AAA91672.1; -.
DR EMBL; U34130; AAA91677.1; -.
DR EMBL; U34131; AAA91678.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.

Query Match 100.0%; Score 49; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLPDLCTEL 9
DB 11 KLPDLCTEL 19

RESULT 9
Q77E16
ID Q77E16 PRELIMINARY; PRT; 151 AA.
AC Q77E16;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE E6 oncoprotein (E6 protein).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AF469197; AAO15691.1; -.
DR EMBL; AJ388063; CAB45118.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;

Query Match 100.0%; Score 49; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLPDLCTEL 9
DB 11 KLPDLCTEL 19

RESULT 10
Q80966
ID Q80966 PRELIMINARY; PRT; 151 AA.
AC Q80966; O12650; O12651; O12652; O12925; O12926; O12927; Q80962;
AC Q80964; Q80965;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";

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DR EMBL; X04354; CAA27879.1; -
 DR EMBL; X05015; CAA28664.1; -
 DR EMBL; M20325; AAA99514.1; -
 DR EMBL; M26798; AAA46946.1; -
 DR EMBL; X04773; CAA28466.1; -
 DR EMBL; A06324; CAA00539.1; -
 DR EMBL; A06328; CAA00542.1; -
 DR PIR; A26165; W6WL18.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 KW DNA-binding; Early protein; Nuclear protein; Oncogene; Zinc-finger.
 FT ZN_FING 32 68 Potential.
 FT ZN_FING 105 141 Potential.
 FT CONFLICT 22 22 N -> S (in Ref. 4).
 FT CONFLICT 22 22 N -> S (in Ref. 4).
 SQ SEQUENCE 158 AA; 18871 MW; 5BCF13CF43D157FA CRC64;

Query Match 100.0%; Score 49; DB 1; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
 |||||
 Db 13 KLPDLCTEL 21

RESULT 13
 ID V66 HPV45 STANDARD; PRT; 158 AA.
 AC P21735;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE E6 protein.
 GN Name=E6;
 OS Human papillomavirus type 45.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94265501; PubMed=8205838;
 RA Kaplan J.B., Burk R.D.;
 RT Submitted (AUG-1990) to the EMBL/GenBank/DBJ databases.
 RL FUNCTION: This protein has transforming activity in vitro.
 CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double
 CC stranded DNA (in vitro).
 CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.

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DR EMBL; X74479; CAA52573.1; -
 DR EMBL; M38198; AAA46973.1; -
 DR PIR; S36561; S36561.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 KW DNA-binding; Early protein; Nuclear protein; Oncogene; Zinc-finger.

FT ZN_FING 32 68 Potential.
 FT ZN_FING 105 141 Potential.
 FT CONFLICT 10 10 R -> P (in Ref. 2).
 FT CONFLICT 30 30 I -> N (in Ref. 2).
 FT CONFLICT 118 118 R -> A (in Ref. 2).
 SQ SEQUENCE 158 AA; 18897 MW; PICF10DD33AA4C3E CRC64;

Query Match 100.0%; Score 49; DB 1; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
 |||||
 Db 13 KLPDLCTEL 21

RESULT 14
 Q9Y4Y4 PRELIMINARY; PRT; 158 AA.
 AC Q9Y4Y4;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein.
 GN Name=HPV45 E6;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sastre-Garau X., Favre M., Couturier J., Orth G.;
 RT "Distinct patterns of alteration of myc genes associated with
 RT integration of human papillomavirus type 16 oe type 45 in two genital
 RT tumors.";
 RL J. Gen. Virol. 81:198-199(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Favre M.G.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ242956; CAB44706.1; -
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 158 AA; 18914 MW; A61AEFP98390AEEB3 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
 |||||
 Db 13 KLPDLCTEL 21

RESULT 15
 O10608 PRELIMINARY; PRT; 158 AA.
 AC O10608;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Oncoprotein E6.
 OS Human papillomavirus type 45.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sastre-Garau X., Favre M., Couturier J., Orth G.;
 RT "Distinct patterns of alteration of myc genes associated with
 RT integration of HPV16 or HPV45 DNA in two genital tumors.";

RL J. Gen. Virol. 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RA Favre M.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBSJ databases.
DR EMBL; Y13218; CAA73660.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 18914 MW; A61AEF98390AEEB3 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
|||
Db 13 KLPDLCTEL 21

Search completed: June 28, 2005, 21:23:44
Job time : 56.1 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-21
Perfect score: 49
Sequence: 1 KLPDLCTEL 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	57	2	E6 protein - human
2	49	100.0	158	1	W6WL18
3	49	100.0	158	2	E6 protein - human
4	43	87.8	158	1	W6WL39
5	43	87.8	158	1	W6WLHS
6	40	81.6	486	2	B86611
7	40	81.6	486	2	A72014
8	37	75.5	100	2	H95283
9	37	75.5	158	1	W6WLPR
10	37	75.5	177	2	S06079
11	36	73.5	84	2	E82288
12	35	71.4	374	2	E36996
13	35	71.4	450	2	D82494
14	35	71.4	743	2	D84545
15	34	69.4	86	2	A80153
16	34	69.4	94	2	S49190
17	34	69.4	273	2	S17695
18	34	69.4	341	1	K1BE36
19	34	69.4	341	1	K1BE40
20	34	69.4	341	1	K1BE73
21	34	69.4	341	1	K1BE87
22	34	69.4	341	1	K1BEGK
23	34	69.4	389	2	S75454
24	34	69.4	397	2	S28274
25	34	69.4	400	2	T44805
26	34	69.4	439	2	T49907
27	34	69.4	450	2	I77426
28	34	69.4	588	2	JC8021
29	34	69.4	609	2	B81528

30 34 69.4 609 2 F86611 glutamine-fructose
31 34 69.4 609 2 E72012 glutamine-fructose
32 34 69.4 1123 2 C96622 probable ATPase P2
33 34 69.4 1132 2 C75259 probable iron-sulf
34 33 67.3 121 2 C95967 probable transcrip
35 33 67.3 193 2 H64174 hypothetical prote
36 33 67.3 213 2 S42585 DNA-invertase - Rh
37 33 67.3 216 2 AH2347 hypothetical prote
38 33 67.3 235 2 T25675 hypothetical prote
39 33 67.3 279 2 T47942 hypothetical prote
40 33 67.3 292 2 A64487 modification methy
41 33 67.3 319 2 S48355 SRS1 protein - yea
42 33 67.3 362 2 D84713 probable dioxygena
43 33 67.3 399 1 F70427 dihydropteroate sy
44 33 67.3 422 1 BMRT2Y synaptotagmin II -
45 33 67.3 422 2 A55417 synaptotagmin II -

ALIGNMENTS

RESULT 1
I56705
E6 protein - human papillomavirus type 18
C:Species: human papillomavirus type 18
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56705
R:Inagaki, Y.; Tsunokawa, Y.; Takebe, N.; Nawa, H.; Nakanishi, S.; Terada, M.; Sugimura, J. Virol. 62, 1640-1646, 1988
A:Title: Nucleotide sequences of cDNAs for human papillomavirus type 18 transcripts in He
A:Reference number: I56705; MUID:88188247; PMID:2833614
A:Accession: I56705
A:Molecule type: mRNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-57 <RES>
A:Cross-references: UNIPROT:Q90133; GB:M20324; NID:G183933; PIDN:AAA99512.1; PID:G306834
C:Superfamily: papillomavirus E6 protein

Query Match 100.0%; Score 49; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
Db 13 KLPDLCTEL 21
|||||

RESULT 2
W6WL18
E6 protein - human papillomavirus type 18
C:Species: human papillomavirus type 18
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: A26165; G26251
R:Seedorf, K.; Oltersdorf, T.; Kraemmer, G.; Roewekamp, W. EMBO J. 6, 139-144, 1987
A:Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)
A:Reference number: A91068; MUID:87218459; PMID:3034571
A:Accession: A26165
A:Molecule type: DNA
A:Residues: 1-158 <SEE>
A:Cross-references: UNIPROT:P06463; GB:X04773; NID:G60876; PIDN:CAA28466.1; PID:G60877
R:Cole, S.T.; Danos, O. J. Mol. Biol. 193, 599-608, 1987
A:Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 18
A:Reference number: A92937; MUID:8723882; PMID:3039146
A:Accession: G26251
A:Molecule type: DNA
A:Residues: 1-158 <COL>
A:Cross-references: GB:X05015; NID:G60975; PIDN:CAA28664.1; PID:G60976
R:Matlahewski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pim, D.; Crawford, L. J. Gen. Virol. 67, 1909-1916, 1986
A:Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the p
A:Reference number: A92791; MUID:86306665; PMID:3018129

A;Contents: annotation; identification of the protein
 C;Superfamily: papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; transforming protein; zinc finger
 F;32-68/Region: zinc finger CCCC motif
 F;105-141/Region: zinc finger CCCC motif

Query Match 100.0%; Score 49; DB 1; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.062;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
 |||||
 Db 13 KLPDLCTEL 21

RESULT 3
 S36561
 E6 protein - human papillomavirus type 45
 C;Species: human papillomavirus type 45
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C;Accession: S36561
 R;Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A;Description: Primer-directed sequencing of human papillomavirus types.
 A;Reference number: S36469
 A;Accession: S36561
 A;Molecule type: DNA
 A;Residues: 1-158
 A;Cross-references: UNIPROT:P21735; EMBL:X74479; PIDN:CAA52573.1; PID:G3970
 C;Superfamily: papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 100.0%; Score 49; DB 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.062;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
 |||||
 Db 13 KLPDLCTEL 21

RESULT 4
 W6WL39
 E6 protein - human papillomavirus type 39
 C;Species: human papillomavirus type 39
 A;Note: host Homo sapiens (man)
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C;Accession: A38502
 R;Volpers, C.; Strebeck, R.E.
 Virology 181, 419-423, 1991
 A;Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
 A;Reference number: A38502; MUID:91135017; PMID:1847266
 A;Accession: A38502
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-158 <VOL>
 A;Cross-references: UNIPROT:P24935; GB:M62849; EMBL:M38185; NID:G333245; PIDN:AAA47050.1
 C;Superfamily: papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; transforming protein; zinc finger
 F;32-68/Region: zinc finger CCCC motif
 F;105-141/Region: zinc finger CCCC motif

Query Match 87.8%; Score 43; DB 1; Length 158;
 Best Local Similarity 88.9%; Pred. No. 0.83;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
 |||||
 Db 13 KLPDLCTEL 21

RESULT 5
 W6WLHS
 E6 protein - human papillomavirus type 16
 C;Species: human papillomavirus type 16
 C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
 C;Accession: A03682; T10427
 R;Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
 Virology 145, 181-185, 1985
 A;Title: Human papillomavirus type 16 DNA sequence.
 A;Reference number: A22355; MUID:85246220; PMID:2990099
 A;Accession: A03682
 A;Molecule type: DNA
 A;Residues: 1-158 <SEE>
 A;Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
 R;Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
 J. Virol. 65, 2093-2097, 1991
 A;Title: A negative element in the human poapillomavirus type 16 genome acts at the level
 A;Reference number: E17014; MUID:91162763; PMID:1848319
 A;Accession: T10427
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: DNA
 A;Residues: 1-158 <KEN>
 A;Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
 C;Genetics:
 C;Superfamily: papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; zinc finger
 F;37-73/Region: zinc finger CCCC motif
 F;110-146/Region: zinc finger CCCC motif

Query Match 87.8%; Score 43; DB 1; Length 158;
 Best Local Similarity 88.9%; Pred. No. 0.83;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
 |||||
 Db 18 KLPDLCTEL 26

RESULT 6
 B86611
 hypothetical protein CPJ0964 [imported] - Chlamydomphila pneumoniae (strain J138)
 C;Species: Chlamydomphila pneumoniae, Chlamydia pneumoniae
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: B86611
 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise
 Nucleic Acids Res. 28, 2311-2314, 2000
 A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A;Reference number: A86491; MUID:20330349; PMID:10871362
 A;Accession: B86611
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-486 <STO>
 A;Cross-references: UNIPROT:Q9J583; GB:BA000008; NID:98979338; PIDN:BA099172.1; GSPDB:GNK
 A;Experimental source: strain J138
 C;Genetics:
 A;Gene: CPJ0964
 C;Superfamily: Chlamydia pneumoniae hypothetical protein CP0896

Query Match 81.6%; Score 40; DB 2; Length 486;
 Best Local Similarity 66.7%; Pred. No. 9.5;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
 |||||
 Db 188 KIPDLCSOL 196

RESULT 7
 A72014
 hypothetical protein CP0896 [imported] - Chlamydomphila pneumoniae (strains CWL029 and AR
 C;Species: Chlamydomphila pneumoniae, Chlamydia pneumoniae
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: A72014; E81526
 R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

protein E6 - human papillomavirus type 16
 C;Species: human papillomavirus type 16
 C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
 C;Accession: A03682; T10427
 R;Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
 Virology 145, 181-185, 1985
 A;Title: Human papillomavirus type 16 DNA sequence.
 A;Reference number: A22355; MUID:85246220; PMID:2990099
 A;Accession: A03682
 A;Molecule type: DNA
 A;Residues: 1-158 <SEE>
 A;Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
 R;Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
 J. Virol. 65, 2093-2097, 1991
 A;Title: A negative element in the human poapillomavirus type 16 genome acts at the level
 A;Reference number: E17014; MUID:91162763; PMID:1848319
 A;Accession: T10427
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: DNA
 A;Residues: 1-158 <KEN>
 A;Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
 C;Genetics:
 C;Superfamily: papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; zinc finger
 F;37-73/Region: zinc finger CCCC motif
 F;110-146/Region: zinc finger CCCC motif

Query Match 87.8%; Score 43; DB 1; Length 158;
 Best Local Similarity 88.9%; Pred. No. 0.83;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
 |||||
 Db 18 KLPDLCTEL 26

RESULT 6
 B86611
 hypothetical protein CPJ0964 [imported] - Chlamydomphila pneumoniae (strain J138)
 C;Species: Chlamydomphila pneumoniae, Chlamydia pneumoniae
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: B86611
 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise
 Nucleic Acids Res. 28, 2311-2314, 2000
 A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A;Reference number: A86491; MUID:20330349; PMID:10871362
 A;Accession: B86611
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-486 <STO>
 A;Cross-references: UNIPROT:Q9J583; GB:BA000008; NID:98979338; PIDN:BA099172.1; GSPDB:GNK
 A;Experimental source: strain J138
 C;Genetics:
 A;Gene: CPJ0964
 C;Superfamily: Chlamydia pneumoniae hypothetical protein CP0896

Query Match 81.6%; Score 40; DB 2; Length 486;
 Best Local Similarity 66.7%; Pred. No. 9.5;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
 |||||
 Db 188 KIPDLCSOL 196

RESULT 7
 A72014
 hypothetical protein CP0896 [imported] - Chlamydomphila pneumoniae (strains CWL029 and AR
 C;Species: Chlamydomphila pneumoniae, Chlamydia pneumoniae
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: A72014; E81526
 R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999
A:Title: Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192398
A:Accession: A72014
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-486 <ARN>
A:Cross-references: UNIPROT:Q9Z6U4; GB:AE001676; GB:AE001363; NID:G4377283; PIDN:AAAD1910
A:Experimental source: strain CWL029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: AB1500; MUID:20150255; PMID:10694935
A:Accession: E81526
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-486 <REA>
A:Cross-references: GB:AE002248; GB:AE002161; NID:G7189806; PIDN:AAF38683.1; PID:G718980
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CPN0964; CP0896
C:Superfamily: Chlamydia pneumoniae hypothetical protein CP0896

Query Match 81.6%; Score 40; DB 2; Length 486;
Best Local Similarity 66.7%; Pred. No. 9.5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
|:||||:|
Db 188 KIPDLCSOL 196

RESULT 8
H95283
Conserved hypothetical protein Sma0325 [imported] - Sinorhizobium meliloti (strain 1021)
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: H95283
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe, R.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: H95283
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-100 <KUR>
A:Cross-references: UNIPROT:Q930L9; GB:AE006469; PIDN:AAK64834.1; PID:G14523247; GSPDB:C
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A56039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Sma0325
A:Genome: plasmid

Query Match 75.5%; Score 37; DB 2; Length 100;
Best Local Similarity 75.0%; Pred. No. 7.1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPDLCTE 8
|:|||||
Db 79 KVPDLCTE 86

RESULT 9

W6WLP
E6 protein - human papillomavirus type ME180 (provirus)
C:Species: human papillomavirus type ME180
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
A:Accession: C40509
R:Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E. J. Virol. 65, 5564-5568, 1991
A:Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma (C) cell line.
A:Reference number: A40509; MUID:91374616; PMID:1716694
A:Accession: C40509
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-158 <REU>
A:Cross-references: UNIPROT:P27962; GB:M73258
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:32-68/Region: zinc finger CCCC motif
F:105-141/Region: zinc finger CCCC motif

Query Match 75.5%; Score 37; DB 1; Length 158;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
|:|||||
Db 13 KLPDLCTEL 21

RESULT 10
S06079
H+-transporting two-sector ATPase (EC 3.6.3.14) delta chain - Vibrio alginolyticus
C:Species: Vibrio alginolyticus
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
A:Accession: S06079
R:Krumholz, L.R.; Esser, U.; Simoni, R.D. Nucleic Acids Res. 17, 7993-7994, 1989
A:Title: Nucleotide sequence of the unc operon of Vibrio alginolyticus.
A:Reference number: S06075; MUID:90016889; PMID:2529481
A:Accession: S06079
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-177 <KRU>
A:Cross-references: UNIPROT:P12987; EMBL:X16050; NID:G48331; PIDN:CAA34178.1; PID:G48336
C:Genetics:
A:Gene: uncH
C:Superfamily: H+-transporting ATP synthase delta chain
C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

Query Match 75.5%; Score 37; DB 2; Length 177;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LPDLCTE 8
|:|||||
Db 89 LPDVCCTE 95

RESULT 11
E82288
ferredoxin VC0716 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 12-Jul-2004
A:Accession: E82288
R:Heidelberg, J.F.; Eissen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P. Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: E82288
A:Status: preliminary
A:Molecule type: DNA

A;Residues: 1-84 <HEI>
A;Cross-references: UNIPROT:Q9KUL4; GB:AE004158; GB:AE003852; NID:g9655156; PIDN:AAF9388
A;Experimental source: serogroup O1; strain N16961; biotype EI Tor
C;Genetics:
A;Gene: VC0716
A;Map position: 1
C;Keywords: 4Fe-4S; metalloproteins
F;9,12,15,54/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
F;19,38,41,50/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 73.5%; Score 36; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PDLCTE 8
| | | | |
Db 35 PDLCTE 40

RESULT 12
E96996
A;P-Dependent RNA helicase, superfamily II [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: E96996
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: E96996
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-374 <KUR>
A;Cross-references: UNIPROT:Q97KY2; GB:AE001437; PIDN:AAK78760.1; PID:gl5023670; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0784
C;Superfamily: translation initiation factor eIF-4A

Query Match 71.4%; Score 35; DB 2; Length 374;
Best Local Similarity 77.8%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
| | | | |
Db 226 KLEDLCTAL 234

RESULT 13
D82494
probable oxidoreductase VCA0151 [imported] - Vibrio cholerae (strain N16961 serogroup O1
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82494
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Charleson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B. N. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: D82494
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-450 <HEI>
A;Cross-references: UNIPROT:Q9KN15; GB:AE004356; GB:AE003853; NID:g9657536; PIDN:AAF9606
A;Experimental source: serogroup O1; strain N16961; biotype EI Tor
C;Genetics:
A;Gene: VCA0151
A;Map position: 2

Query Match 71.4%; Score 35; DB 2; Length 450;
Best Local Similarity 85.7%; Pred. No. 77;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PDLCTEL 9
| | | | |
Db 370 PDLCAEL 376

RESULT 14
D84545
probable salt-inducible protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: D84545
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84545
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-743 <STO>
A;Cross-references: UNIPROT:Q9ZVK5; GB:AE002093; NID:g3757517; PIDN:AAC64219.1; GSPDB:GN
C;Genetics:
A;Gene: At2g16880
A;Map position: 2

Query Match 71.4%; Score 35; DB 2; Length 743;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LPDLCT 7
| | | | |
Db 307 LPDLCT 312

RESULT 15
AB0153
probable bacteriophage protein YPO1250a [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0153
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; i l, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, i Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0153
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 <KUR>
A;Cross-references: UNIPROT:Q8ZGN6; GB:AL590842; PIDN:CAC90085.1; PID:gl5979305; GSPDB:G
C;Genetics:
A;Gene: YPO1250a

Query Match 69.4%; Score 34; DB 2; Length 86;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LPDLCTEL 9
| | | | |
Db 74 LPDLCAEL 81

Search completed: June 28, 2005, 21:27:35
Job time : 13.15 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-20
Perfect score: 47
Sequence: 1 TLGIVAPIC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	91.5	26	Q84267	Q84267 human papil
2	43	91.5	94	Q8B5P6	Q8B5P6 human papil
3	43	91.5	98	VE7_HPV16	P03129 human papil
4	43	91.5	98	O11650	O11650 human papil
5	43	91.5	98	O12337	O12337 human papil
6	43	91.5	98	O12338	O12338 human papil
7	43	91.5	98	Q8QRD2	Q8QRD2 human papil
8	43	91.5	98	Q8QRD3	Q8QRD3 human papil
9	43	91.5	98	Q8QRD4	Q8QRD4 human papil
10	43	91.5	98	O8V1J0	O8V1J0 human papil
11	43	91.5	98	Q778H3	Q778H3 human papil
12	43	91.5	98	Q778H5	Q778H5 human papil
13	41	87.2	104	VE7_HPV32	P36827 human papil
14	39	83.0	348	Q8KBQ8	Q8KBQ8 chlorobium
15	38	80.9	99	O90724	O90724 human papil
16	37	78.7	98	VE7_HPV11	P04020 human papil
17	37	78.7	98	VE7_HPV6B	P04464 human papil
18	37	78.7	98	O9QLP4	O9QLP4 human papil
19	37	78.7	561	Q8G4W0	Q8G4W0 bifidobacte
20	36	76.6	97	Q82006	Q82006 human papil
21	36	76.6	98	VE7_HPV6A	Q84292 human papil
22	36	76.6	213	Q8SV04	Q8SV04 encephalito
23	36	76.6	226	Q8BZC0	Q8BZC0 lactobacilli
24	36	76.6	351	Q861J0	Q861J0 dictyosteli
25	36	76.6	428	Q6CX65	Q6CX65 kluyveromyc
26	36	76.6	487	Q8NC61	Q8NC61 homo sapien
27	36	76.6	516	O8EKT7	O8EKT7 shewanella
28	36	76.6	3056	Q898M4	Q898M4 rhizobium 1
29	35	74.5	94	Q6EGQ1	Q6EGQ1 human papil
30	35	74.5	94	Q6EGQ8	Q6EGQ8 human papil
31	35	74.5	101	VE7_HPV13	Q02271 human papil

32	35	74.5	134	2	Q7VDC9	Q7VDC9 prochloroco
33	35	74.5	219	2	Q50798	Q50798 methanobact
34	35	74.5	232	2	Q95KA7	Q95KA7 macaca fasc
35	35	74.5	300	2	Q6LZ28	Q6LZ28 methanococc
36	35	74.5	326	2	Q8NCF8	Q8NCF8 homo sapien
37	35	74.5	336	2	Q9C7E9	Q9C7E9 arabidopsis
38	35	74.5	339	2	Q7M7S8	Q7M7S8 wolinnella s
39	35	74.5	344	2	Q8BHI3	Q8BHI3 m mus muscu
40	35	74.5	367	2	Q97IP8	Q97IP8 clostridium
41	35	74.5	413	2	Q8NCD8	Q8NCD8 homo sapien
42	35	74.5	431	1	PROA_BIFLO	Q8G5H9 bifidobacte
43	35	74.5	446	2	Q9HLT4	Q9HLT4 thermoplasma
44	35	74.5	449	2	Q9CGJ0	Q9CGJ0 lactococcus
45	35	74.5	461	2	Q9LIF70	Q9LIF70 arabidopsis

ALIGNMENTS

RESULT 1

Q84267 PRELIMINARY; PRT; 26 AA.
AC Q84267;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE E7 ORF (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8905007; PubMed=2536104;
RA Choo K.-B., Cheung W.-F., Liew L.-N., Lee H.-H., Han S.-H.;
RT "Presence of Caenated Human Papillomavirus Type 16 Episomes in a
RT Cervical Carcinoma Cell Line."
RL J. Virol. 63:782-789 (1989).
DR EMBL; M24215; AAA46944.1; .
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 1
SQ SEQUENCE 26 AA; 2799 MW; 91C16F1D34D18B34 CRC64;

Query Match Similarity 91.5%; Score 43; DB 2; Length 26;
Best Local Similarity 88.9%; Pred. No. 0.53;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
Db 14 TLGIVCPIC 22

RESULT 2

Q8B5P6 PRELIMINARY; PRT; 94 AA.
AC Q8B5P6;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE E7 oncoprotein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469137; AA015692.1; .
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 94

SQ SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;

Query Match 91.5%; Score 43; DB 2; Length 94;
Best Local Similarity 88.9%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLGIVAPIC 9
| | | | |
DB 86 TLGIVCPIC 94

RESULT 3
VE7 HPV16
ID VE7 HPV16 STANDARD; PRT; 98 AA.
AC P03129;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85246220; PubMed=2990099;
RA Seedorf K., Kramer G., Durst M., Suhai S., Rowekamp W.G.;
RT "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90218027; PubMed=2157796;
RA Schneider-Maunoury S., Pehau-Arnauudet G., Breitbart F., Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-v cells,
a line derived from a vulvar intraepithelial neoplasia.";
RL J. Gen. Virol. 71:809-817(1990).
RN [3]
RP SEQUENCE FROM N.A.
RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Tornesello M.L., Buonaguro P.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP FUNCTION.
RX MEDLINE=88223347; PubMed=2836062;
RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;
RT "The human papillomavirus type 16 E7 gene encodes transactivation and
transformation functions similar to those of adenovirus E1A.";
RL Cell 53:539-547(1988).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating
activities.
CC
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CC
CC EMBL; K02718; AAA46940.1; -
DR EMBL; D00735; BAA00633.1; -
DR EMBL; U76411; AAB18962.1; -
DR EMBL; U76412; AAB18963.1; -
DR EMBL; U76413; AAB18964.1; -
DR EMBL; AF003020; AAB70737.1; -
DR EMBL; AF003023; AAB70740.1; -
DR EMBL; AF003024; AAB70741.1; -
DR EMBL; AF003025; AAB70742.1; -

DR EMBL; AF003026; AAB70743.1; -
DR PIR; A03688; W7WLHS.
DR InterPro; IPR00148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW Transcription regulation.
FT SITE 58 61 C-XX-C motif-1.
FT SITE 91 94 C-XX-C motif-2.
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 91.5%; Score 43; DB 1; Length 98;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLGIVAPIC 9
| | | | |
DB 86 TLGIVCPIC 94

RESULT 4
O11650
ID O11650 PRELIMINARY; PRT; 98 AA.
AC O11650;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Putative transforming protein E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
RA Lee H.P.;
RT "Major sequence variants in E7 gene of human papillomavirus type 16
from cervical cancerous and noncancerous lesions of Korean women.";
RL Gynecol. Oncol. 66:275-281(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
RA Lee H.-P.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Terai M., Ma Z., Burk R.D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.-S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
RN [5]
RP SEQUENCE FROM N.A.
RA Terai M., Fu L., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U76404; AAC58243.1; -
DR EMBL; AF472509; AA015706.1; -
DR EMBL; AF486326; AAL96631.1; -
DR EMBL; AF486327; AAL96632.1; -
DR EMBL; AF486330; AAL96635.1; -
DR EMBL; AF486331; AAL96636.1; -
DR EMBL; AF486332; AAL96637.1; -
DR EMBL; AF486333; AAL96638.1; -
DR EMBL; AF486334; AAL96639.1; -
DR EMBL; AF486336; AAL96641.1; -
DR EMBL; AF486338; AAL96643.1; -
DR EMBL; AF486346; AAL96651.1; -
DR EMBL; AF486350; AAL96655.1; -

DR EMBL; AF486351; AAL96656.1; -;
DR EMBL; AF534061; AAQ0404.1; -;
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 91.5%; Score 43; DB 2; Length 98;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
|||||
Db 86 TLGIVCPIC 94

RESULT 5

O12337
ID O12337 PRELIMINARY; PRT; 98 AA.
AC O12337;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesillo M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003021; AAB70739.1; -;
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11056 MW; 19DEB8E14CD2C705 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 98;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
|||||
Db 86 TLGIVCPIC 94

RESULT 6

O12338
ID O12338 PRELIMINARY; PRT; 98 AA.
AC O12338;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesillo M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Jinhu X., Xinxiang W., Yun T.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF003022; AAB70739.1; -;
DR EMBL; AF477385; AAM03025.1; -;
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10969 MW; 9BD612534CCEA59B CRC64;

Query Match 91.5%; Score 43; DB 2; Length 98;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
|||||
Db 86 TLGIVCPIC 94

RESULT 7

O8QRD2
ID O8QRD2 PRELIMINARY; PRT; 98 AA.
AC O8QRD2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486345; AAL96650.1; -;
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 91.5%; Score 43; DB 2; Length 98;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
|||||
Db 86 TLGIVCPIC 94

RESULT 8

O8QRD3
ID O8QRD3 PRELIMINARY; PRT; 98 AA.
AC O8QRD3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486344; AAL96649.1; -;
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 98;
 Best Local Similarity 88.9%; Pred. No. 1.7; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 1 TLGIVAPIC 9
 |||||
 Db 86 TLGIVCPIC 94

RESULT 9

Q8ORD4 PRELIMINARY; PRT; 98 AA.
 AC Q8ORD4;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22182962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RA "Human papillomavirus type 16 intratypic variant infection and risk
 RT for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700(2002).
 DR EMBL; AF486329; AAL96634.1; -.
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 DR NON TER 98
 SQ SEQUENCE 98 AA; 11025 MW; 86E24B234CC3281B CRC64;

Query Match 91.5%; Score 43; DB 2; Length 98;
 Best Local Similarity 88.9%; Pred. No. 1.7; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 1 TLGIVAPIC 9
 |||||
 Db 86 TLGIVCPIC 94

RESULT 10

Q8VLJ0 PRELIMINARY; PRT; 98 AA.
 AC Q8VLJ0;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jinhu X., Xinling W., Yun T.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF461264; AAL66736.1; -.
 DR Pfam; PF00527; E7; 1.
 DR NON TER 98
 SQ SEQUENCE 98 AA; 10997 MW; 9BD610834CCEA59B CRC64;

Query Match 91.5%; Score 43; DB 2; Length 98;
 Best Local Similarity 88.9%; Pred. No. 1.7; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 1 TLGIVAPIC 9
 |||||
 Db 86 TLGIVCPIC 94

RESULT 11

Q778H3 PRELIMINARY; PRT; 98 AA.
 AC Q778H3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE E7 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
 RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 B6 variants in relation to
 RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325(2000).
 DR EMBL; AJ388063; CAB45117.1; -.
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 DR NON TER 98
 SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 91.5%; Score 43; DB 2; Length 98;
 Best Local Similarity 88.9%; Pred. No. 1.7; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 1 TLGIVAPIC 9
 |||||
 Db 86 TLGIVCPIC 94

RESULT 12

Q778H5 PRELIMINARY; PRT; 98 AA.
 AC Q778H5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE E7 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
 RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 B6 variants in relation to
 RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325(2000).
 DR EMBL; AJ388062; CAB45117.1; -.
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 DR NON TER 98
 SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 91.5%; Score 43; DB 2; Length 98;
 Best Local Similarity 88.9%; Pred. No. 1.7; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 1 TLGIVAPIC 9
 |||||
 Db 86 TLGIVCPIC 94

RESULT 13

VE7 HPV32 STANDARD; PRT; 104 AA.
 ID - VE7 HPV32


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DR ENBL; AE012926; AAM72949.1; -.
DR TIGR; C11726; -.
DR InterPro; IPR005524; DUF318.
DR Pfam; PF03773; DUF318; 1.
KW Complete proteome.
SQ SEQUENCE 348 AA; 36990 MW; 9B098EDD8CEB981A CRC64;

Query Match      83.0%; Score 39; DB 2; Length 348;
Best Local Similarity 77.8%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TLGIVAPIC 9
    |||||
DB 106 TLGIVTPFC 114

RESULT 15
O90724 PRELIMINARY; PRT; 99 AA.
AC O90724;
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE ORF E7.
OS Human papillomavirus type 67.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=371120;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=990737695; Pubmed=9857984; DOI=10.1023/A:1008002905588;
RA Kirii Y., Matsukura T.;
RT "Nucleotide sequence and phylogenetic classification of human
RL papillomavirus type 67.";
RL Virus Genes 17:117-121(1998).
DR ENBL; D21208; BAA28853.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 99 AA; 11156 MW; 81A4A636D7588C44 CRC64;

Query Match      80.9%; Score 38; DB 2; Length 99;
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TLGIVAPIC 9
    |||||
DB 88 TLGIVPTC 96

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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 Seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-20
Perfect score: 47
Sequence: 1 TLGIVAPIC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	91.5	98	1 W7WLS	E7 protein - human
2	41	87.2	104	2 S36510	E7 protein - human
3	37	78.7	98	1 W7WLS	E7 protein - human
4	37	78.7	98	1 W7WLS	E7 protein - human
5	37	78.7	98	1 W7WLS	E7 protein - human
6	35	74.5	101	1 W7WLS	E7 protein - human
7	35	74.5	219	2 T45262	hypothetical prote
8	35	74.5	336	2 A86406	probable RING zinc
9	35	74.5	367	2 D70996	probable permease,
10	35	74.5	449	2 B86763	hypothetical prote
11	35	74.5	461	2 T51458	hypothetical prote
12	35	74.5	487	2 JCT328	amino acid transpo
13	35	74.5	508	2 B81212	fatty acid efflux
14	35	74.5	516	2 E81789	multidrug resistan
15	34	72.3	93	1 W7WLS	E7 protein - human
16	34	72.3	337	2 H64432	spore coat polysac
17	34	72.3	441	2 H82642	hypothetical prote
18	34	72.3	460	2 T03274	hst201 protein, hy
19	34	72.3	656	2 T35408	probable transketo
20	34	72.3	2051	2 T30938	receptor tyrosine
21	34	72.3	3624	2 AD0835	large repetitive p
22	33	70.2	119	2 S46108	probable membrane
23	33	70.2	222	2 H69039	cobalamin biosynth
24	33	70.2	262	2 B96937	chemotaxis motilit
25	33	70.2	297	1 A30586	B-cell surface ant
26	33	70.2	360	1 JH0692	protein-tyrosine-p
27	33	70.2	433	2 AG1044	anaerobic C4-dicar
28	33	70.2	454	2 AC1413	PTS system, cellob
29	33	70.2	454	2 AB1789	PTS system, cellob

30 33 70.2 479 2 T51919 related to aldehyd
31 33 70.2 518 2 B71545 probable oligopept
32 33 70.2 587 2 F90044 hypothetical prote
33 33 70.2 599 2 F87682 TrkA family protei
34 33 70.2 930 2 A84668 Argonaute (AGO1)-1
35 33 70.2 1180 2 A47202 adenylate cyclase
36 32 68.1 148 2 AH0712 probable membrane
37 32 68.1 148 2 F85789 hypothetical prote
38 32 68.1 148 2 B90941 hypothetical prote
39 32 68.1 148 2 B64939 hypothetical prote
40 32 68.1 150 2 AH0371 probable membrane
41 32 68.1 152 2 B97865 proline/betaine tr
42 32 68.1 191 2 AB1670 hypothetical prote
43 32 68.1 210 2 AS0761 conserved hypotnet
44 32 68.1 228 2 S48116 integral membrane
45 32 68.1 249 2 JQ2287 SPCP1 protein - so

ALIGNMENTS

RESULT 1
W7WLS
E7 protein - human papillomavirus type 16
C:Species: human papillomavirus type 16
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A03688; S12367; T10428
R:Seedorf, K.; Kramer, G.; Duret, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A:Title: Human papillomavirus type 16 DNA sequence.
A:Reference number: A22355; MUID:85246220; PMID:2990099
A:Accession: A03688
A:Molecule type: DNA
A:Residues: 1-98 <SEB>
A:Cross-references: UNIPROT:P03129; GB:K02718; NID:G333031; PIDN:AAA46940.1; PID:G333033
R:Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Voutsden, K.H.
EMBO J. 9, 153-160, 1990
A:Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 large
A:Reference number: S12367; MUID:90107938; PMID:2153075
A:Accession: S12367
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-98 <BAR>
R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A:Reference number: Z17014; MUID:91162763; PMID:1848319
A:Accession: T10428
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-98 <KEN>
A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46940.1; PID:G333033
C:Genetics:
C:Gene: E7
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:58-94/Region: zinc finger CCCC motif

Query Match 91.5%; Score 43; DB 1; Length 98;
Best Local Similarity 88.9%; Pred. No. 0.33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
Db 86 TLGIVCPIC 94

RESULT 2
S36510
E7 protein - human papillomavirus type 32
C:Species: human papillomavirus type 32
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36510

R;Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A:Description: Primer-directed sequencing of human papillomavirus types.
 A:Reference number: S36469
 A:Accession: S36510
 A:Molecule type: DNA
 A:Residues: 1-104
 A:Cross-references: UNIPROT:P36827; EMBL:X74475; NID:g396981; PIDN:CAA52550.1; PID:g396981
 C:Superfamily: papillomavirus E7 protein
 C:Keywords: DNA binding; early protein; transcription regulation

Query Match 87.2%; Score 41; DB 2; Length 104;
 Best Local Similarity 77.8%; Pred. No. 0.86;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
 |||||
 Db 92 TLGIVCPIC 100

RESULT 3
 W7WLI1
 E7 protein - human papillomavirus type 11
 C:Species: human papillomavirus type 11
 C:Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
 C:Accession: A03690
 R:Dartmann, K.; Schwarz, E.; Gissmann, L.; zur Hausen, H.
 Virology 151, 124-130, 1986
 A:Title: The nucleotide sequence and genome organization of human papilloma virus type 1
 A:Reference number: A94338; MUID:86181601; PMID:3008427
 A:Accession: A03690
 A:Molecule type: DNA
 A:Residues: 1-98 <DAR>
 A:Cross-references: UNIPROT:P04020; GB:J14119; NID:g333026; PIDN:AAA46928.1; PID:g496194
 C:Superfamily: papillomavirus E7 protein
 C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
 F:58-94/Region: zinc finger CCCC motif

Query Match 78.7%; Score 37; DB 1; Length 98;
 Best Local Similarity 77.8%; Pred. No. 4.9;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
 |||||
 Db 86 TLNIVCPIC 94

RESULT 4
 W7WLI6
 E7 protein - human papillomavirus type 6b
 C:Species: human papillomavirus type 6b
 C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
 C:Accession: D20558
 R;Schwarz, E.; Durst, M.; Denankowski, C.; Lattermann, O.; Zech, R.; Wolfsperger, E.; Sur
 EMBO J. 2, 2341-2348, 1983
 A:Title: DNA sequence and genome organization of genital human papillomavirus type 6b.
 A:Reference number: A90975; MUID:84131949; PMID:6321162
 A:Accession: D20558
 A:Molecule type: DNA
 A:Residues: 1-98 <SCH>
 A:Cross-references: UNIPROT:P06464; GB:X00203; NID:g60955; PIDN:CAA25019.1; PID:g60957
 C:Superfamily: papillomavirus E7 protein
 C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
 F:58-94/Region: zinc finger CCCC motif

Query Match 78.7%; Score 37; DB 1; Length 98;
 Best Local Similarity 77.8%; Pred. No. 4.9;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
 |||||
 Db 86 TLNIVCPIC 94

RESULT 5

T33432
 Hypothetical protein T17A3.9 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T33432
 R:Clarke, K.; Rohlfing, T.; Morris, M.
 submitted to the EMBL Data Library, July 1998
 A:Description: The sequence of C. elegans cosmid T17A3.
 A:Reference number: Z21343
 A:Accession: T33432
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-466 <CLA>
 A:Cross-references: EMBL:AF078787; PIDN:AC36955.1; GSPDB:GN00021; CESP:T17A3.9
 A:Experimental source: strain Bristol N2; clone T17A3
 C:Genetics:
 A:Gene: CESP:T17A3.9
 A:Map position: 3
 A:Introns: 27/1; 114/3; 198/3; 318/3; 405/3

Query Match 78.7%; Score 37; DB 2; Length 466;
 Best Local Similarity 62.5%; Pred. No. 20;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LGIVAPIC 9

|||
 Db 324 LGVSPVC 331

RESULT 6

W7WLI3
 E7 protein - human papillomavirus type 13
 C:Species: human papillomavirus type 13
 A:Note: host Homo sapiens (man)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
 C:Accession: B42955
 R:van Ranst, M.; Fuse, A.; Piten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; Opdenakker, G.
 Virology 190, 587-596, 1992
 A:Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Compari
 A:Reference number: A42955; MUID:92391075; PMID:1325697
 A:Accession: B42955
 A:Molecule type: DNA
 A:Residues: 1-101 <VAN>
 A:Cross-references: UNIPROT:Q02271; EMBL:X62843; NID:g60295; PIDN:CAA44648.1; PID:g60297
 C:Superfamily: papillomavirus E7 protein
 C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
 F:61-97/Region: zinc finger CCCC motif

Query Match 74.5%; Score 35; DB 1; Length 101;
 Best Local Similarity 66.7%; Pred. No. 12;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9

|||
 Db 89 TLNIVCPIC 97

RESULT 7

T45262
 cobalamin biosynthesis protein M homolog [imported] - Methanobacterium thermoautotrophic
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T45262
 R:Eberhardt, S.; Korn, S.; Lottspeich, F.; Bacher, A.
 J. Bacteriol. 179, 2938-2943, 1997
 A:Title: Biosynthesis of riboflavin: an unusual riboflavin synthase of Methanobacterium t
 A:Reference number: Z22951; MUID:97284497; PMID:9139911
 A:Accession: T45262
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-219 <EBE>

A;Cross-references: UNIPROT:Q50798; EMBL:X94292; NID:g1419074; PIDN:CAA63955.1; PID:g1419074
 A;Experimental source: strain Marburg
 C;Genetics:
 A;Gene: cblM
 C;Superfamily: cobalamin biosynthesis protein M

Query Match 74.5%; Score 35; DB 2; Length 219;
 Best Local Similarity 44.4%; Pred. No. 25;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
 Db 111 SMGIIPVC 119

RESULT 8
 A86406
 probable RING zinc finger protein [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: A86406
 R;Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huijzer, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: A86406
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-336 <STO>
 A;Cross-references: UNIPROT:Q9CTE9; GB:AE005172; NID:g11024872; PIDN:AG26956.1; GSPDB:G
 C;Genetics:
 A;Map position: 1

Query Match 74.5%; Score 35; DB 2; Length 336;
 Best Local Similarity 66.7%; Pred. No. 36;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
 Db 285 TNGIICPIC 293

RESULT 9
 D97096
 probable permealase, YCGR B. subtilis ortholog [imported] - Clostridium acetobutylicum
 C;Species: Clostridium acetobutylicum
 C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C;Accession: D97096
 R;Nolling, J.; Bretton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
 A;Reference number: A96900; MUID:21359325; PMID:21359325
 A;Accession: D97096
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-367 <KUR>
 A;Cross-references: UNIPROT:Q97IP8; GB:AE001437; PIDN:AAK79559.1; PID:g15024547; GSPDB:G
 A;Experimental source: Clostridium acetobutylicum ATCC824
 C;Genetics:
 A;Gene: CAC1592

Query Match 74.5%; Score 35; DB 2; Length 367;
 Best Local Similarity 44.4%; Pred. No. 39;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
 Db 99 TIGLIPVC 107

RESULT 10

B86763
 hypothetical protein ylbD [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
 C;Species: Lactococcus lactis subsp. lactis
 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C;Accession: B86763
 R;Bolotin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich
 Genome Res. 11, 731-753, 2001
 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssi
 A;Reference number: A86625; MUID:21235186; PMID:111337471
 A;Accession: B86763
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-449 <STO>
 A;Cross-references: UNIPROT:Q9CGJ0; GB:AE005176; PID:g12724063; PIDN:AAK05204.1; GSPDB:G
 A;Experimental source: strain IL1403
 C;Genetics:
 A;Gene: ylbD

Query Match 74.5%; Score 35; DB 2; Length 449;
 Best Local Similarity 66.7%; Pred. No. 47;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
 Db 202 TEGIVCPVC 210

RESULT 11

T51458
 hypothetical protein K10A8.20 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
 C;Accession: T51458
 R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew
 submitted to the Protein Sequence Database, August 2000
 A;Reference number: 225394
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-461 <SAT>
 A;Cross-references: UNIPROT:Q9LF70; EMBL:AL391151
 A;Experimental source: cultivar Columbia, BAC clone K10A8
 C;Genetics:
 A;Map position: 5
 A;Introns: 147/3
 A;Note: K10A8.20

Query Match 74.5%; Score 35; DB 2; Length 461;
 Best Local Similarity 62.5%; Pred. No. 48;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LGIVAPIC 9
 Db 416 IGIVPVC 423

RESULT 12

JC7328
 amino acid transporter At1 - human
 C;Species: Homo sapiens (man)
 C;Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 09-Jul-2004
 C;Accession: JC7328
 R;Wang, H.; Huang, W.; Sugawara, M.; Devoe, L.D.; Leibach, F.H.; Prasad, P.D.; Ganapathy,
 Biochem. Biophys. Res. Commun. 273, 1175-1179, 2000
 A;Title: Cloning and functional expression of AtAT1, a subtype of amino acid transporter
 A;Reference number: JC7328
 A;Contents: Placenta

A;Accession: JC7328
 A;Molecule type: mRNA
 A;Residues: 1-487 <WAN>
 A;Cross-references: UNIPROT:Q9H2H9; GB:AF271070
 C;Comment: This transporter that is capable of mediating Na+-coupled transport of the symporter
 no acid, is a transmembrane protein.
 C;Genetics:
 A;Gene: atai

A;Map position: 12
 A;Superfamily: Arabidopsis amino acid transport protein I
 C;Keywords: amino acid transport; placenta; transmembrane protein

Query Match 74.5%; Score 35; DB 2; Length 487;
 Best Local Similarity 55.6%; Pred. No. 50;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
 |||:|:|
 Db 202 TFGIILPLC 210

RESULT 13

B81212
 fatty acid efflux system protein NMB0319 [imported] - Neisseria meningitidis (strain MCS
 C;Species: Neisseria meningitidis
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: B81212
 R;Fetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 Xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Masignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
 A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
 A;Reference number: A81000; MUID:20175755; PMID:10710307

A;Accession: B81212
 A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-508 <TEP>

A;Cross-references: UNIPROT:Q9K159; GB:AE002389; GB:AE002098; NID:g7225537; PIDN:AAF4076
 A;Experimental source: serogroup B, strain MCS8

C;Genetics:

A;Gene: NMB0319

C;Superfamily: lincomycin-resistance protein lmrB

Query Match 74.5%; Score 35; DB 2; Length 508;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
 |||:|:|
 Db 235 TLGVVALVC 243

RESULT 14

E81789
 multidrug resistance translocase NMA2168 [imported] - Neisseria meningitidis (strain Z24
 C;Species: Neisseria meningitidis
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C;Accession: E81789
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A;Reference number: A81775; MUID:2022556; PMID:10761919

A;Accession: E81789

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-516 <PAR>

A;Cross-references: UNIPROT:Q9JSR9; GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB8538
 A;Experimental source: serogroup A, strain Z2491

C;Genetics:

A;Gene: emrB; NMA2168

C;Superfamily: lincomycin-resistance protein lmrB

Query Match 74.5%; Score 35; DB 2; Length 516;
 Best Local Similarity 66.7%; Pred. No. 53;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
 |||:|:|
 Db 243 TLGVVALVC 251

RESULT 15

W7ML42

E7 protein - human papillomavirus type 42

C;Species: human papillomavirus type 42

A;Note: host Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Accession: F39451

R;Philipp, W.; Honore, N.; Sapp, M.; Cole, S.T.; Streeck, R.E.

Virology 186, 331-334, 1992

A;Title: Human papillomavirus type 42: new sequence, conserved genome organization.

A;Reference number: A39451; MUID:92087479; PMID:1309278

A;Accession: F39451

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-93 <PHI>

A;Cross-references: UNIPROT:P27231; GB:M73236

C;Superfamily: papillomavirus E7 protein

C;Keywords: DNA binding; early protein; transcription regulation

Query Match

72.3%; Score 34; DB 1; Length 93;

Best Local Similarity 66.7%; Pred. No. 18;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
 |||:|:|
 Db 81 TLDIVCPLC 89

Search completed: June 28, 2005, 19:23:46

Job time : 13.2 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-19

Perfect score: 49

Sequence: 1 GTLGIVCPI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	26	2	Q84267 human papil
2	49	100.0	93	2	Q9QDH2 human papil
3	49	100.0	93	2	Q9QDH4 human papil
4	49	100.0	93	2	Q9QDH6 human papil
5	49	100.0	93	2	Q9QDH8 human papil
6	49	100.0	94	2	Q8B5P6 human papil
7	49	100.0	98	1	VE7 HPV16
8	49	100.0	98	2	O11650 human papil
9	49	100.0	98	2	O12337 human papil
10	49	100.0	98	2	O12338 human papil
11	49	100.0	98	2	Q8QRD2 human papil
12	49	100.0	98	2	Q8QRD3 human papil
13	49	100.0	98	2	Q8QRD4 human papil
14	49	100.0	98	2	Q8V1J0 human papil
15	49	100.0	98	2	Q778H3 human papil
16	49	100.0	98	2	Q778H5 human papil
17	45	91.8	97	2	Q82006 human papil
18	43	87.8	98	1	VE7 HPV11
19	43	87.8	98	1	VE7 HPV6B
20	43	87.8	98	2	Q9QLP4 human papil
21	42	85.7	98	1	VE7 HPV6A
22	41	83.7	88	2	Q76959 manduca sex
23	41	83.7	94	2	Q8EGQ1 human papil
24	41	83.7	94	2	Q8EGQ8 human papil
25	41	83.7	99	1	VE7 HPV35
26	41	83.7	99	2	Q76WP2 human papil
27	41	83.7	101	1	VE7 HPV13
28	41	83.7	104	1	VE7 HPV32
29	41	83.7	336	2	Q9C7E9 human papil
30	41	83.7	753	2	Q6A9S6 arabidopsis
31	40	81.6	93	1	VE7 HPV42

32 40 81.6 904 2 Q7Q6E8 07q6e8 anopheles g
33 39 79.6 74 2 Q8NVJ9 Q8nvj9 staphylococ
34 39 79.6 74 2 Q99SK8 Q99sk8 staphylococ
35 39 79.6 74 2 Q7A4I1 Q7a4i1 staphylococ
36 39 79.6 74 2 Q8CRR0 Q8crr0 staphylococ
37 39 79.6 74 2 Q6G7R3 Q6g7r3 staphylococ
38 39 79.6 74 2 Q6GF28 Q6gf28 staphylococ
39 39 79.6 95 2 Q8B5W9 Q8b5w9 human papil
40 39 79.6 96 2 Q98005 Q98005 human papil
41 39 79.6 98 2 Q8JTG7 Q8jtg7 human papil
42 39 79.6 99 2 Q90724 Q90724 human papil
43 39 79.6 99 2 Q705H9 Q705h9 human papil
44 39 79.6 111 1 VE7 HPV07 P36816 human papil
45 38 77.6 113 1 VE7_RHPV1 P22161 rhesus papi

ALIGNMENTS

RESULT 1
Q84267 PRELIMINARY; PRT; 26 AA.
AC Q84267;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E7 ORF (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RX MEDLINE=8905007; PubMed=2536104;
RA Choo K.-B., Cheung W.-F., Liew L.-N., Lee H.-H., Han S.-H.;
RT "Presence of Caenated Human Papillomavirus Type 16 Episomes in a
RL Cervical Carcinoma Cell Line.";
RL J. Virol. 63:782-789(1989).
DR EMBL; M24215; AAA46944.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 1
SQ SEQUENCE 26 AA; 2799 MW; 91C16FD34D18B34 CRC64;

Query Match Similarity 100.0%; Score 49; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 13 GTLGIVCPI 21

RESULT 2
Q9QDH2 PRELIMINARY; PRT; 93 AA.
AC Q9QDH2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RX SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SRP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF197859; AAF13399.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 93

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SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 49; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 85 GTLGIVCPI 93

RESULT 3
Q9QDH4 PRELIMINARY; PRT; 93 AA.
AC Q9QDH4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON TER 93
FT SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 49; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 85 GTLGIVCPI 93

RESULT 4
Q9QDH6 PRELIMINARY; PRT; 93 AA.
AC Q9QDH6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187867; AAF13395.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON TER 93
FT SEQUENCE 93 AA; 10513 MW; 92C7054341326A1F CRC64;

Query Match 100.0%; Score 49; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 85 GTLGIVCPI 93

RESULT 5
Q9QDH8 PRELIMINARY; PRT; 93 AA.
AC Q9QDH8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON TER 93
FT SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 49; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 85 GTLGIVCPI 93

RESULT 6
Q8B5P6 PRELIMINARY; PRT; 94 AA.
AC Q8B5P6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E7 oncoprotein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469197; AAO15692.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON TER 94
FT SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;

Query Match 100.0%; Score 49; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 85 GTLGIVCPI 93

RESULT 7
VE7 HPV16 STANDARD; PRT; 98 AA.
AC VE7 HPV16
ID P03129;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE E7 protein.
DE Name=E7;
GN Human papillomavirus type 16.
OS Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

```


CC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85246220; PubMed=2990099;
 RA Seedorf K., Kramer G., Durst M., Suhai S., Rowekamp W.G.;
 RT "Human Papillomavirus type 16 DNA sequence.";
 RL Virology 145:181-185 (1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90218027; PubMed=2157796;
 RA Schneider-Maunoury S., Pehau-Arnauudet G., Breitburd F., Orth G.;
 RT "Expression of the human papillomavirus type 16 genome in SK-v cells,
 a line derived from a vulvar intraepithelial neoplasia.";
 RL J. Gen. Virol. 71:809-817 (1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP FUNCTION.
 RX MEDLINE=89223347; PubMed=2836062;
 RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;
 RT "The human papillomavirus type 16 E7 gene encodes transactivation and
 transformation functions similar to those of adenovirus E1A.";
 RL Cell 53:539-547 (1988).
 CC -1- FUNCTION: E7 protein has both transforming and trans-activating
 activities.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; K02718; AAA46940.1; -
 DR EMBL; D00735; BAA00633.1; -
 DR EMBL; U76411; AAB18962.1; -
 DR EMBL; U76412; AAB18963.1; -
 DR EMBL; U76413; AAB18964.1; -
 DR EMBL; AF003020; AAB70737.1; -
 DR EMBL; AF003023; AAB70740.1; -
 DR EMBL; AF003024; AAB70741.1; -
 DR EMBL; AF003025; AAB70742.1; -
 DR EMBL; AF003026; AAB70743.1; -
 DR PIR; A03688; W7WLHS.
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
 KW Transcription regulation.
 FT SITE 58 61 C-XX-C motif-1.
 FT SITE 91 94 C-XX-C motif-2.
 SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;
 Query Match 100.0%; Score 49; DB 1; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTLGIVCP1 9
 Db 85 GTLGIVCP1 93
 RESULT 8
 OI1650 PRELIMINARY; PRT; 98 AA.
 ID OI1650

AC OI1650;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative transforming protein E7.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
 RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
 RA Lee H.P.;
 RT "Major sequence variants in E7 gene of human papillomavirus type 16
 from cervical cancerous and noncancerous lesions of Korean women.";
 RL Gynecol. Oncol. 66:275-281 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
 RA Lee H.-P.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX Terai M., Ma Z., Burk R.D.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22182962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RT "Human papillomavirus type 16 intratypic variant infection and risk
 for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700 (2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX Terai M., Fu L., Ma Z., Burk R.D.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U76404; AAC58243.1; -
 DR EMBL; AF472509; AAO15706.1; -
 DR EMBL; AF486326; AAL96631.1; -
 DR EMBL; AF486327; AAL96632.1; -
 DR EMBL; AF486330; AAL96635.1; -
 DR EMBL; AF486331; AAL96636.1; -
 DR EMBL; AF486332; AAL96637.1; -
 DR EMBL; AF486333; AAL96638.1; -
 DR EMBL; AF486334; AAL96639.1; -
 DR EMBL; AF486336; AAL96641.1; -
 DR EMBL; AF486338; AAL96643.1; -
 DR EMBL; AF486346; AAL96651.1; -
 DR EMBL; AF486350; AAL96655.1; -
 DR EMBL; AF486351; AAL96656.1; -
 DR EMBL; AF534061; AAQ10404.1; -
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;
 Query Match 100.0%; Score 49; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTLGIVCP1 9
 Db 85 GTLGIVCP1 93
 RESULT 9
 OI2337 PRELIMINARY; PRT; 98 AA.
 ID OI2337
 AC OI2337;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

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DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Torressello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003021; AAB70738.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 85 GTLGIVCPI 93

RESULT 10
O12338
ID O12338 PRELIMINARY; PRT; 98 AA.
AC O12338;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Torressello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003021; AAB70738.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10969 MW; 9BD612534CCEA59B CRC64;

Query Match 100.0%; Score 49; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 85 GTLGIVCPI 93

RESULT 11
O8QRD2
ID O8QRD2 PRELIMINARY; PRT; 98 AA.
AC O8QRD2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Torressello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003021; AAB70738.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10969 MW; 9BD612534CCEA59B CRC64;

Query Match 100.0%; Score 49; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 85 GTLGIVCPI 93

RESULT 12
O8QRD3
ID O8QRD3 PRELIMINARY; PRT; 98 AA.
AC O8QRD3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Torressello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003021; AAB70738.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 100.0%; Score 49; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 85 GTLGIVCPI 93

RESULT 13
O8QRD4
ID O8QRD4 PRELIMINARY; PRT; 98 AA.
AC O8QRD4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Torressello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003021; AAB70738.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 85 GTLGIVCPI 93
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RN SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486329; AAL96634.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11025 MW; 86E24B234CC3281B CRC64;

Query Match 100.0%; Score 49; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTLGIVCPI 9
Db 85 GTLGIVCPI 93

RESULT 14
Q8VLJ0 PRELIMINARY; PRT; 98 AA.
AC Q8VLJ0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]_
RP SEQUENCE FROM N.A.
RA Jinhu X., Xinling W., Yun T.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461264; AAL66736.1; -.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10997 MW; 9BD610834CCEA59B CRC64;

Query Match 100.0%; Score 49; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTLGIVCPI 9
Db 85 GTLGIVCPI 93

RESULT 15
Q778H3 PRELIMINARY; PRT; 98 AA.
AC Q778H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388063; CAB45119.1; -.
DR InterPro; IPR000148; Papvi_E7.
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DR Pfam; PF00527; E7; 1.
FT NON TER 98 98
SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 49; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTLGIVCPI 9
Db 85 GTLGIVCPI 93

Search completed: June 28, 2005, 19:19:32
Job time : 57.3 secs
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 Seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-19
Perfect score: 49
Sequence: 1 GTLGIVCP1 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	98	1 W7WLS	E7 protein - human
2	43	87.8	98	1 W7WLS	E7 protein - human
3	43	87.8	98	1 W7WLS	E7 protein - human
4	41	83.7	99	1 W7WLS	E7 protein - human
5	41	83.7	101	1 W7WLS	E7 protein - human
6	41	83.7	104	2 S36510	E7 protein - human
7	41	83.7	336	2 A86406	probable RING zinc
8	40	81.6	93	1 W7WLS	E7 protein - human
9	39	79.6	74	2 B89996	conserved hypothet
10	39	79.6	111	2 S36585	E7 protein - human
11	38	77.6	113	1 W7WLS	E7 protein - rhesu
12	38	77.6	183	2 B86622	hypothetical prote
13	38	77.6	183	2 D72003	hypothetical prote
14	38	77.6	2703	1 A24420	notch protein - fr
15	37	75.5	98	1 W7WLS	E7 protein - pygmy
16	37	75.5	98	1 W7WLS	E7 protein - human
17	37	75.5	111	2 S36556	E7 protein - human
18	37	75.5	111	2 S72737	adenine phosphorib
19	37	75.5	125	2 A90694	probable gene 58 l
20	37	75.5	125	2 C64777	probable membrane
21	37	75.5	125	2 S85544	probable gene 58 p
22	37	75.5	258	2 T41212	hypothetical wt16
23	37	75.5	402	2 T41253	hypothetical wt15
24	37	75.5	418	2 T41027	hypothetical wt15
25	37	75.5	433	1 B65058	fixC protein homol
26	37	75.5	433	2 E91081	hypothetical prote
27	37	75.5	433	2 F85926	hypothetical prote
28	37	75.5	561	2 JN0797	site-specific DNA-
29	37	75.5	575	2 S57648	nicotinic acetylch

30 37 75.5 1010 2 T16616
31 37 75.5 2318 2 S45306
32 37 75.5 2321 2 S78549
33 36 73.5 55 2 T19907
34 36 73.5 97 1 W7WLS
35 36 73.5 99 2 S36574
36 36 73.5 125 2 A80562
37 36 73.5 217 2 F87372
38 36 73.5 555 2 D96598
39 36 73.5 563 2 T38766
40 36 73.5 788 2 A31153
41 36 73.5 798 2 F98134
42 36 73.5 800 2 T26683
43 36 73.5 3624 2 A08835
44 35.5 72.4 560 2 I59302
45 35 71.4 86 2 S36533

ALIGNMENTS

RESULT 1

W7WLS

E7 protein - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03688; S12367; T10428

R:Seedorf, K.; Kramer, G.; Durat, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03688

A:Molecule type: DNA

A:Residues: 1-98 <SEE>

A:Cross-references: UNIPROT:P03129; GB:K02718; NID:G333031; PIDN:AAA46940.1; PID:G333033

R:Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vousden, K.H.

EMBO J. 9, 153-160, 1990

A:Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 large

A:Reference number: S12367; MUID:90107938; PMID:2153075

A:Accession: S12367

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-98 <BAR>

R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human papillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10428

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-98 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46940.1; PID:G333033

C:Genetics:

A:Gene: E7

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:58-94/Region: zinc finger CCCC motif

Query Match 100.0%; Score 49; DB 1; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.071;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTLGIVCP1 9

Db 85 GTLGIVCP1 93

RESULT 2

W7WLS

E7 protein - human papillomavirus type 11

C:Species: human papillomavirus type 11

C:Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004

C:Accession: A03690

R:Dartmann, K.; Schwarz, E.; Gissmann, L.; zur Hausen, H.
 Virology 151, 124-130, 1986
 A:Title: The nucleotide sequence and genome organization of human papilloma virus type 1
 A:Reference number: A94338; MUID:86181601; PMID:3008427
 A:Accession: A03690
 A:Molecule type: DNA
 A:Residues: 1-98 <DAR>
 A:Cross-references: UNIPROT:P04020; GB:M14119; NID:g333026; PIDN:AAA46928.1; PID:g496194
 C:Superfamily: papillomavirus E7 protein
 C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
 F:58-94/Region: zinc finger CCCC motif

Query Match 87.8%; Score 43; DB 1; Length 98;
 Best Local Similarity 88.9%; Pred. No. 0.88;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
 Db 85 GTLNIVCPI 93

RESULT 3
 W7WL6
 E7 protein - human papillomavirus type 6b
 C:Species: human papillomavirus type 6b
 C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
 C:Accession: D20558
 R:Schwarz, E.; Durst, M.; Demankowski, C.; Luttermann, O.; Zech, R.; Wolfspurger, E.; Su
 EMBO J. 2, 2341-2348, 1983
 A:Title: DNA sequence and genome organization of Genital human papillomavirus type 6b.
 A:Reference number: A90975; MUID:84131949; PMID:6321162
 A:Accession: D20558
 A:Molecule type: DNA
 A:Residues: 1-98 <SCH>
 A:Cross-references: UNIPROT:P06464; GB:X00203; NID:g60955; PIDN:CAA25019.1; PID:g60957
 C:Superfamily: papillomavirus E7 protein
 C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
 F:58-94/Region: zinc finger CCCC motif

Query Match 87.8%; Score 43; DB 1; Length 98;
 Best Local Similarity 88.9%; Pred. No. 0.88;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
 Db 85 GTLNIVCPI 93

RESULT 4
 W7WL35
 E7 protein - human papillomavirus type 35
 C:Species: human papillomavirus type 35
 A:Note: host Homo sapiens (man)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: F40824; S36522
 R:Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
 Virology 186, 770-776, 1992
 A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillo
 A:Reference number: A40824; MUID:92124753; PMID:1310198
 A:Accession: F40824
 A>Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-99 <MAR>
 A:Cross-references: UNIPROT:P27230; GB:M74117; NID:g333050; PIDN:AAA46967.1; PID:g333052
 R:Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A:Description: Primer-directed sequencing of human papillomavirus types.
 A:Reference number: S36469
 A:Molecule type: DNA
 A:Residues: 1-99
 A:Cross-references: ENBL:X74477; NID:g396997; PIDN:CAA52562.1; PID:g396999

A:Experimental source: strain 35H
 C:Superfamily: papillomavirus E7 protein
 C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
 F:59-95/Region: zinc finger CCCC motif

Query Match 83.7%; Score 41; DB 1; Length 99;
 Best Local Similarity 87.5%; Pred. No. 2.1;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTLGIVCP 8
 Db 86 GTFGIVCP 93

RESULT 5
 W7WL13
 E7 protein - human papillomavirus type 13
 C:Species: human papillomavirus type 13
 A:Note: host Homo sapiens (man)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
 C:Accession: B42955
 R:van Ranst, M.; Fuse, A.; Piten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; Opdenakker, G.
 Virology 190, 587-596, 1992
 A:Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Compari
 A:Reference number: A42955; MUID:92391075; PMID:1325697
 A:Accession: B42955
 A:Molecule type: DNA
 A:Residues: 1-101 <VAN>
 A:Cross-references: UNIPROT:Q02271; EMBL:X62843; NID:g60295; PIDN:CAA44648.1; PID:g60297
 C:Superfamily: papillomavirus E7 protein
 C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
 F:61-97/Region: zinc finger CCCC motif

Query Match 83.7%; Score 41; DB 1; Length 101;
 Best Local Similarity 77.8%; Pred. No. 2.1;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
 Db 88 GTLNIVCPL 96

RESULT 6
 S36510
 E7 protein - human papillomavirus type 32
 C:Species: human papillomavirus type 32
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C:Accession: S36510
 R:Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A:Description: Primer-directed sequencing of human papillomavirus types.
 A:Reference number: S36469
 A:Accession: S36510
 A:Molecule type: DNA
 A:Residues: 1-104
 A:Cross-references: UNIPROT:P36827; EMBL:X74475; NID:g396981; PIDN:CAA52550.1; PID:g39698
 C:Superfamily: papillomavirus E7 protein
 C:Keywords: DNA binding; early protein; transcription regulation

Query Match 83.7%; Score 41; DB 2; Length 104;
 Best Local Similarity 87.5%; Pred. No. 2.1;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLGIVCPI 9
 Db 92 TLGIVCPL 99

RESULT 7
 A86406
 probable RING zinc finger protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: A86406
R;Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maif, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86406
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-336 <STO>
A;Cross-references: UNIPROT:Q9C7E9; GB:AE005172; NID:gil1024872; PIDN:AAG26956.1; GSPDB:C
C;Genetics:
A;Map position: 1

Query Match 83.7%; Score 41; DB 2; Length 336;
Best Local Similarity 77.8%; Pred. No. 6;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTLGIIVCP1 9
Db 284 GTNGIICPI 292

RESULT 8
W7WLR1
E7 protein - human papillomavirus type 42
C;Species: human papillomavirus type 42
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: F39451
R;Philipp, W.; Honore, N.; Sapp, M.; Cole, S.T.; Strecek, R.E.
Virology 186, 331-334, 1992
A;Title: Human papillomavirus type 42: new sequence, conserved genome organization.
A;Reference number: A39451; MUID:92087479; PMID:1309278
A;Accession: F39451
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-93 <PHI>
A;Cross-references: UNIPROT:P27231; GB:M73236
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation

Query Match 81.6%; Score 40; DB 1; Length 93;
Best Local Similarity 77.8%; Pred. No. 3;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTLGIIVCP1 9
Db 80 GTLDIVCPL 88

RESULT 9
B89996
conserved hypothetical protein SA1849 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B89996
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: B89996
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-74 <KUR>

A;Cross-references: UNIPROT:Q99SK8; GB:BA000018; PID:g13701838; PIDN:BA843131.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1849
C;Superfamily: conserved hypothetical protein HI0721

Query Match 79.6%; Score 39; DB 2; Length 74;
Best Local Similarity 75.0%; Pred. No. 3.7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIIVCP 8
Db 6 GTVGWVCP 13

RESULT 10
S36585
E7 protein - human papillomavirus type 7
C;Species: human papillomavirus type 7
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36585
R;Deliuss, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36585
A;Molecule type: DNA
A;Residues: 1-111
A;Cross-references: UNIPROT:P36816; EMBL:X74463; NID:g397060; PIDN:CAAS2477.1; PID:g39706
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation

Query Match 79.6%; Score 39; DB 2; Length 111;
Best Local Similarity 87.5%; Pred. No. 5.3;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTLGIIVCP 8
Db 98 GTLNIIVCP 105

RESULT 11
W7WLR1
E7 protein - rhesus papillomavirus (type 1)
C;Species: rhesus papillomavirus
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: B38503
R;Ostrow, R.S.; LaBresh, K.V.; Faras, A.J.
Virology 181, 424-429, 1991
A;Title: Characterization of the complete RHPV 1 genomic sequence and an integration loci
A;Reference number: A38503; MUID:91135018; PMID:1847267
A;Accession: B38503
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-113 <OST>
A;Cross-references: UNIPROT:P22161; EMBL:M37717
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation

Query Match 77.6%; Score 38; DB 1; Length 113;
Best Local Similarity 87.5%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTLGIIVCP 8
Db 100 GTLDIVCP 107

RESULT 12
B86622
hypothetical protein CPJ1053 [imported] - Chlamydomydia pneumoniae (strain J138)
C;Species: Chlamydomydia pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: B86622
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ie
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: B86622
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-183 <STO>
A;Cross-references: UNIPROT:Q9Z6K6; GB:BA000008; NID:g9879426; PIDN:BA099260.1; GSPDB:GN
A;Experimental source: strain J138
C;Genetics:
A;Gene: CP1053
C;Superfamily: Chlamydia pneumoniae hypothetical protein CP0799

Query Match 77.6%; Score 38; DB 2; Length 183;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTLGIVCP1 9
| | | | |
Db 17 GDLGVACPI 25
| | | | |

RESULT 13
D72003
Hypothetical protein CP0799 [imported] - Chlamydia pneumoniae (strains CWL029 and AR
C;Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: D72003; C81537
R;Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: D72003
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-183 <ARN>
A;Cross-references: UNIPROT:Q9Z6K6; GB:AE001685; GB:AE001363; NID:g4373738; PIDN:AAD1919
A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: C81537
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-183 <REA>
A;Cross-references: GB:AE002239; GB:AE002161; NID:g7189708; PIDN:AAF38598.1; PID:g718971
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CP1053; CP0799
C;Superfamily: Chlamydia pneumoniae hypothetical protein CP0799

Query Match 77.6%; Score 38; DB 2; Length 183;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTLGIVCP1 9
| | | | |
Db 17 GDLGVACPI 25
| | | | |

RESULT 14
A24420
notch protein - fruit fly (Drosophila melanogaster)
N;Alternate names: neurogenic repetitive locus protein
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: A24420; A24768; S09358; A05267
R;Kidd, S.; Kelley, M.R.; Young, M.W.
Mol. Cell. Biol. 6, 3094-3108, 1986

A;Reference number: A24420; MUID:87064624; PMID:3097517
A;Accession: A24420
A;Molecule type: DNA
A;Residues: 1-2703 <KID>
A;Cross-references: UNIPROT:P07207; GB:K03508; NID:g157991; PIDN:AAA28725.1; PID:g157993
R;Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.
Cell 43, 567-581, 1985
A;Reference number: A24768; MUID:86079539; PMID:3935325
A;Accession: A24768
A;Molecule type: mRNA
A;Residues: 1-48; I' 50-118, 'R', 120-230, 'I', 232-256, 'N', 258-266, 'A', 268-872, 'R', 874-958, '
A;Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044
R;Tautz, D.
Nucleic Acids Res. 17, 6463-6471, 1989
A;Title: Hypervariability of simple sequences as a general source for polymorphic DNA mar
A;Reference number: S09358; MUID:89385974; PMID:2780284
A;Accession: S09358
A;Molecule type: DNA
A;Residues: 2505-2551, 'OQQQ', 2552-2576, 'E', 2578-2604 <TAU>
R;Wharton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artavanis-Tsakonas, S.
Cell 40, 55-62, 1985
A;Title: opa: a novel family of transcribed repeats shared by the Notch locus and other c
A;Reference number: A05267; MUID:85099329; PMID:2981631
A;Accession: A05267
A;Molecule type: DNA
A;Residues: 2504-2576, 'E', 2578-2611 <WHA2>
C;Genetics:
A;Gene: notch; opa
A;Cross-references: FlyBase:FBgn0004647
A;Map position: 8.96-9.36
A;Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology
C;Keywords: differentiation; tandem repeat; transmembrane protein
F;27-43/Domain: transmembrane #status predicted <TMM1>
F;297-328/Domain: EGF homology <EGX1>
F;530-561/Domain: EGF homology <EGF1>
F;568-599/Domain: EGF homology <EGF>
F;988-1019/Domain: EGF homology <EGX2>
F;1064-1095/Domain: EGF homology <EGF3>
F;1187-1218/Domain: EGF homology <EGX3>
F;1746-1762/Domain: transmembrane #status predicted <TMM2>
F;1950-1982/Domain: ankyrin repeat homology <AN1>
F;1983-2015/Domain: ankyrin repeat homology <AN2>
F;1988-2004/Domain: transmembrane #status predicted <TMM3>
F;2017-2049/Domain: ankyrin repeat homology <AN3>
F;2050-2082/Domain: ankyrin repeat homology <AN4>
F;2083-2115/Domain: ankyrin repeat homology <AN5>
F;2538-2568/Region: glutamine-rich
F;2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>

Query Match 77.6%; Score 38; DB 1; Length 2703;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTLGIVCP1 9
| | | | |
Db 1250 GTMGIICEI 1258
| | | | |

RESULT 15
W7MLC1
E7 protein - pygmy chimpanzee papillomavirus (type 1)
C;Species: pygmy chimpanzee papillomavirus
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Jul-1999
C;Accession: B36818
R;van Ranst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; Opdenakker, G.
Virology 190, 587-596, 1992
A;Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Compari
A;Reference number: A42955; MUID:92391075; PMID:1325697
A;Accession: B36818
A;Molecule type: DNA
A;Residues: 1-98 <VAN>
A;Cross-references: EMBL:X62844; NID:g61010; PIDN:CAA44656.1; PID:g61012

C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; transforming protein;
P:58-94/Region: zinc finger CCCC motif

Query Match 75.5%; Score 37; DB 1; Length 98;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTLGIVCPI 9
|:| |||:
Db 85 GSLNIVCPL 93

Search completed: June 28, 2005, 19:23:44
Job time : 12.2 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-18
Perfect score: 42
Sequence: 1 LLMGTLGIV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	26	2 Q84267	Q84267 human papil
2	42	100.0	93	2 Q9QDH2	Q9qdh2 human papil
3	42	100.0	93	2 Q9QDH4	Q9qdh4 human papil
4	42	100.0	93	2 Q9QDH6	Q9qdh6 human papil
5	42	100.0	93	2 Q9QDH8	Q9qdh8 human papil
6	42	100.0	94	2 Q8B5P6	Q8b5p6 human papil
7	42	100.0	97	2 Q82006	Q82006 human papil
8	42	100.0	98	1 V57_HPV16	P03129 human papil
9	42	100.0	98	2 O11650	O11650 human papil
10	42	100.0	98	2 O12337	O12337 human papil
11	42	100.0	98	2 O12338	O12338 human papil
12	42	100.0	98	2 Q9QRD2	Q9qrd2 human papil
13	42	100.0	98	2 Q9QRD3	Q9qrd3 human papil
14	42	100.0	98	2 Q9QRD4	Q9qrd4 human papil
15	42	100.0	98	2 Q8V1J0	Q8v1j0 human papil
16	42	100.0	98	2 Q778H3	Q778h3 human papil
17	42	100.0	98	2 Q778H5	Q778h5 human papil
18	38	90.5	99	1 V57_HPV35	P27230 human papil
19	38	90.5	99	2 Q76WF2	Q76wf2 human papil
20	37	88.1	27	2 Q71P18	Q71p18 eurhynchio
21	37	88.1	28	2 Q6Y3V3	Q6y3v3 brachytheci
22	37	88.1	28	2 Q6Y3W8	Q6y3w8 brachytheci
23	37	88.1	28	2 Q5FHQ0	Q5fhn0 chiloecephu
24	37	88.1	28	2 Q71PB1	Q71pb1 aerobrydiu
25	37	88.1	28	2 Q85UP7	Q85up7 cryphaea he
26	37	88.1	29	2 Q71NH9	Q71nh9 sinskea fla
27	37	88.1	29	2 Q71NP6	Q71np6 weymouthia
28	37	88.1	29	2 Q71PA8	Q71pa8 brachytheci
29	37	88.1	30	2 Q71NG1	Q71ng1 brachytheci
30	37	88.1	31	1 PSBT_CHLRE	P37256 chlamydomon
31	37	88.1	31	1 PSBT_CHLVU	P56327 chlorella v

32 37 88.1 31 1 PSBT_MESVI Q8muvc mesostigma
33 37 88.1 31 2 Q6T795 Q6t795 homalia bes
34 37 88.1 31 2 Q6T798 Q6t798 pilotrichel
35 37 88.1 31 2 Q71NJ7 Q71nj7 helicodonti
36 37 88.1 31 2 Q71NN9 Q71nn9 trachypodop
37 37 88.1 31 2 Q71NY2 Q71ny2 chrysocradi
38 37 88.1 31 2 Q7YN21 Q7yn21 meteorium p
39 37 88.1 32 2 Q6T783 Q6t783 fifea aciph
40 37 88.1 32 2 Q6T789 Q6t789 rigodium to
41 37 88.1 32 2 Q6T792 Q6t792 rigodium ps
42 37 88.1 32 2 Q71KP1 Q71kp1 chlorokybus
43 37 88.1 32 2 Q7YN24 Q7yn24 meteorium b
44 37 88.1 32 2 Q85UN4 Q85un4 orthostiche
45 37 88.1 32 2 Q85UQ9 Q85uq9 orthotrichu

ALIGNMENTS

RESULT 1
Q84267 PRELIMINARY; PRT; 26 AA.
AC Q84267;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E7 ORF (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP MEDLINE=89095007; PubMed=2536104;
RA Choo K.-B., Cheung W.-P., Liew L.-N., Lee H.-H., Han S.-H.;
RT "Presence of Caenated Human Papillomavirus Type 16 Episomes in a
RT Cervical Carcinoma Cell Line.";
RL J. Virol. 63:782-789(1989).
DR EMBL; M24215; AAA46944.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 1
SQ SEQUENCE 26 AA; 2799 MW; 91C16F1D34D18B34 CRC64;
Query Match 100.0%; Score 42; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
| | | | |
Db 10 LLMGTLGIV 18

RESULT 2
Q9QDH2 PRELIMINARY; PRT; 93 AA.
AC Q9QDH2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187869; AA13399.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 93

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SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 42; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
Db 82 LLMGTLGIV 90

RESULT 3
Q9QDH4 PRELIMINARY; PRT; 93 AA.
AC Q9QDH4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 42; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
Db 82 LLMGTLGIV 90

RESULT 4
Q9QDH6 PRELIMINARY; PRT; 93 AA.
AC Q9QDH6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187867; AAF13395.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10513 MW; 92C7054341326A1F CRC64;

Query Match 100.0%; Score 42; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
Db 82 LLMGTLGIV 90

RESULT 5
Q9QDH8 PRELIMINARY; PRT; 93 AA.
AC Q9QDH8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 42; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
Db 82 LLMGTLGIV 90

RESULT 6
Q8B5P6 PRELIMINARY; PRT; 94 AA.
AC Q8B5P6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E7 oncoprotein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469197; AAO15692.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 94
SQ SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;

Query Match 100.0%; Score 42; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
Db 82 LLMGTLGIV 90

RESULT 7
Q82006 PRELIMINARY; PRT; 97 AA.
AC Q82006;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 73.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.

```

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OX NCBI_TaxID=51033;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=96213783; PubMed=8635859;
RA Voelter C., He Y., Delius H., Roy-Burman A., Greenspan J.S.,
RA Greenspan D., de Villiers E.M.;
RT "Novel HPV types present in oral papillomatous lesions from patients
RT with HIV infection.";
RL Int. J. Cancer 66:453-456(1996).
DR EMBL; X94165; CAA63883.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 97 AA; 10970 MW; 651D0345D048F022 CRC64;

Query Match 100.0%; Score 42; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMGTLGIV 9
DB 81 LLMGTLGIV 89

RESULT 8
VE7_HPVI6 STANDARD; PRT; 98 AA.
ID VE7_HPVI6
AC P03129;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85246220; PubMed=2990099;
RA Seedorf K., Kramer G., Durst M., Suhai S., Rowekamp W.G.;
RT "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90218027; PubMed=2157796;
RA Schneider-Maunoury S., Pehau-Arnudet G., Breitburd F., Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-v cells,
RT a line derived from a vulvar intraepithelial neoplasia.";
RL J. Gen. Virol. 71:809-817(1990).
RN [3]
RP SEQUENCE FROM N.A.
RA Song Y.-S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP FUNCTION.
RX MEDLINE=88223347; PubMed=2836062;
RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;
RT "The human papillomavirus type 16 E7 gene encodes transactivation and
RT transformation functions similar to those of adenovirus E1A.";
RL Cell 53:539-547(1988).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC
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-----
DR EMBL; K02718; AAA46940.1; -.
DR EMBL; D00735; BAA00633.1; -.
DR EMBL; U76411; AAB18962.1; -.
DR EMBL; U76412; AAB18963.1; -.
DR EMBL; U76413; AAB18964.1; -.
DR EMBL; AF003020; AAB70737.1; -.
DR EMBL; AF003023; AAB70740.1; -.
DR EMBL; AF003024; AAB70741.1; -.
DR EMBL; AF003025; AAB70742.1; -.
DR EMBL; AF003026; AAB70743.1; -.
DR PIR; A03688; W7MLHS.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW Transcription regulation.
FT SITE 58 61 C-XX-C motif-1.
FT SITE 91 94 C-XX-C motif-2.
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 100.0%; Score 42; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMGTLGIV 9
DB 82 LLMGTLGIV 90

RESULT 9
O11650 PRELIMINARY; PRT; 98 AA.
ID O11650
AC O11650;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transforming protein E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
RA Song Y.-S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
RA Lee H.P.;
RT "Major sequence variants in E7 gene of human papillomavirus type 16
RT from cervical cancerous and noncancerous lesions of Korean women.";
RL Gynecol. Oncol. 66:275-281(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Song Y.-S., Kee S.H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
RA Lee H.-P.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Terai M., Ma Z., Burk R.D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.B.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
RN [5]
RP SEQUENCE FROM N.A.
RA Terai M., Fu L., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U76404; AAC58243.1; -.

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DR EMBL; AF472509; AAO15706.1; -
 DR EMBL; AF486326; AAL96631.1; -
 DR EMBL; AF486327; AAL96632.1; -
 DR EMBL; AF486330; AAL96635.1; -
 DR EMBL; AF486331; AAL96636.1; -
 DR EMBL; AF486332; AAL96637.1; -
 DR EMBL; AF486333; AAL96638.1; -
 DR EMBL; AF486334; AAL96639.1; -
 DR EMBL; AF486336; AAL96641.1; -
 DR EMBL; AF486338; AAL96643.1; -
 DR EMBL; AF486346; AAL96651.1; -
 DR EMBL; AF486350; AAL96655.1; -
 DR EMBL; AF486351; AAL96656.1; -
 DR EMBL; AF534061; AAO1404.1; -
 DR InterPro: IPR000148; Papvi_E7.
 DR Pfam: PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 10995 MW; 81853B534CC3281B CRC64;

Query Match 100.0%; Score 42; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
 |||||
 Db 82 LLMGTLGIV 90

RESULT 10

O12337 PRELIMINARY; PRT; 98 AA.
 AC O12337;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Tonnesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus
 RT type 16 in penile carcinomas from Ugandan patients."
 RL J. Gen. Virol. 78:2199-2208(1997).
 DR EMBL; AF003021; AAB70738.1; -
 DR InterPro: IPR000148; Papvi_E7.
 DR Pfam: PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;

Query Match 100.0%; Score 42; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
 |||||
 Db 82 LLMGTLGIV 90

RESULT 11

O12338 PRELIMINARY; PRT; 98 AA.
 AC O12338;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;

RN SEQUENCE FROM N.A.
 RP MEDLINE=97437474; PubMed=9292007;
 RA Tonnesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus
 RT type 16 in penile carcinomas from Ugandan patients."
 RL J. Gen. Virol. 78:2199-2208(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Jinhu X., Xinxiang W., Yun T.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003022; AAB70739.1; -
 DR EMBL; AF477385; AAM03025.1; -
 DR InterPro: IPR000148; Papvi_E7.
 DR Pfam: PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 10969 MW; 9BD612534CCEA59B CRC64;

Query Match 100.0%; Score 42; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
 |||||
 Db 82 LLMGTLGIV 90

RESULT 12

O8QRD2 PRELIMINARY; PRT; 98 AA.
 AC O8QRD2;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22182962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RT "Human papillomavirus type 16 intratypic variant infection and risk
 RT for cervical neoplasia in southern China."
 RL J. Infect. Dis. 186:696-700(2002).
 DR EMBL; AF486345; AAL96650.1; -
 DR InterPro: IPR000148; Papvi_E7.
 DR Pfam: PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 100.0%; Score 42; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
 |||||
 Db 82 LLMGTLGIV 90

RESULT 13

O8QRD3 PRELIMINARY; PRT; 98 AA.
 AC O8QRD3;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486344; AAL96649.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;

Query Match 100.0%; Score 42; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMGTLGIV 9
DB 82 LLMGTLGIV 90

RESULT 14
OSQORD4 PRELIMINARY; PRT; 98 AA.
AC Q8QRD4;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486329; AAL96634.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11025 MW; 86E24B234CC3281B CRC64;

Query Match 100.0%; Score 42; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMGTLGIV 9
DB 82 LLMGTLGIV 90

RESULT 15
OSQV1J0 PRELIMINARY; PRT; 98 AA.
AC Q8VLJ0;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Jinhui X., Xinxiang W., Yun T.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461264; AAL66736.1; -.

DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10997 MW; 9BD610834CCEA59B CRC64;

Query Match 100.0%; Score 42; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMGTLGIV 9
DB 82 LLMGTLGIV 90

Search completed: June 28, 2005, 19:19:30
Job time : 56.3 secs
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 Seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-18
Perfect score: 42
Sequence: 1 LLMGTLGIV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: Piri: *
2: Piri: *
3: Piri: *
4: Piri: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	98	1 W7WLS	E7 protein - human
2	38	90.5	99	1 W7WL35	E7 protein - human
3	37	88.1	31	2 S20491	hypothetical prote
4	37	88.1	31	2 T07276	photosystem II pro
5	37	88.1	35	2 A05057	hypothetical prote
6	37	88.1	715	2 G86634	hypothetical prote
7	37	88.1	715	2 B43943	ATP-dependent memb
8	36	85.7	31	2 A53841	ycf8 protein - Eug
9	36	85.7	111	2 S3585	E7 protein - human
10	35	83.3	113	1 W7WLR1	E7 protein - rhesu
11	35	83.3	469	2 E82264	probable polyacach
12	35	83.3	617	2 T01227	glutathione-regula
13	34	81.0	98	1 W7WL31	E7 protein - human
14	34	81.0	99	2 T11886	NADH2 dehydrogenas
15	34	81.0	103	2 T01283	hypothetical prote
16	34	81.0	103	2 T08546	hypothetical prote
17	34	81.0	111	2 S36556	E7 protein - human
18	34	81.0	131	2 G70326	hypothetical prote
19	34	81.0	176	2 AF1738	hypothetical prote
20	34	81.0	667	2 G82208	GGDEF family prote
21	33	78.6	55	2 S19907	E7-C protein - hum
22	33	78.6	86	2 AE1645	holin from bacteri
23	33	78.6	97	1 W7WL33	E7 protein - human
24	33	78.6	98	1 W7WL11	E7 protein - human
25	33	78.6	98	1 W7WL6	E7 protein - human
26	33	78.6	101	1 W7WL13	E7 protein - human
27	33	78.6	112	2 A72717	hypothetical prote
28	33	78.6	205	2 B75253	Deda family protei
29	33	78.6	234	2 B72254	glycerol uptake fa

30	33	78.6	379	2 D82481	multidrug resistan
31	33	78.6	417	2 G44614	conserved hypothet
32	33	78.6	432	2 T43476	hypothetical prote
33	33	78.6	455	1 W0EBST	phosphotransferase
34	33	78.6	456	2 S62331	phosphotransferase
35	33	78.6	472	2 T34748	transmembrane tran
36	33	78.6	486	2 E87566	hypothetical prote
37	33	78.6	641	2 A71163	hypothetical prote
38	32	76.2	125	2 AE0562	probable membrane
39	32	76.2	125	2 A90694	probable gene 58 (
40	32	76.2	125	2 C64777	probable membrane
41	32	76.2	125	2 E85544	probable gene 58 p
42	32	76.2	215	2 T36153	probable permease
43	32	76.2	272	2 F75157	probable ABC trans
44	32	76.2	289	2 D90494	tatC-like protein,
45	32	76.2	309	2 AD3594	transporter, dme f

ALIGNMENTS

RESULT 1

W7WLS

E7 protein - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03688; S12367; T10428

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virolgy 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03688

A:Molecule type: DNA

A:Residues: 1-98 <SEE>

A:Cross-references: UNIPROT:P03129; GB:K02718; NID:G333031; PIDN:AAA46940.1; PID:G333033

R:Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vousden, K.H.

EMBO J. 9, 153-160, 1990

A:Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 larg

A:Reference number: S12367; MUID:90107938; PMID:2153075

A:Accession: S12367

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-98 <BAR>

R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10428

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-98 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46940.1; PID:G333033

C:Genetics:

A:Gene: E7

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:58-94/Region: zinc finger CCCC motif

Query Match 100.0%; Score 42; DB 1; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.31;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9

Db 82 LLMGTLGIV 90

RESULT 2

W7WLS

E7 protein - human papillomavirus type 35

C:Species: human papillomavirus type 35

A:Note: host Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: lcnC

C:Superfamily: hemolysin secretion protein B; ATP-binding cassette homology

Query Match 88.1%; Score 37; DB 2; Length 715;

Best Local Similarity 87.5%; Pred. No. 24; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LMGTGLGIV 9

Db 201 LMGTGLGII 208

RESULT 7

B43943

ATP-dependent membrane translocator homolog LcnC - Lactococcus lactis

C:Species: Lactococcus lactis

C:Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: B43943

R:Stoddard, G.W.; Petzel, J.P.; van Belkum, M.J.; Kok, J.; McKay, L.L.

Appl. Environ. Microbiol. 58, 1952-1961, 1992

A:Title: Molecular analyses of the lactococcal A gene cluster from Lactococcus lactis su

A:Reference number: A43943; MUID:93231840; PMID:1622271

A:Accession: B43943

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-715 <STO>

A:Cross-references: UNIPROT:Q00564

A:Experimental source: subsp. lactis biovar diacetylactis WM4

A:Note: sequence extracted from NCBI backbone (NCBI:107872, NCBI:107875)

C:Superfamily: hemolysin secretion protein B; ATP-binding cassette homology

C:Keywords: ATP; nucleotide binding; P-loop; transmembrane protein

F:498-691/Domain: ATP-binding cassette homology <ABC>

F:515-522/Region: nucleotide-binding motif A (P-loop)

Query Match 88.1%; Score 37; DB 2; Length 715;

Best Local Similarity 87.5%; Pred. No. 24;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LMGTGLGIV 9

Db 201 LMGTGLGII 208

RESULT 8

A53841

ycf8 protein - Euglena gracilis chloroplast

N:Alternate names: hypothetical protein 35

C:Species: chloroplast Euglena gracilis

C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C:Accession: S34917; S07547; A53841; S34550

R:Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.R.; Monfort, A.; Orsat, B.; Spielman

Nucleic Acids Res. 21, 3537-3544, 1993

A:Title: Complete sequence of Euglena gracilis chloroplast DNA.

A:Reference number: S34862; MUID:93347989; PMID:8346031

A:Accession: S34917

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-31 <HAL>

A:Cross-references: UNIPROT:P20176; EMBL:X70810; NID:G415327; PIDN:CAAS0132.1; PID:G4157

A:Experimental source: strain Pringheim 2

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993

R:Keller, M.; Weil, J.H.; Nair, C.K.K.

Plant Mol. Biol. 13, 723-725, 1989

A:Title: Nucleotide sequence of the psbB gene of Euglena gracilis.

A:Reference number: S07546; MUID:91370857; PMID:2518836

A:Accession: S07547

A:Molecule type: DNA

A:Residues: 1-8 <KEL>

A:Cross-references: EMBL:X15903; GB:S55899; NID:G434001

A:Note: the sequence in GenBank entry CHECAPO, release 106.0, (PID:G434003) translates a

R:Hong, L.; Hallick, R.B.

Genes Dev. 8, 1589-1599, 1994

A:Title: A group III intron is formed from domains of two individual group II introns.

A:Reference number: A53841; MUID:95047317; PMID:7958842

A:Contents: annotation; characterization of two splicing pathways for ycf8 gene

C:Genetics:

A:Gene: ycf8

A:Genome: chloroplast

A:Introns: 9/1

A:Note: the major splicing pathway for removal of the 1352-nucleotide intron is removal

s of removal of one of the group II introns followed by removal of the remaining intronic

C:Keywords: alternative splicing; chloroplast; transmembrane protein

Query Match 85.7%; Score 36; DB 2; Length 31;

Best Local Similarity 66.7%; Pred. No. 1.5;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9

Db 9 LLIGTLGVI 17

RESULT 9

S36585

E7 protein - human papillomavirus type 7

C:Species: human papillomavirus type 7

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S36585

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36585

A:Molecule type: DNA

A:Residues: 1-111

A:Cross-references: UNIPROT:P36816; EMBL:X74463; NID:G397060; PIDN:CAAS2477.1; PID:G39706

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 85.7%; Score 36; DB 2; Length 111;

Best Local Similarity 88.9%; Pred. No. 5.5;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9

Db 95 LLMGTLNIV 103

RESULT 10

W7WLR1

E7 protein - rhesus papillomavirus (type 1)

C:Species: rhesus papillomavirus

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C:Accession: S38503

R:Ostrow, R.S.; LaBresh, K.V.; Faras, A.J.

Virology 181, 424-429, 1991

A:Title: Characterization of the complete RHPV 1 genomic sequence and an integration locu

A:Reference number: A38503; MUID:91135018; PMID:1847267

A:Accession: S38503

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-113 <OST>

A:Cross-references: UNIPROT:P22161; EMBL:M37717

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 83.3%; Score 35; DB 1; Length 113;

Best Local Similarity 88.9%; Pred. No. 8.9;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9

Db 97 LLMGTLDIV 105

RESULT 11
EB2264
probable polysaccharide export protein VC0921 [imported] - Vibrio cholerae (strain N1696)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: E82264
R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Winn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoti, I.; Sellers, R.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833; PMID:10952301
A:Accession: E82264
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-469 <HEI>
A:Cross-references: UNIPROT:Q9KTI1; GB:AE004175; GB:AE003852; NID:g9655366; PIDN:AAF9408
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0921
A:Map position: 1

Query Match 83.3%; Score 35; DB 2; Length 469;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLMGTGLGIV 9
|||||
Db 240 LLMGVLGLV 248

RESULT 12
T01227
glutathione-regulated potassium-efflux system protein kefB homolog F6N23.15 - Arabidopsis
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01227
R:Geisels, C.
submitted to the EMBL Data Library, April 1998
A:Description: The sequence of A. thaliana F6N23.
A:Reference number: Z14281
A:Accession: T01227
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-617 <GEI>
A:Cross-references: UNIPROT:O6S272; EMBL:AF058919; NID:g3047100; PID:g3047127; GSPDB:GNC
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: ATSP:F6N23.15
A:Map position: 5
A:Introns: 46/2; 90/3; 110/3; 150/3; 173/3; 195/3; 225/3; 260/3; 303/3; 398/2; 455/3; 47
C:Superfamily: glutathione-regulated potassium efflux system protein kefC

Query Match 83.3%; Score 35; DB 2; Length 617;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTGLGIV 9
|||||
Db 319 LLMGTGLGL 327

RESULT 13
W7WL31
E7 protein - human papillomavirus type 31
C:Species: human papillomavirus type 31
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: B32444
R:Goldsbrough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-assoc

A:Reference number: A94398; MUID:89299478; PMID:2545036
A:Accession: B32444
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-98 <GOL>
A:Cross-references: UNIPROT:P17387; GB:J04353; NID:g333048; PIDN:AAA46951.1; PID:g459917
C:Comment: This protein may be involved in the oncogenic potential of this virus.
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:58-94/Region: zinc finger CCCC motif

Query Match 81.0%; Score 34; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLMGTGLGIV 9
|||||
Db 82 LLMGSFGIV 90

RESULT 14
T11886
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - sea anemone (Metridium senile) n
C:Species: mitochondrion Metridium senile (brown sea anemone, frilled sea anemone)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T11886
R:Beagley, C.T.; Okimoto, R.; Wolstenholme, D.R.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z17371
A:Accession: T11886
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-99 <BEA>
A:Cross-references: UNIPROT:O47492; EMBL:AF000023; NID:g2920983; PID:g2920987; PIDN:AAC04
A:Experimental source: white color morphe
C:Genetics:
A:Genome: mitochondrion
A:Note: ND4L
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c

Query Match 81.0%; Score 34; DB 2; Length 99;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLMGTGLGIV 9
|||||
Db 13 LLLGLVLGIV 21

RESULT 15
T01283
hypothetical protein At2g19350 [imported] - Arabidopsis thaliana
A:Alternate names: hypothetical protein F27F23.15
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01283; F84575
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
submitted to the EMBL Data Library, May 1998
A:Description: Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence.
A:Reference number: Z14177
A:Accession: T01283
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-103 <ROU>
A:Cross-references: UNIPROT:O64568; EMBL:AC003058; NID:g3135250; PID:g3135265
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: F84575
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-103 <STO>
A:Cross-references: GB:AE002093; NID:g3135265; PIDN:AAC16465.1; GSPDB:GN00139
C:Genetics:
A:Gene: F27F23.15; At2g19350
A:Map position: 2
A:Introns: 64/1

Query Match 81.0%; Score 34; DB 2; Length 103;
Best Local Similarity 77.8%; Pred No. 13;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
| : |||||
Db 39 LVFGTLGIV 47

Search completed: June 28, 2005, 19:23:43
Job time : 12.2 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 Seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-17

Perfect score: 44

Sequence: 1 TLEDLLMGT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	44	100.0	98	1	W7WLS	E7 protein - human
2	39	88.6	99	1	W7WLS35	E7 protein - human
3	39	88.6	113	1	W7WLR1	E7 protein - rhesu
4	36	81.8	687	2	D95553	hypothetical prote
5	35	79.5	98	1	W7WLS8	E7 protein - human
6	34	77.3	62	2	A97972	degenerate transpo
7	34	77.3	97	2	S36516	E7 protein - human
8	34	77.3	129	2	E95062	IS1381, transposas
9	34	77.3	129	2	B97977	transposase (orf1)
10	34	77.3	132	2	H95108	IS1381, transposas
11	34	77.3	132	2	B95152	IS1381, transposas
12	34	77.3	189	2	G98114	degenerate transpo
13	34	77.3	235	2	A97996	degenerate transpo
14	34	77.3	249	2	AB3063	mandelate racemase
15	34	77.3	346	2	T48049	hypothetical prote
16	34	77.3	372	2	F98223	hypothetical prote
17	33	75.0	55	2	S19907	E7-C protein - hum
18	33	75.0	97	1	W7WLS33	E7 protein - human
19	33	75.0	98	1	W7WLR11	E7 protein - human
20	33	75.0	129	2	B95225	IS1381, transposas
21	33	75.0	146	2	AH3401	hypothetical membr
22	32	72.7	145	2	S03298	Ig alpha chain C r
23	32	72.7	189	2	H90079	hypothetical prote
24	32	72.7	220	2	C22360	Ig alpha-2 chain C
25	32	72.7	274	2	AC1866	hypothetical prote
26	32	72.7	340	1	A2HU	Ig alpha-2 chain C
27	32	72.7	340	2	I56230	Ig alpha-2 chain -
28	32	72.7	340	2	B22360	Ig alpha-2 chain C
29	32	72.7	342	2	A45966	Ig alpha chain C r

30 32 72.7 344 1 AHMS
31 32 72.7 352 2 S05500
32 32 72.7 353 1 A1HU
33 32 72.7 354 2 F71623
34 32 72.7 521 2 D72518
35 32 72.7 622 1 H69480
36 32 72.7 678 2 H96552
37 32 72.7 794 2 T46073
38 32 72.7 943 1 S07776
39 32 72.7 979 2 T41006
40 32 72.7 1139 2 B54962
41 32 72.7 1141 2 A54962
42 32 72.7 1354 2 T13363
43 31 70.5 76 2 F75522
44 31 70.5 101 1 W7WLR13
45 31 70.5 151 2 E69760

Ig alpha chain C r
Ig alpha-1 chain C
Ig alpha-1 chain C
protein with DnaJ
probable glycine d
carbon-monoxide de
hypothetical prote
hypothetical prote
oxoglutarate dehyd
ubiquitin carboxyl
sterol regulatory
sterol regulatory
phosphoribosylform
hypothetical prote
E7 protein - human
conserved hypothet

ALIGNMENTS

RESULT 1

W7WLS

E7 protein - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03688; S12367; T10428

R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Viology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03688

A:Molecule type: DNA

A:Residues: 1-98 <SEE>

A:Cross-references: UNIPROT:P03129; GB:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333033

R:Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vousden, K.H.

EMBO J. 9, 153-160, 1990

A:Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 large

A:Reference number: S12367; MUID:90107938; PMID:2153075

A:Accession: S12367

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-98 <BAR>

R:Kennedy, I.M.; Haddock, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10428

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-98 <KEN>

A:Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333033

C:Genetics:

A:Gene: E7

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

P:58-94/Region: zinc finger CCCC motif

Query Match 100.0%; Score 44; DB 1; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.035;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9

Db 78 TLEDLLMGT 86

RESULT 2

W7WLS

E7 protein - human papillomavirus type 35

C:Species: human papillomavirus type 35

A:Note: host Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Accession: F40824; S36522
 R;Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
 Virology 186, 770-776, 1992
 A;Title: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 16
 A;Reference number: A40824; MUID:92124753; PMID:1310198
 A;Accession: F40824
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-99 <VAR>
 A;Cross-references: UNIPROT:P27230; GB:M74117; NID:g333050; PIDN:AAA46967.1; PID:g333052
 R;Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A;Description: Primer-directed sequencing of human papillomavirus types.
 A;Reference number: S36469
 A;Accession: S36522
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-99
 A;Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52562.1; PID:g396999
 A;Experimental source: strain 35H
 C;Superfamily: papillomavirus E7 protein
 C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
 F;59-95/Region: zinc finger CCCC motif

Query Match 88.6%; Score 39; DB 1; Length 99;
 Best Local Similarity 100.0%; Pred. No. 0.43;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEDLLMG 9
 |||||
 Db 80 LEDLLMG 87

RESULT 3
 W7WLR1
 E7 protein - rhesus papillomavirus (type 1)
 C;Species: rhesus papillomavirus
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C;Accession: B38503
 R;Ostrow, R.S.; Labresh, K.V.; Faras, A.J.
 Virology 181, 424-429, 1991
 A;Title: Characterization of the complete RHPV 1 genomic sequence and an integration loc
 A;Reference number: A38503; MUID:91135018; PMID:1847267
 A;Accession: B38503
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-113 <OST>
 A;Cross-references: UNIPROT:P22161; EMBL:M37717
 C;Superfamily: papillomavirus E7 protein
 C;Keywords: DNA binding; early protein; transcription regulation

Query Match 88.6%; Score 39; DB 1; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEDLLMG 9
 |||||
 Db 94 LEDLLMG 101

RESULT 4
 D96553
 hypothetical protein F5D21.6 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: D96553
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Creasy, K.;
 ansen, N.F.; Hughes, B.; Huijzar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: D96553
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-687 <STO>
 A;Cross-references: UNIPROT:Q9C8K2; GB:AE005173; NID:gl0092349; PIDN:AAG12758.1; GSPDB:G
 C;Genetics:
 A;Gene: F5D21.6
 A;Map position: 1
 C;Superfamily: Arabidopsis thaliana probable ATP-binding cassette protein F12L6.1; ATP-b
 Query Match 81.8%; Score 36; DB 2; Length 687;
 Best Local Similarity 77.8%; Pred. No. 19;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLEDLLMG 9
 |||||
 Db 107 TQEDILMG 115

RESULT 5
 W7WLS8
 E7 protein - human papillomavirus type 58
 C;Species: human papillomavirus type 58
 A;Note: host Homo sapiens (man)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C;Accession: F36779
 R;Kirii, Y.; Iwamoto, S.; Matsukura, T.
 Virology 185, 424-427, 1991
 A;Title: Human papillomavirus type 58 DNA sequence.
 A;Reference number: A36779; MUID:92024102; PMID:1656594
 A;Accession: F36779
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-98 <KIR>
 A;Cross-references: UNIPROT:P26557; GB:D90400; NID:g222386; PIDN:BA31846.1; PID:g3337095
 C;Superfamily: papillomavirus E7 protein
 C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
 F;59-95/Region: zinc finger CCCC motif

Query Match 79.5%; Score 35; DB 1; Length 98;
 Best Local Similarity 77.8%; Pred. No. 3.1;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLEDLLMG 9
 |||||
 Db 79 TLQQLMG 87

RESULT 6
 A97972
 degenerate transposase (orf1) [imported] - Streptococcus pneumoniae (strain R6)
 C;Species: Streptococcus pneumoniae
 C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C;Accession: A97972
 R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Es
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 e, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A;Reference number: A97872; MUID:21429245; PMID:11544234
 A;Accession: A97972
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-62 <KUR>
 A;Cross-references: UNIPROT:Q8DQ83; GB:AE007317; PIDN:AAK99605.1; PID:gl5458400; GSPDB:G
 C;Genetics:
 A;Gene: ISI381-truncation


```

Query Match      77.3%; Score 34; DB 2; Length 62;
Best Local Similarity 77.8%; Pred. No. 3;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 TLEDLLMGT 9
      :|||||
Db      50 SLEDLLMAT 58

RESULT 7
S36516
E7 protein - human papillomavirus type 34
C:Species: human papillomavirus type 34
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36516
R:Delius, H.; Hofmann, B.
A:Submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36516
A:Molecule type: DNA
A:Residues: 1-97 <DEL>
A:Cross-references: UNIPROT:P36828; EMBL:X74476; NID:G396989; PIDN:CAA52556.1; PID:G3969
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match      77.3%; Score 34; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LEDLLMG 8
      :|||||
Db      78 LEDLLMG 84

RESULT 8
E95062
IS1381, transposase Orfa [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: E95062
R:Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzap
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: E95062
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <KUR>
A:Cross-references: UNIPROT:Q9EW63; GB:AE005672; PIDN:AAK74694.1; PID:gl4972011; GSPDB:G
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0537

Query Match      77.3%; Score 34; DB 2; Length 129;
Best Local Similarity 77.8%; Pred. No. 7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 TLEDLLMGT 9
      :|||||
Db      50 SLEDLLMAT 58

RESULT 9
B97977
transposase (orf1) [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: B97977
R:Hoakins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; B

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e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: B97977
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <KUR>
A:Cross-references: UNIPROT:Q8D052; GB:AE007317; PIDN:AAK99646.1; PID:gl15458444; GSPDB:G
C:Genetics:
A:Gene: IS1381

```

```

Query Match      77.3%; Score 34; DB 2; Length 129;
Best Local Similarity 77.8%; Pred. No. 7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 TLEDLLMGT 9
      :|||||
Db      50 SLEDLLMAT 58

```

```

RESULT 10
H95108
IS1381, transposase Orfa [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: H95108
R:Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzap
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: H95108
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-132 <KUR>
A:Cross-references: UNIPROT:Q9TR85; GB:AE005672; PIDN:AAK75065.1; PID:gl4972417; GSPDB:G
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0942

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Query Match      77.3%; Score 34; DB 2; Length 132;
Best Local Similarity 77.8%; Pred. No. 7.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 TLEDLLMGT 9
      :|||||
Db      50 SLEDLLMAT 58

```

```

RESULT 11
B95152
IS1381, transposase Orfa [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: B95152
R:Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzap
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: B95152
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-132 <KUR>
A:Cross-references: UNIPROT:Q97QB2; GB:AE005672; PIDN:AAK75411.1; PID:gl4972793; GSPDB:G
A:Experimental source: strain TIGR4

```

C:Genetics:
A:Gene: SP1310

Query Match 77.3%; Score 34; DB 2; Length 132;
Best Local Similarity 77.8%; Pred. No. 7.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 50 SLEDLLMAT 58
:|||||

RESULT 12
G98114
degenerate transposase (orf1) [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: G98114
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.W.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: G98114
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-189 <KUR>
A:Cross-references: UNIPROT:Q8DN37; GB:AE007317; PIDN:AAL00748.1; PID:GI5459645; GSPDB:G
C:Genetics:
A:Gene: IS1381-truncation

Query Match 77.3%; Score 34; DB 2; Length 189;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 109 SLEDLLMAT 117
:|||||

RESULT 13
A97996
degenerate transposase (orf1) [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: A97996
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.W.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: A97996
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-235 <KUR>
A:Cross-references: UNIPROT:Q8DPV0; GB:AE007317; PIDN:AAK99797.1; PID:GI5458608; GSPDB:G
C:Genetics:
A:Gene: IS1381-truncation

Query Match 77.3%; Score 34; DB 2; Length 235;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 153 SLEDLLMAT 161
:|||||

RESULT 14

AB3063
mandelate racemase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AB3063
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AB3063
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <KUR>
A:Cross-references: UNIPROT:Q8U8H2; GB:AB008689; PIDN:AAL44920.1; PID:GI7742573; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu4120
A:Map position: linear chromosome

Query Match 77.3%; Score 34; DB 2; Length 249;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 28 TLEDLLAGS 36
:|||||

RESULT 15
T48049
hypothetical protein F26K9.30 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T48049
R:Blöcker, H.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.; Quétier, F.; Salanoubat
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24465
A:Accession: T48049
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-346 <BLO>
A:Cross-references: UNIPROT:Q9LZK5; EMBL:AL162651
A:Experimental source: cultivar Columbia; BAC clone F26K9
C:Genetics:
A:Map position: 3
A:Insertions: 24/2; 74/1; 119/2; 156/3; 195/3; 224/3; 244/3; 270/3; 294/3
A:Note: F26K9.30
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F:26-91/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 77.3%; Score 34; DB 2; Length 346;
Best Local Similarity 87.5%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLEDLLMG 8
Db 145 TLEDLYMG 152
:|||||

Search completed: June 28, 2005, 19:23:42
Job time : 18.2 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 Seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-15

Perfect score: 46

Sequence: 1 MLDLQPETT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	98	1 W7WLS	E7 protein - human
2	42	91.3	99	2 S36574	E7 protein - human
3	41	89.1	99	2 B75019	ssu ribosomal prot
4	37	80.4	98	1 W7WLS	E7 protein - human
5	37	80.4	599	2 D83764	chitinase BH0916 [
6	35	76.1	252	2 AC0391	conserved hypotet
7	35	76.1	542	2 S72474	site-specific DNA-
8	34	73.9	99	1 W7WLS	E7 protein - human
9	34	73.9	277	1 MNTH32	32K nonstructural
10	34	73.9	324	2 F81126	fructose-1,6-bisph
11	34	73.9	589	2 A34341	poly(3-hydroxybuty
12	34	73.9	698	2 S49206	G1 cyclin CLN1 - y
13	34	73.9	3670	2 T36249	CDA peptide synthe
14	33	71.7	300	2 T08292	hypothetical prote
15	33	71.7	333	2 F64108	biotin synthase (E
16	33	71.7	477	2 T46917	hypothetical prote
17	33	71.7	544	2 S2081	diphosphate-fructo
18	33	71.7	652	2 S25265	outer membrane pro
19	32	69.6	52	2 G97873	hypothetical prote
20	32	69.6	111	2 S36585	E7 protein - human
21	32	69.6	276	2 AD1210	DTDP-L-rhamnose sy
22	32	69.6	291	2 AC1302	hypothetical prote
23	32	69.6	291	2 AC1674	hypothetical prote
24	32	69.6	304	2 A49098	N-hydroxyarylamine
25	32	69.6	345	2 A12560	hypothetical prote
26	32	69.6	459	2 E86726	cell division prot
27	32	69.6	489	2 T46450	hypothetical prote
28	32	69.6	563	2 T38766	probable transcrip
29	32	69.6	567	2 T03948	probable glucose-6

glucose-6-phosphat
probable glucose-6
hypothetical prote
ribonucleoside-dip
hypothetical prote
hypothetical prote
probable exported
hypothetical prote
laminin alpha-4 ch
cell wall-associat
E7 protein - human
conserved hypotet
transcription fact
ATP-binding cassat
conserved hypotet
probable ion chann

ALIGNMENTS

RESULT 1

W7WLS

E7 protein - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03688; S12367; T10428

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virolgy 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03688

A:Molecule type: DNA

A:Residues: 1-98 <SEE>

A:Cross-references: UNIPROT:P03129; GB:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333033

R:Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Voutsden, K.H.

EMBO J. 9, 153-160, 1990

A:Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 large

A:Reference number: S12367; MUID:90107938; PMID:2153075

A:Accession: S12367

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-98 <BAR>

R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10428

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-98 <KEN>

A:Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333033

C:Genetics:

A:Gene: E7

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:58-94/Region: zinc finger CCCC motif

Query Match 100.0%; Score 46; DB 1; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.057;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MLDLQPETT 9

|||||

Db 12 MLDLQPETT 20

RESULT 2

S36574

E7 protein - human papillomavirus type 52

C:Species: human papillomavirus type 52

C:Date: 08-May-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C:Accession: S36574

R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36574
A:Molecule type: DNA
A:Residues: 1-99
A:Cross-references: UNIPROT:P36831; EMBL:X74481; NID:g397038; PIDN:CAA52586.1; PID:g397038
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 91.3%; Score 42; DB 2; Length 99;
Best Local Similarity 88.9%; Pred. No. 0.36;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
:|||||
Db 12 ILDLQPETT 20

RESULT 3
B75019
ssu ribosomal protein s24e (rps24e) PAB3419 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: B75019
R:Anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Reference number: A75001
A:Accession: B75019
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <XAW>
A:Cross-references: UNIPROT:Q9UY20; GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB5059
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: rps24E; PAB3419

Query Match 89.1%; Score 41; DB 2; Length 99;
Best Local Similarity 88.9%; Pred. No. 0.56;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
:|||||
Db 43 MLDLNPETT 51

RESULT 4
W7ML31
E7 protein - human papillomavirus type 31
C:Species: human papillomavirus type 31
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: B32444
R:Goldsbrough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated virus
A:Reference number: A94398; MUID:89299478; PMID:2545036
A:Accession: B32444
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-98 <COL>
A:Cross-references: UNIPROT:P17387; GB:J04353; NID:g333048; PIDN:AAA46951.1; PID:g459917
C:Comment: This protein may be involved in the oncogenic potential of this virus.
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:58-94/Region: zinc finger CCCC motif

Query Match 80.4%; Score 37; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 3.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
:|||||
Db 12 VLDLQPEAT 20

RESULT 5
D83764
chitinase BH0916 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: D83764
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: D83764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-599 <STO>
A:Cross-references: UNIPROT:Q9KED7; GB:AF001510; GB:BA000004; NID:gi10173440; PIDN:BAB0461
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0916

Query Match 80.4%; Score 37; DB 2; Length 599;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DLQPETT 9
:|||||
Db 509 DLQPETT 515

RESULT 6
AC0391
conserved hypothetical protein YPO3220 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AC0391
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, I
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AC0391
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-252 <KUR>
A:Cross-references: UNIPROT:Q8ZC10; GB:AL590842; PIDN:CAC92455.1; PID:gi15981156; GSPDB:G
C:Genetics:
A:Gene: YPO3220

Query Match 76.1%; Score 35; DB 2; Length 252;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPET 8
:|||||
Db 47 ILDIQPET 54

RESULT 7
S72474
site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) BsoBI - Bacillus st
C:Species: Bacillus stearothermophilus
C:Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 05-May-2000
C:Accession: S72474
R:Ruan, H.; Lunnen, K.D.; Scott, M.E.; Moran, L.S.; Slatko, B.E.; Pelletier, J.J.; Hess,
Mol. Gen. Genet. 252, 695-699, 1996
A:Title: Cloning and sequence comparison of AvaI and BsoBI restriction-modification syste
A:Reference number: S72471; MUID:97074885; PMID:8917312
A:Accession: S72474

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-542 <RNA>

A:Cross-references: EMBL:X98287

A:Experimental source: strain JN209

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Genetics:

A:Gene: bsoBIM

A:Start codon: GTG

C:Function:

A:Description: catalyzes N4 cytosine modification of 5'CYCGRG3'

C:Keywords: methyltransferase; restriction modification system; S-adenosylmethionine

Query Match 76.1%; Score 35; DB 2; Length 542;

Best Local Similarity 87.5%; Pred. No. 52;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LDLOPETT 9

Db 8 LDLOPETD 15

RESULT 8

W7ML35

E7 protein - human papillomavirus type 35

C:Species: human papillomavirus type 35

A>Note: host Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: F40824; S36522

R:Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.

Virology 186, 770-776, 1992

A>Title: The phylogenetic relationship and complete nucleotide sequence of human papillom

A:Reference number: A40824; MUID:92124753; PMID:1310198

A:Accession: F40824

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-99 <VAR>

A:Cross-references: UNIPROT:P27230; GB:M74117; NID:G333050; PIDN:AAA46967.1; PID:G333052

R:Delius, H.; Hofmann, B.

A:Submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36522

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-99

A:Cross-references: EMBL:X74477; NID:G396997; PIDN:CAA52562.1; PID:G396999

A:Experimental source: strain 35H

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:59-95/Region: zinc finger CCCC motif

Query Match 73.9%; Score 34; DB 1; Length 99;

Best Local Similarity 66.7%; Pred. No. 14;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLDLOPETT 9

Db 12 VLDLEPEAT 20

RESULT 9

MNIH32

32K nonstructural protein - bovine coronavirus (strain Québec)

C:Species: bovine coronavirus

C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004

C:Accession: A34039

R:Cox, G.J.; Parker, M.D.; Babiuk, L.A.

Nucleic Acids Res. 17, 5947, 1989

A>Title: The sequence of cDNA of bovine coronavirus 32K nonstructural gene.

A:Reference number: A34039; MUID:89345182; PMID:2762160

A:Accession: A34039

A:Molecule type: genomic RNA

A:Residues: 1-277 <COX>

A:Cross-references: UNIPROT:P18517; EMBL:X15445; NID:G58906; PIDN:CAA33485.1; PID:G58907

C:Superfamily: phosphoesterase, coronavirus type

C:Keywords: nonstructural protein

Query Match 73.9%; Score 34; DB 1; Length 277;

Best Local Similarity 85.7%; Pred. No. 40;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLOPE 7

Db 53 MLDLOPE 59

RESULT 10

F81126

fructose-1,6-bisphosphatase NM1060 [imported] - Neisseria meningitidis (strain MC58 sero

C:Species: Neisseria meningitidis

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: F81126

R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Masignani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver

A>Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: F81126

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-324 <TET>

A:Cross-references: UNIPROT:Q9JZH1; GB:AE002456; GB:AE002098; NID:G7226293; PIDN:AAF41451

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NM1060

C:Superfamily: fructose-1,6-bisphosphatase

Query Match 73.9%; Score 34; DB 2; Length 324;

Best Local Similarity 85.7%; Pred. No. 48;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLOPE 7

Db 293 MLDLOPE 299

RESULT 11

A34341

poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus

C:Species: Alcaligenes eutrophus

C>Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004

C:Accession: A34341; A39190

R:Peoples, O.P.; Sinskey, A.J.

J. Biol. Chem. 264, 15298-15303, 1989

A>Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Ident

A:Reference number: A34341; MUID:89359357; PMID:2670936

A:Accession: A34341

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-589 <PEO>

A:Cross-references: UNIPROT:P23608; GB:J05003; NID:G141958; PIDN:AAA21975.1; PID:G141959

A:Experimental source: strain H16

R:Schubert, P.; Krueger, N.; Steinbuechel, A.

J. Bacteriol. 173, 188-175, 1991

A>Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynt

emoter.

A:Reference number: A39190; MUID:91100279; PMID:1987116

A:Accession: A39190

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-219 <SCH>

A:Cross-references: GB:M64341; NID:G141964; PIDN:AAA21979.1; PID:G141965

A>Note: the authors translated the codon TAC for residue 120 as Thr

C;Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC
C;Keywords: acyltransferase

Query Match 73.9%; Score 34; DB 2; Length 589;
Best Local Similarity 66.7%; Pred. No. 89;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLDLQPEPT 9
:|||||:
252 ILDLQPESS 260

RESULT 12

G1 cyclin CLN1 - yeast (Candida albicans)

C;Species: Candida albicans

C;Date: 16-Feb-1995 #sequence_revision 14-Jul-1995 #text_change 12-Jul-2004

C;Accession: S49206; S51612; S27406; B47211; S51631

R;Sherlock, G.

Submitted to the EMBL Data Library, July 1994

A;Description: Molecular cloning and analysis of CDC28 and cyclin homologues from the hu

A;Reference number: S47030

A;Accession: S49206

A;Molecule type: DNA

A;Residues: 1-698 <SHE>

A;Cross-references: EMBL:X80032

R;Sherlock, G.; Bahman, A.M.; Mahal, A.; Shieh, J.C.; Ferreira, M.; Rosamond, J.

Mol. Gen. Genet. 245, 716-723, 1994

A;Title: Molecular cloning and analysis of CDC28 and cyclin homologues from the human fu

A;Reference number: S51611; MUID:95131949; PMID:7830719

A;Accession: S51612

A;Molecule type: DNA

A;Residues: 1-4,6-187;637-698 <SHW>

A;Cross-references: EMBL:X80032

R;Whiteaway, M.; Dignard, D.; Thomas, D.Y.

Submitted to the EMBL Data Library, September 1991

A;Description: Uncomplementary genes: Isolation of foreign regulatory genes by dominant

A;Reference number: S27406

A;Accession: S27406

A;Molecule type: DNA

A;Residues: 1-646 <WHI>

A;Cross-references: EMBL:M76587; NID:G170836; PIDN:AAA34330.1; PID:G170837

R;Whiteaway, M.; Dignard, D.; Thomas, D.Y.

Proc. Natl. Acad. Sci. U.S.A. 89, 9410-9414, 1992

A;Title: Dominant negative selection of heterologous genes: isolation of Candida albican

A;Reference number: A47211; MUID:93028473; PMID:1409649

A;Accession: B47211

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 37-188 <WH2>
A;Note: sequence extracted from NCBI backbone (NCBIP:115748)

C;Genetics:

A;Gene: CLN1

C;Superfamily: cyclin, G1 CLN1/CLN2/Puc1 type

Query Match 73.9%; Score 34; DB 2; Length 698;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLDLQPE 7
:|||||
66 MIDLQPE 72

RESULT 13

T36249

CDA peptide synthetase II SCP63.02c [imported] - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 12-Jul-2004

C;Accession: T36249

R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A

submitted to the EMBL Data Library, March 1999

A;Reference number: Z21602

A;Accession: T36249
A;Status: preliminary; translated from GB/EMBL/DBDJB

A;Molecule type: DNA

A;Residues: 1-3670 <SAU>

A;Cross-references: UNIPROT:Q9Z4X5; EMBL:AL035640; PIDN:CAB38517.1; GSPDB:GN00070; SCOED

A;Experimental source: strain A3(2)

C;Genetics:

A;Gene: cdaPS2; SCOEDB:SCE63.02c

C;Superfamily: non-ribosomal peptide synthetase; acetate-CoA ligase homology; acyl carrier

C;Keywords: carrier protein; phosphopantetheine; phosphoprotein

F;512-932/Domain: acetate-CoA ligase homology <ACL1>

F;948-1016/Domain: acyl carrier protein homology <ACP1>

F;1545-1981/Domain: acetate-CoA ligase homology <ACL2>

F;1997-2065/Domain: acyl carrier protein homology <ACP2>

F;2608-3064/Domain: acetate-CoA ligase homology <ACL3>

F;3080-3147/Domain: acyl carrier protein homology <ACP3>

F;980,2029,3112/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 73.9%; Score 34; DB 2; Length 3670;

Best Local Similarity 66.7%; Pred. No. 6.2e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLDLQPEPT 9
:|||||:
Db 3396 VLDDLPDPTT 3404

RESULT 14

T08292

hypothetical protein H0844 [imported] - Halobacterium sp. (strain NRC-1) plasmid pNRC100

C;Species: Halobacterium sp.

A;Variety: strain NRC-1

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: T08292

R;Ng, W.V.; Ciufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, B.; I

Genome Res. 8, 1131-1141, 1998

A;Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid or m

A;Reference number: Z16408; MUID:99063795; PMID:9847077

A;Accession: T08292

A;Status: translated from GB/EMBL/DBDJB

A;Molecule type: DNA

A;Residues: 1-300 <NGW>

A;Cross-references: UNIPROT:O51979; EMBL:AF016485; NID:G2822278; PID:G28222353; HALOSP:H08

A;Experimental source: strain NRC-1

C;Genetics:

A;Gene: HALOSP:H0844

A;Genome: plasmid pNRC100

C;Superfamily: Halobacterium plasmid pNRC100 hypothetical protein H0844

Query Match 71.7%; Score 33; DB 2; Length 300;

Best Local Similarity 75.0%; Pred. No. 69;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LDLPQPEPT 9
:|||||:
Db 140 LDLPQPEPT 147

RESULT 15

F64108

biotin synthase (EC 2.8.1.6) H11022 [similarity] - Haemophilus influenzae (strain Rd KW2)

C;Species: Haemophilus influenzae

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004

C;Accession: F64108

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.

Science 269, 456-512, 1995

A;Anchors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: F64108

A;Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-333 <TIGR>
A:Cross-references: UNIPROT:P44987; GB:U32783; GB:L42023; MID:g1574053; PIDN:AAC22682.1;
C:Function:
A:Description: catalyzes the conversion of dethiobiotin to biotin
A:Pathway: last step in biotin biosynthesis
C:Superfamily: biotin synthetase
C:Keywords: 2Fe-2S; biotin biosynthesis; iron-sulfur protein; metalloprotein; sulfurtransferase
P:66,70,73,201/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 71.7%; Score 33; DB 2; Length 333;
Best Local Similarity 85.7%; Pred No. 77;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LDLPQET 8
|||:
Db 321 LDLPQET 327

Search completed: June 28, 2005, 19:23:31
Job time : 12.2 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 Seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-14
Perfect score: 48
Sequence: 1 YMLDLQPET 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	98	1 W7WLS	E7 protein - human
2	44	91.7	99	2 S36574	E7 protein - human
3	40	83.3	589	2 A34341	poly(3-hydroxybuty
4	39	81.2	98	1 W7WLS3	E7 protein - human
5	38	79.2	440	2 E71625	variant-specific s
6	37	77.1	759	2 AE2429	hypothetical prote
7	36	75.0	99	1 W7WLS35	E7 protein - human
8	36	75.0	99	2 B75019	ssu ribosomal prot
9	36	75.0	498	2 S68588	nicotinic acetylch
10	36	75.0	536	2 TS1771	poly(3-hydroxybuty
11	35	72.9	252	2 AC0391	conserved hypothet
12	35	72.9	808	2 T49233	sucrose synthase-1
13	34	70.8	46	2 G82758	hypothetical prote
14	34	70.8	98	1 W7WLS8	E7 protein - human
15	34	70.8	105	2 S36504	E7 protein - human
16	34	70.8	232	2 G69029	hypothetical prote
17	34	70.8	277	1 MNH32	32K nonstructural
18	34	70.8	324	2 F81126	fructose-1,6-bisph
19	34	70.8	390	1 TVMVCB	transforming prote
20	34	70.8	580	2 C81352	lipid export ABC t
21	34	70.8	604	2 I36917	glycoprotein IIB -
22	34	70.8	698	2 S49206	G1 cyclin CLN1 - y
23	34	70.8	764	2 I36916	glycoprotein IIB -
24	34	70.8	896	2 B43817	transforming prote
25	34	70.8	906	2 A43817	transforming prote
26	34	70.8	1039	2 A34269	integrin alpha-2b
27	34	70.8	1138	2 G85077	probable polypept
28	33	68.8	61	2 A34340	alpha IIB beta 3 i
29	33	68.8	97	1 W7WLS3	E7 protein - human

30	33	68.8	333	2	F64108	biotin synthase (E
31	33	68.8	398	2	F69863	probable transamin
32	33	68.8	544	2	S52081	diphosphate-fructo
33	33	68.8	587	2	E87420	poly-beta-hydroxyb
34	33	68.8	935	1	A35367	methyleneretrahedr
35	33	68.8	935	1	A31903	methyleneretrahedr
36	33	68.8	1884	2	JC4975	plexin 2 precursor
37	32	66.7	52	2	G97873	hypothetical prote
38	32	66.7	111	2	S36585	E7 protein - human
39	32	66.7	211	2	AB3178	glutathione S-tran
40	32	66.7	270	2	T26480	hypothetical prote
41	32	66.7	276	2	AD1210	DTDP-L-rhamnose sy
42	32	66.7	291	2	AC1302	hypothetical prote
43	32	66.7	291	2	AC1674	hypothetical prote
44	32	66.7	304	2	A49098	N-hydroxyarylamine
45	32	66.7	345	2	AI2560	hypothetical prote

ALIGNMENTS

RESULT 1

W7WLS

E7 protein - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03688; S12367; T10428

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virolgy 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03688

A:Molecule type: DNA

A:Residues: 1-98 <SEE>

A:Cross-references: UNIPROT:P03129; GB:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333033

R:Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vousden, K.H.

EMBO J. 9, 153-160, 1990

A:Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 large

A:Reference number: S12367; MUID:90107938; PMID:2153075

A:Accession: S12367

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-98 <BAR>

R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10428

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-98 <KEN>

A:Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333033

C:Genetics:

A:Gene: E7

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

P:58-94/Region: zinc finger CCCC motif

Query Match 100.0%; Score 48; DB 1; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.018;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy

1 YMLDLQPET 9

|||||

Db

11 YMLDLQPET 19

RESULT 2

S36574

E7 protein - human papillomavirus type 52

C:Species: human papillomavirus type 52

C:Date: 08-May-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C:Accession: S36574

Db 727 YEFDLQPET 735

RESULT 7
W7ML35

E7 protein - human papillomavirus type 35
C:Species: human papillomavirus type 35
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: F40824; S36522

R:Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
ViROLOGY 186, 770-776, 1992

A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35
A:Reference number: F40824; MUID:92124753; PMID:1310198

A:Accession: F40824
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-99 <VAR>

A:Cross-references: UNIPROT:P27230; GB:M74117; NID:g333050; PIDN:AAA46967.1; PID:g333052

R:Deilus, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469

A:Accession: S36522
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99

A:Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52562.1; PID:g396999

C:Superfamily: Papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:59-95/Region: zinc finger CCCC motif

Query Match 75.0%; Score 36; DB 1; Length 99;
Best Local Similarity 75.0%; Pred. No. 4.8;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPE 8
|:|:|:|
Db 11 YVLDLEPE 18

RESULT 8

ssu ribosomal protein s24e (rps24e) PAB3419 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: B75019

R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A:Reference number: A75001

A:Accession: B75019
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <RAW>

A:Cross-references: UNIPROT:Q9UY20; GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB5059

A:Experimental source: strain Orsay
C:Genetics:
A:Gene: rps24E; PAB3419

Query Match 75.0%; Score 36; DB 2; Length 99;
Best Local Similarity 87.5%; Pred. No. 4.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MLDLQPE 9
|:|:|:|
Db 43 MLDLNPET 50

RESULT 9

S68588
nicotinic acetylcholine receptor alpha-1 chain precursor (clone Ce21) - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C:Accession: S68588; S57496

R:Ballivet, M.; Alliod, C.; Bertrand, S.; Bertrand, D.
J. Mol. Biol. 258, 261-269, 1996

A:Title: Nicotinic acetylcholine receptors in the nematode *Caenorhabditis elegans*.
A:Reference number: S68587; MUID:96196478; PMID:8627624

A:Accession: S68588
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-498 <BAL>

A:Cross-references: UNIPROT:P48180; EMBL:X83887; NID:g872087; PIDN:CAA58764.1; PID:g87208

C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane; F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-498/Product: nicotinic acetylcholine receptor alpha-1 chain #status predicted <NAT>

Query Match 75.0%; Score 36; DB 2; Length 498;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YMLDLQPE 9
|:|:|:|
Db 173 YKLDLQPAT 181

RESULT 10

T51771
poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) [validated] - Alcaligenes latus
C:Species: Alcaligenes latus
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: T51771

R:Choi, J.I.; Lee, S.Y.; Han, K.
Appl. Environ. Microbiol. 64, 4897-4903, 1998

A:Title: Cloning of the *Alcaligenes latus* polyhydroxyalkanoate biosynthesis genes and use of the *Alcaligenes latus* polyhydroxyalkanoate synthase gene as a reporter gene
A:Reference number: Z25450; MUID:99054931; PMID:9835580

A:Accession: T51771
A:Status: preliminary; translated from GB/EMBL/DDDBJ
A:Molecule type: DNA
A:Residues: 1-536 <CHO>

A:Cross-references: UNIPROT:Q9Z3D5; EMBL:AF078795; PIDN:AAC83658.1
C:Genetics:
A:Gene: phaC
C:Function:
A:Description: (EC 2.3.1.-); poly(3-hydroxybutyrate) synthase [validated, MUID:99054931]
C:Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC
C:Keywords: acyltransferase

Query Match 75.0%; Score 36; DB 2; Length 536;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPE 8
|:|:|:|
Db 198 YILDLPD 205

RESULT 11

AC0391
conserved hypothetical protein YPO3220 [imported] - *Yersinia pestis* (strain CO92)
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AC0391

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F.11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B. Nature 413, 523-527, 2001

A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AC0391
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-252 <KUR>

A;Cross-references: UNIPROT:Q8ZC10; GB:AL590842; PIDN:CAC92455.1; PID:gl5981156; GSPDB:G82758
C;Genetics:
A;Gene: YPO3220

Query Match 72.9%; Score 35; DB 2; Length 252;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 MLDLQPET 9
|:|:|:|:|
DB 47 ILDIQPET 54

RESULT 12
T49233
sucrose synthase-like protein - Arabidopsis thaliana
N;Alternate names: protein F7K15.40
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49233
R;Obermayer, B.; Ottenwaelder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Rudd, S.; Lem
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25019
A;Accession: T49233
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-808 <OBS>
A;Cross-references: UNIPROT:Q9LXL5; EMBL:AL353871; GSPDB:GN00061; ATSP:F7K15.40
A;Experimental source: cultivar Columbia; BAC clone F7K15
C;Genetics:
A;Gene: ATSP:F7K15.40
A;Map position: 3
A;Introns: 35/2; 128/2; 192/3; 304/3; 336/3; 394/3; 433/3; 489/2; 564/2; 752/2; 798/3
C;Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology

Query Match 72.9%; Score 35; DB 2; Length 808;
Best Local Similarity 55.6%; Pred. No. 73;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMLDLQPET 9
|:|:|:|:|
DB 216 YLMELKPKET 224

RESULT 13
G82758
hypothetical protein XF0812 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: G82758
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: G82758
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-46 <SIM>
A;Cross-references: UNIPROT:Q9PF66; GB:AE003921; GB:AE003849; NID:g9105710; PIDN:AAF8362
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H
as-Neto, E.; Docena, C.; El-Borri, H.; Facinani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuchako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0812

Query Match 70.8%; Score 34; DB 2; Length 46;
Best Local Similarity 55.6%; Pred. No. 5.3;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMLDLQPET 9
|:|:|:|:|
DB 32 YVVDLRPDT 40

RESULT 14
WTJL58
E7 protein - human papillomavirus type 58
C;Species: human papillomavirus type 58
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: F36779
R;Kirii, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
A;Title: Human papillomavirus type 58 DNA sequence.
A;Reference number: A36779; MUID:92024102; PMID:1656594
A;Accession: F36779
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-98 <KIR>
A;Cross-references: UNIPROT:P26557; GB:D90400; NID:g222386; PIDN:BAA31846.1; PID:g333709;
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:59-95/Region: zinc finger CCCC motif

Query Match 70.8%; Score 34; DB 1; Length 98;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMLDLQPE 8
|:|:|:|:|
DB 11 YILDHPE 18

RESULT 15
S36504
E7 protein - human papillomavirus type 30
C;Species: human papillomavirus type 30
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36504
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36504
A;Molecule type: DNA
A;Residues: 1-105
A;Cross-references: UNIPROT:P36826; EMBL:X74474; NID:g396973; PIDN:CAA52544.1; PID:g3969;
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation

Query Match 70.8%; Score 34; DB 2; Length 105;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMLDLQPET 9
|:|:|:|:|
DB 11 YILDLPVPT 19

Search completed: June 28, 2005, 19:23:30
Job time : 12.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-13
Perfect score: 48
Sequence: 1 TLHEYMLDL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	16	2 Q919C3	Q919C3 human papil
2	48	100.0	17	2 Q919B0	Q919B0 human papil
3	48	100.0	18	2 Q919A8	Q919A8 human papil
4	48	100.0	18	2 Q919B3	Q919B3 human papil
5	48	100.0	18	2 Q919B5	Q919B5 human papil
6	48	100.0	18	2 Q919B7	Q919B7 human papil
7	48	100.0	18	2 Q919B9	Q919B9 human papil
8	48	100.0	18	2 Q919C1	Q919C1 human papil
9	48	100.0	18	2 Q919C5	Q919C5 human papil
10	48	100.0	18	2 Q919C7	Q919C7 human papil
11	48	100.0	18	2 Q919C9	Q919C9 human papil
12	48	100.0	18	2 Q919D1	Q919D1 human papil
13	48	100.0	18	2 Q919D3	Q919D3 human papil
14	48	100.0	18	2 Q919D5	Q919D5 human papil
15	48	100.0	43	2 Q91194	Q91194 human papil
16	48	100.0	65	2 Q8B563	Q8B563 human papil
17	48	100.0	77	2 Q8B5P5	Q8B5P5 human papil
18	48	100.0	93	2 Q9QDH2	Q9QDH2 human papil
19	48	100.0	93	2 Q9QDH4	Q9QDH4 human papil
20	48	100.0	93	2 Q9QDH6	Q9QDH6 human papil
21	48	100.0	93	2 Q9QDH8	Q9QDH8 human papil
22	48	100.0	94	2 Q8B5P6	Q8B5P6 human papil
23	48	100.0	98	1 VE7 HPV16	P03129 human papil
24	48	100.0	98	2 O11650	O11650 human papil
25	48	100.0	98	2 O12337	O12337 human papil
26	48	100.0	98	2 O12338	O12338 human papil
27	48	100.0	98	2 Q8QRD2	Q8QRD2 human papil
28	48	100.0	98	2 Q8QRD3	Q8QRD3 human papil
29	48	100.0	98	2 Q8QRD4	Q8QRD4 human papil
30	48	100.0	98	2 Q8V1J0	Q8V1J0 human papil
31	48	100.0	98	2 Q778H3	Q778H3 human papil

32	48	100.0	98	2 Q778H5	Q778H5 human papil
33	37	77.1	109	2 Q52874	Q52874 coxiella bu
34	37	77.1	596	2 Q87285	Q87285 neurospora
35	37	77.1	1121	1 EX5C HAEIN	P44945 haemophilus
36	37	77.1	1270	1 Q8EF44	Q8ef44 shewanella
37	36	75.0	98	1 VE7 HPV58	P25557 human papil
38	36	75.0	98	2 Q8QHN7	Q8qhn7 human papil
39	36	75.0	98	2 Q8QHQ2	Q8qhq2 human papil
40	36	75.0	98	2 Q8QSE8	Q8qse8 human papil
41	36	75.0	98	2 Q8QSF0	Q8qsf0 human papil
42	36	75.0	98	2 Q9QC21	Q9qcz1 human papil
43	36	75.0	98	2 Q9QC22	Q9qcz2 human papil
44	36	75.0	127	2 Q74BC7	Q74bc7 geobacter s
45	36	75.0	317	2 Q81HX9	Q81hx9 bacillus ce

ALIGNMENTS

RESULT 1

Q919C3 PRELIMINARY; PRT; 16 AA.
AC Q919C3;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404698; AAL01354.1; -.
FT NON TER 16
SQ SEQUENCE 16 AA; 1901 MW; D1DB6BF776889B26 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
Db 7 TLHEYMLDL 15

RESULT 2

Q919B0 PRELIMINARY; PRT; 17 AA.
AC Q919B0;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404705; AAL01367.1; -.
FT NON TER 17
SQ SEQUENCE 17 AA; 1998 MW; 4471DB6BF776889B CRC64;

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Query Match          100.0%; Score 48; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
   |||||
Db 7 TLHEYMLDL 15

RESULT 3
Q919A8 PRELIMINARY; PRT; 18 AA.
AC Q919A8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404706; AAL01369.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match          100.0%; Score 48; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
   |||||
Db 7 TLHEYMLDL 15

RESULT 4
Q919B3 PRELIMINARY; PRT; 18 AA.
AC Q919B3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01364.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match          100.0%; Score 48; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
   |||||
Db 7 TLHEYMLDL 15

```

```

RESULT 5
Q919B5 PRELIMINARY; PRT; 18 AA.
AC Q919B5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404702; AAL01362.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match          100.0%; Score 48; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
   |||||
Db 7 TLHEYMLDL 15

RESULT 6
Q919B7 PRELIMINARY; PRT; 18 AA.
AC Q919B7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01360.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match          100.0%; Score 48; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
   |||||
Db 7 TLHEYMLDL 15

RESULT 7
Q919B9 PRELIMINARY; PRT; 18 AA.
AC Q919B9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE E7 protein (Fragment).

```

```
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040469; AAL01358.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
Db 7 TLHEYMLDL 15

RESULT 8
Q919C1 ID Q919C1 PRELIMINARY; PRT; 18 AA.
AC Q919C1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040469; AAL01358.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2136 MW; A76466EB6BF77688 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
Db 7 TLHEYMLDL 15

RESULT 9
Q919C5 ID Q919C5 PRELIMINARY; PRT; 18 AA.
AC Q919C5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040469; AAL01358.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
Db 7 TLHEYMLDL 15

RESULT 10
Q919C7 ID Q919C7 PRELIMINARY; PRT; 18 AA.
AC Q919C7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040469; AAL01350.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
Db 7 TLHEYMLDL 15

RESULT 11
Q919C9 ID Q919C9 PRELIMINARY; PRT; 18 AA.
AC Q919C9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040469; AAL01348.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
Db 7 TLHEYMLDL 15
```

```

QY      1 TLHEYMLDL 9
Db      7 TLHEYMLDL 15

RESULT 12
Q919D1 ID Q919D1 PRELIMINARY; PRT; 18 AA.
AC Q919D1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE E7 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040694; AAL01346.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TLHEYMLDL 9
Db      7 TLHEYMLDL 15

RESULT 13
Q919D3 ID Q919D3 PRELIMINARY; PRT; 18 AA.
AC Q919D3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE E7 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040693; AAL01344.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TLHEYMLDL 9
Db      7 TLHEYMLDL 15

RESULT 14
Q919D5 ID Q919D5 PRELIMINARY; PRT; 18 AA.

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```

Q919D5;
AC Q919D5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE E7 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040692; AAL01341.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TLHEYMLDL 9
Db      7 TLHEYMLDL 15

RESULT 15
Q91194 ID Q91194 PRELIMINARY; PRT; 43 AA.
AC Q91194;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Truncated E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhao M., Wu X.X., Ding X.H.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF393782; AAK84003.1; -.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 43 AA; 4903 MW; 19A57D4E52FB14D6 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TLHEYMLDL 9
Db      7 TLHEYMLDL 15

Search completed: June 28, 2005, 19:19:24
Job time : 56.3 secs

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 Seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-13
Perfect score: 48
Sequence: 1 TLHEYMLDL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: Piri:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	100.0	98	1	W7WLS	E7 protein - human
2	37	77.1	1121	2	G64103	exodeoxyribonuclease
3	36	75.0	98	1	W7WLS	E7 protein - human
4	35	72.9	97	1	W7WLS	E7 protein - human
5	35	72.9	495	2	S43294	bone morphogenetic
6	35	72.9	501	2	JC2347	growth/differentia
7	35	72.9	501	2	A35452	cartilage-derived
8	34	70.8	47	2	D40605	hmc 3'-region hypo
9	34	70.8	266	2	S77446	nitrate transport
10	34	70.8	268	2	F75100	acetyltransferase
11	34	70.8	513	2	S54590	2'-O-ribosyl phosph
12	34	70.8	617	2	B70425	hypothetical prote
13	34	70.8	764	2	A45321	protein-glutamine
14	34	70.8	805	2	S48411	SEC6 protein - yea
15	34	70.8	924	2	T50996	probable AMP deami
16	34	70.8	1032	2	H4100	acriflavine resist
17	34	70.8	1333	2	S38635	blastopodia polyprot
18	34	70.8	4151	2	G70944	probable polyketid
19	33	68.8	98	1	W7WLS	E7 protein - human
20	33	68.8	98	2	AB0739	hypothetical prote
21	33	68.8	99	1	W7WLS	E7 protein - human
22	33	68.8	161	2	J50306	Id4 protein - huma
23	33	68.8	444	2	E96905	TPR-repeat-contain
24	33	68.8	484	2	JU0091	sucrose alpha-gluc
25	33	68.8	720	2	A36526	choline O-acetyltr
26	33	68.8	728	2	A24889	choline O-acetyltr
27	33	68.8	731	2	T15664	hypothetical prote
28	33	68.8	926	2	F88632	protein F56B3.4 [i
29	33	68.8	1025	1	JC1266	beta-galactosidase

30	33	68.8	1498	2	AG1439	B. subtilis Yuka p
31	32	66.7	105	2	S36504	E7 protein - human
32	32	66.7	141	2	F72483	hypothetical prote
33	32	66.7	157	2	E97838	hypothetical prote
34	32	66.7	171	1	B60010	early E1A 20K prot
35	32	66.7	232	1	WNA0C2	early E1A 25K prot
36	32	66.7	336	2	C84297	hypothetical prote
37	32	66.7	361	2	T39008	probable mating pr
38	32	66.7	381	2	C82907	conserved hypotet
39	32	66.7	413	2	H97315	hypothetical prote
40	32	66.7	425	2	G71374	probable UDP-N-ace
41	32	66.7	614	2	T19963	hypothetical prote
42	32	66.7	695	2	F86547	hypothetical prote
43	32	66.7	695	2	F81592	hypothetical prote
44	32	66.7	695	2	E72075	hypothetical prote
45	32	66.7	716	2	T37830	probable glutamate

ALIGNMENTS

RESULT 1
W7WLS

E7 protein - human papillomavirus type 16
C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A03688; S12367; T10428

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03688

A:Molecule type: DNA

A:Residues: 1-98 <SE>

A:Cross-references: UNIPROT:P03129; GB:K02718; NID:g333033; PIDN:AAA46940.1; PID:g333033

R:Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Voutsden, K.H.

EMBO J. 9, 153-160, 1990

A:Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 large

A:Reference number: S12367; MUID:90107938; PMID:2153075

A:Accession: S12367

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-98 <BAR>

R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human papillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10428

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-98 <KEN>

A:Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333033

C:Genetics:

A:Gene: E7

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

P:58-94/Region: zinc finger CCCC motif

Query Match 100.0%; Score 48; DB 1; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.022;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9

Db 7 TLHEYMLDL 15

RESULT 2

G64103

exodeoxyribonuclease V 125K chain homolog - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004

C:Accession: G64103

A; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Frichman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995

A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Reference number: A64000; MUID:95350630; PMID:7542800

A; Accession: G64103

A; Status: nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-1121 <TTGR>

A; Cross-references: UNIPROT:P44945; GB:U32775; GB:L42023; NID:g1573951; PIDN:AAC22596.1; C:Genetics:

A; Start codon: GTG

C; Superfamily: exodeoxyribonuclease V 125K chain

Query Match 77.1%; Score 37; DB 2; Length 1121;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LHEYMVLDL 9
|||:|||||
Db 402 LHDYLLDL 409

RESULT 3

W7ML58

E7 protein - human papillomavirus type 58

C; Species: human papillomavirus type 58

A; Note: host Homo sapiens (man)

C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C; Accession: F36779

R; Kirii, Y.; Iwamoto, S.; Matsukura, T. Virology 185, 424-427, 1991

A; Title: Human papillomavirus type 58 DNA sequence.

A; Reference number: A36779; MUID:92024102; PMID:1656594

A; Accession: F36779

A; Status: translation not shown

A; Molecule type: DNA

A; Residues: 1-98 <KIR>

A; Cross-references: UNIPROT:P26557; GB:D90400; NID:g222386; PIDN:BAA31846.1; PID:g333709

C; Superfamily: papillomavirus E7 protein

C; Keywords: DNA binding; early protein; transcription regulation; zinc finger

F; 59-95/Region: zinc finger CCCC motif

Query Match 75.0%; Score 36; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 5.1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
|||:|||||
Db 7 TLREYVLDL 15

RESULT 4

W7ML33

E7 protein - human papillomavirus type 33

C; Species: human papillomavirus type 33

C; Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004

C; Accession: A03689; S23831; S23827

R; Cole, S.T.; Strebeck, R.E. J. Virol. 58, 991-995, 1986

A; Title: Genome organization and nucleotide sequence of human papillomavirus type 33, which is a member of the genus gamma 1. A; Reference number: A93020; MUID:86200464; PMID:3009902

A; Accession: A03689

A; Molecule type: DNA

A; Residues: 1-97 <COL>

A; Cross-references: UNIPROT:P06429; GB:M12732; NID:g333049; PIDN:AAA46959.1; PID:g463178

R; Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Meijer, H.J.M.; et al. submitted to the EMBL Data Library, January 1992

A; Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via transcription of a 1.1 kb DNA fragment. A; Reference number: S19906

A; Accession: S23831

A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-97 <SNI>

A; Cross-references: EMBL:X64085; NID:g60278; PIDN:CAA45434.1; PID:g60281; EMBL:X64084; NID:g60282

C; Superfamily: papillomavirus E7 protein

C; Keywords: DNA binding; early protein; transcription regulation; zinc finger

F; 58-94/Region: zinc finger CCCC motif

Query Match 72.9%; Score 35; DB 1; Length 97;
Best Local Similarity 77.8%; Pred. No. 7.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
|||:|||||
Db 7 TLREYVLDL 15

RESULT 5

S43294

bone morphogenetic protein-related protein (GDF5) - mouse

C; Species: Mus musculus (house mouse)

C; Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C; Accession: S43294

R; Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J. Nature 368, 639-643, 1994

A; Title: Limb alterations in brachypodism mice due to mutations in a new member of the TGF-beta superfamily.

A; Reference number: S43294; MUID:94195427; PMID:8145850

A; Accession: S43294

A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-495 <STO>

A; Cross-references: UNIPROT:P43027; GB:U08337; NID:g488461; PIDN:AAA18778.1; PID:g488462

C; Superfamily: inhibin

Query Match 72.9%; Score 35; DB 2; Length 495;
Best Local Similarity 77.8%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
|||:|||||
Db 162 TPHEYMLSL 170

RESULT 6

JC2347

growth/differentiation factor 5 - human

C; Species: Homo sapiens (man)

C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C; Accession: JC2347

R; Hoetten, G.; Neidhardt, H.; Jacobowsky, B.; Pohl, J. Biochem. Biophys. Res. Commun. 204, 646-652, 1994

A; Title: Cloning and expression of recombinant human growth/differentiation factor 5.

A; Reference number: JC2347; MUID:95071375; PMID:7980526

A; Accession: JC2347

A; Molecule type: DNA

A; Residues: 1-501 <HOB>

A; Cross-references: UNIPROT:P43026; GB:X80915; NID:g671524; PIDN:CAA56874.1; PID:g671525

C; Genetics:

A; Gene: GDB:BMP9

A; Cross-references: GDB:433948

A; Introns: 211/1

C; Superfamily: inhibin

C; Keywords: Glycoprotein

F; 189/Binding site: carbohydrate (Asn) (covalent) #status predicted

F; 381-382/Cleavage site: Arg-Ala (unidentified proteinase) #status predicted

Query Match 72.9%; Score 35; DB 2; Length 501;
Best Local Similarity 77.8%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
|||:|||||
Db 168 TPHEYMLSL 176

RESULT 7

A55452
Cartilage-derived morphogenetic protein 1 precursor - human
C:Species: Homo sapiens (man)
C>Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C:Accession: A55452
R:Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak
J. Biol. Chem. 269, 28227-28234, 1994
A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming growth
A:Reference number: A55452; MUID:95050604; PMID:7961761
A:Accession: A55452
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-501 <CHA>
A:Cross-references: UNIPROT:P43026; GB:U13660; NID:G600731; PID:G600732
C:Genetics:
A:Gene: GDB:CDMP1
A:Cross-References: GDB:438940
C:Superfamily: inhibin

Query Match 72.9%; Score 35; DB 2; Length 501;

Best Local Similarity 77.8%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9

Db 168 TPHEYMLSL 176

RESULT 8

D40605
hmc 3'-region hypothetical peptide 4 - Desulfovibrio vulgaris
C:Species: Desulfovibrio vulgaris
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: D40605
R:Rossi, M.; Pollock, W.B.R.; Reij, M.W.; Keon, R.G.; Fu, R.; Voordouw, G.
J. Bacteriol. 175, 4699-4711, 1993
A:Title: The hmc operon of Desulfovibrio vulgaris subsp. vulgaris Hildenborough encodes
A:Reference number: A40605; MUID:93328674; PMID:8335628
A:Accession: D40605
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-47 <ROS>
A:Cross-references: UNIPROT:P33391; GB:L16784; NID:G290377; PIDN:AAA1997.1; PID:G290380
A:Experimental source: subsp. vulgaris
C:Keywords: transmembrane protein

Query Match 70.8%; Score 34; DB 2; Length 47;

Best Local Similarity 85.7%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLHEYML 7

Db 7 TLHEFML 13

RESULT 9

S77446
nitrate transport protein D-2 - Synecchocystis sp. (strain PCC 6803)
N:Alternate names: protein sll1082
C:Species: Synecchocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 16-Aug-2004
C:Accession: S77446
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocystis
S.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S77446

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-266 <KAN>

A:Cross-references: UNIPROT:P73265; EMBL:D90905; GB:AB001339; NID:G1652360; PIDN:BAAL729;

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Genetics:

A:Gene: nrtb-2

C:Superfamily: ATP-binding cassette homology

C:Keywords: ATP; nucleotide binding; P-loop

F:22-210/Domain: ATP-binding cassette homology <ABC>

F:39-46/Region: nucleotide-binding motif A (P-loop)

Query Match 70.8%; Score 34; DB 2; Length 266;

Best Local Similarity 50.0%; Pred. No. 38;

Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LHEYMLDL 9

Db 172 MHEYLIDI 179

RESULT 10

F75100

acetyltransferase PAB1583 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi

C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C:Accession: F75100

R:anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc

A:Reference number: A75001

A:Accession: F75100

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-268 <KAW>

A:Cross-references: UNIPROT:Q9UZF2; GB:AJ248286; GB:AL096836; NID:G5458366; PIDN:CABS010;

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: PAB1583

Query Match 70.8%; Score 34; DB 2; Length 268;

Best Local Similarity 75.0%; Pred. No. 39;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LHEYMLDL 9

Db 83 LHNFMIDL 90

RESULT 11

S54590

2'-O-ribosyl phosphate transferase RIT1 - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C>Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C:Accession: S54590; A55096; S19047; S48306

R:Pearson, D.; Bowman, S.

submitted to the EMBL Data Library, May 1995

A:Reference number: S54582

A:Accession: S54590

A:Molecule type: DNA

A:Residues: 1-513 <PEA>

A:Cross-references: UNIPROT:P23796; EMBL:Z49704; NID:G825540; PIDN:CAA89781.1; PID:G82554;

A:Experimental source: strain AB972

R:Aastrom, S.U.; Bystrom, A.S.

Cell 79, 535-546, 1994

A:Title: RIT1, a tRNA backbone-modifying enzyme that mediates initiator and elongator tri

A:Reference number: A55096; MUID:95042750; PMID:7954819

A:Accession: A55096

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 20-513 <AST>

A:Cross-references: EMBL:X80795; NID:G556674; PIDN:CAA566770.1; PID:G556675

R;Finnegan, P.M.; Payne, M.J.; Keramidaris, E.; Lukins, H.B.
Curr. Genet. 20, 53-61, 1991
A:Title: Characterization of a yeast nuclear gene, AEP2, required for accumulation of mi
A:Reference number: S19045; MUID:92035073; PMID:1718609
A:Accession: S19047
A:Molecule type: DNA
A:Residues: 418-513 <FIN>
A:Cross-references: EMBL:M59860
C:Genetics:
A:Gene: SGD:RIT1
A:Cross-references: SGD:S0004896; MIPS:YMR283C
A:Map position: 13R
C:Function:
A:Description: modifies the initiator tRNA and thus mediates discrimination between ini
C:Superfamily: Saccharomyces cerevisiae 2'-O-ribosyl phosphate transferase RIT1

Query Match 70.8%; Score 34; DB 2; Length 513;
Best Local Similarity 62.5%; Pred. No. 80;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHEYMLDL 9
| | | | |
DB 311 LHDYIMDL 318

RESULT 12
B70425
hypothetical protein aq_1439 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: B70425
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: B70425
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-617 <AQF>
A:Cross-references: UNIPROT:O67428; GB:AE000740; NID:g2983826; PIDN:AAC07393.1; PID:g298
A:Experimental source: strain VF5
C:Genetics:
A:Gene: aq_1439
C:Superfamily: Aquifex aeolicus hypothetical protein aq_1439

Query Match 70.8%; Score 34; DB 2; Length 617;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
| | | | |
DB 394 TYHEYELDI 402

RESULT 13
A45321
protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) - horseshoe crab (Tachyples b
N:Alternate names: TGase; transglutaminase
C:Species: Tachyples tridentatus
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 22-Oct-1999
C:Accession: A45321
R;Tokunaga, F.; Muta, T.; Iwanaga, S.; Ichinose, A.; Davie, E.W.; Kuma, K.; Miyata, T.
J. Biol. Chem. 268, 262-268, 1993
A:Title: Limulus hemocyte transglutaminase. cDNA cloning, amino acid sequence, and tissu
A:Reference number: A45321; MUID:93107012; PMID:8093243
A:Accession: A45321
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-764 <TOK>
A:Experimental source: hemocytes
A:Note: sequence extracted from NCBI backbone (NCBIP:121409)
C:Superfamily: protein-glutamine gamma-glutamyltransferase

C:Keywords: aminoacyltransferase
F;343/Active site: Cys #status predicted

Query Match 70.8%; Score 34; DB 2; Length 764;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HEYMLDL 9
| | | | |
DB 29 HSYMLDL 35

RESULT 14
S48411
SEC6 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YIL068c
C:Species: Saccharomyces cerevisiae
C:Date: 31-Mar-1992 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C:Accession: S48411; S25362; S20130
R;Smith, V.
submitted to the EMBL Data Library, September 1994
A:Reference number: S48407
A:Accession: S48411
A:Molecule type: DNA
A:Residues: 1-805 <SMI>
A:Cross-references: UNIPROT:P32844; GB:Z47047; EMBL:Z38060; NID:g603997; PID:g763278; MII
R;Potenza, M.; Bowser, R.; Mueller, H.; Novick, P.
Yeast 8, 549-558, 1992
A:Title: SEC6 encodes an 85 kDa soluble protein required for exocytosis in yeast.
A:Reference number: S25362; MUID:92397592; PMID:1523887
A:Accession: S25362
A:Molecule type: DNA
A:Residues: 'MKLINWMIIDLIQIVMIV' 92-500, 'E', 502-626, 'HE', 629-805 <POT>
A:Cross-references: EMBL:X64738; NID:g4449; PIDN:CAA46004.1; PID:g4450
C:Genetics:
A:Gene: SGD:SEC6
A:Cross-references: SGD:S0001330; MIPS:YIL068c
A:Map position: 9L

Query Match 70.8%; Score 34; DB 2; Length 805;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
| | | | |
DB 632 TLDBYLLDI 640

RESULT 15
T50996
probable AMP deaminase [imported] - Neurospora crassa
N:Alternate names: protein B7F18.150
C:Species: Neurospora crassa
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C:Accession: T50996
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, July 2000
A:Reference number: Z25286
A:Accession: T50996
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-924 <SCH>
A:Cross-references: UNIPROT:Q9P3N4; EMBL:AL389891; GSPDB:GN00116; NCSP:B7F18.150
A:Experimental source: SAC clone B7F18; strain OR74A
C:Genetics:
A:Gene: NCSP:B7F18.150
A:Map position: 6
A:Introns: 795/2
C:Superfamily: AMP deaminase

Query Match 70.8%; Score 34; DB 2; Length 924;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TLREYMLDL 9
Db 294 TLREYLDL 302

Search completed: June 28, 2005, 19:23:29
Job time : 13.2 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-12
Perfect score: 52
Sequence: 1 PLCDLLIRC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	81	2	Q80886 human papil
2	52	100.0	84	2	Q80882 human papil
3	52	100.0	90	2	Q80883 human papil
4	52	100.0	90	2	Q80884 human papil
5	52	100.0	90	2	Q80885 human papil
6	52	100.0	91	2	Q80887 human papil
7	52	100.0	99	2	Q919B2 human papil
8	52	100.0	103	2	Q919D6 human papil
9	52	100.0	130	2	Q919B4 human papil
10	52	100.0	130	2	Q919B8 human papil
11	52	100.0	130	2	Q919C0 human papil
12	52	100.0	130	2	Q919C2 human papil
13	52	100.0	130	2	Q919C8 human papil
14	52	100.0	130	2	Q919D0 human papil
15	52	100.0	138	2	Q919D2 human papil
16	52	100.0	143	2	Q919B6 human papil
17	52	100.0	143	2	Q919C4 human papil
18	52	100.0	151	2	O12335 human papil
19	52	100.0	151	2	O12336 human papil
20	52	100.0	151	2	Q76TS0 human papil
21	52	100.0	151	2	Q778I6 human papil
22	52	100.0	151	2	Q778I6 human papil
23	52	100.0	151	2	Q77JZ7 human papil
24	52	100.0	151	2	Q77ZJ5 human papil
25	52	100.0	151	2	Q80963 human papil
26	52	100.0	151	2	Q80966 human papil
27	52	100.0	151	2	Q89640 human papil
28	52	100.0	151	2	Q89648 human papil
29	52	100.0	151	2	Q89708 human papil
30	52	100.0	151	2	Q89755 human papil
31	52	100.0	151	2	Q89852 human papil

32	52	100.0	151	2	Q89887 human papil
33	52	100.0	151	2	Q8B564 human papil
34	52	100.0	151	2	Q8BB19 human papil
35	52	100.0	151	2	Q8BB20 human papil
36	52	100.0	151	2	Q8BB21 human papil
37	52	100.0	151	2	Q8BB21 human papil
38	52	100.0	151	2	Q9W931 human papil
39	52	100.0	151	2	Q9WMP2 human papil
40	52	100.0	151	2	Q9WMP3 human papil
41	52	100.0	151	2	Q9WMP5 human papil
42	52	100.0	158	1	VE6 HPV16
43	52	100.0	158	2	Q8JMU8 human papil
44	52	100.0	158	2	Q8QHN0 human papil
45	52	100.0	158	2	Q8QHP5 human papil

ALIGNMENTS

RESULT 1
Q80886 PRELIMINARY; PRT; 81 AA.
AC Q80886;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14515; AAB60569.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
FT NON TER 81
SQ SEQUENCE 81 AA; 9784 MW; DD5PEDBC9F845B97 CRC64;

Query Match Similarity 100.0%; Score 52; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. NO. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
| | | | |
Db 54 PLCDLLIRC 62

RESULT 2
Q80882 PRELIMINARY; PRT; 84 AA.
AC Q80882;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14511; AAB60565.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

```

DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 84
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;
Query Match 100.0%; Score 52; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 51 PLCDLLIRC 59

RESULT 3
Q80883 PRELIMINARY; PRT; 90 AA.
AC Q80883;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14512; AAB60566.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10904 MW; 5D3ADF843AD6060B CRC64;
Query Match 100.0%; Score 52; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 54 PLCDLLIRC 62

RESULT 4
Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.

```

```

FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFACCCC01 CRC64;
Query Match 100.0%; Score 52; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 54 PLCDLLIRC 62

RESULT 5
Q80885 PRELIMINARY; PRT; 90 AA.
AC Q80885;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14514; AAB60568.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10964 MW; BC2531643ACBA76C CRC64;
Query Match 100.0%; Score 52; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 54 PLCDLLIRC 62

RESULT 6
Q80887 PRELIMINARY; PRT; 91 AA.
AC Q80887;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14516; AAB60570.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 11136 MW; 22PDF3EA185ACBA7 CRC64;

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Query Match          100.0%; Score 52; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCOLLIRC 9
Db 54 PLCOLLIRC 62

RESULT 7
ID Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040704; AAL01342.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT NON TER 99
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;

Query Match          100.0%; Score 52; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCOLLIRC 9
Db 71 PLCOLLIRC 79

RESULT 8
ID Q919D6 PRELIMINARY; PRT; 103 AA.
AC Q919D6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040692; AAL01342.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT NON TER 103
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;

Query Match          100.0%; Score 52; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCOLLIRC 9
Db 74 PLCOLLIRC 82

RESULT 9
ID Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT NON TER 130
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;

Query Match          100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCOLLIRC 9
Db 74 PLCOLLIRC 82

RESULT 10
ID Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040701; AAL01359.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT NON TER 130
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match          100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 PLCDLLIRC 9
Db 74 PLCDLLIRC 82

RESULT 11
Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404700; AAL01357.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
SQ

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 74 PLCDLLIRC 82

RESULT 12
Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404699; AAL01355.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
SQ

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 74 PLCDLLIRC 82

RESULT 13
Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404696; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;
SQ

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 74 PLCDLLIRC 82

RESULT 14
Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404695; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;
SQ

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 74 PLCDLLIRC 82

RESULT 15
```

```
Qy 1 PLCDLLIRC 9
Db 74 PLCDLLIRC 82

RESULT 11
Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404700; AAL01357.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
SQ

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 74 PLCDLLIRC 82

RESULT 12
Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404699; AAL01355.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
SQ

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 74 PLCDLLIRC 82

RESULT 13
Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404696; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;
SQ

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 74 PLCDLLIRC 82

RESULT 14
Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404695; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;
SQ

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 74 PLCDLLIRC 82

RESULT 15
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Q919D2
 ID Q919D2 PRELIMINARY; PRT; 138 AA.
 AC Q919D2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404694; AAL01345.1; --
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;
 Query Match 100.0%; Score 52; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 0.052;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PLCDLLIRC 9
 Db 82 PLCDLLIRC 90

Search completed: June 28, 2005, 19:19:23
 Job time : 55.3 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-3
Perfect score: 47
Sequence: 1 QLCTELQTT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	158	1 W6WLS	protein E6 - human
2	39	83.0	455	2 AE0181	hypothetical prote
3	36	76.6	470	1 S30830	fumarate reductase
4	35	74.5	158	2 E89818	hypothetical prote
5	35	74.5	187	2 A90126	hypothetical prote
6	35	74.5	239	1 LNM5MA	mannose-binding le
7	34	72.3	182	2 AI2373	hypothetical prote
8	34	72.3	342	2 AB3116	transcription regu
9	34	72.3	356	2 C98171	hypothetical prote
10	34	72.3	511	2 T23189	hypothetical prote
11	34	72.3	527	2 E89240	protein K01D12.6 [
12	33	70.2	57	2 I56705	E6 protein - human
13	33	70.2	156	2 S36966	probable H-transp
14	33	70.2	158	1 W6WLS	E6 protein - human
15	33	70.2	158	2 S36561	E6 protein - human
16	33	70.2	221	2 AB2190	hypothetical prote
17	33	70.2	243	2 D84629	hypothetical prote
18	33	70.2	390	2 E70793	hypothetical prote
19	33	70.2	484	2 E59095	hypothetical prote
20	32	68.1	189	2 AF0372	glycine cleavage s
21	32	68.1	530	2 A84847	probable Ca2+ depe
22	32	68.1	656	2 T31884	hypothetical prote
23	32	68.1	751	2 T40462	ser-lys rich hypot
24	32	68.1	824	2 T23923	hypothetical prote
25	32	68.1	930	2 T42241	myotubularin prote
26	32	68.1	938	2 T25215	hypothetical prote
27	32	68.1	980	2 T39630	valine-tRNA ligase
28	32	68.1	2042	2 T18399	variant-specific s
29	32	68.1	2344	1 RRWRH	genome polyprotein

30 31 66.0 33 2 PQ0417 nucleoprotein - in
31 31 66.0 32 2 TI0551 hypothetical prote
32 31 66.0 153 1 A25946 interleukin-4 prec
33 31 66.0 158 1 W6WLS39 E6 protein - human
34 31 66.0 195 2 S50522 hypothetical prote
35 31 66.0 244 1 LKRTMC mannose-binding le
36 31 66.0 361 2 E75610 conserved hypotet
37 31 66.0 446 2 A40896 Ca2+/calmodulin-de
38 31 66.0 461 2 AC3592 response regulator
39 31 66.0 492 1 T03271 calcium-dependent
40 31 66.0 498 1 A60028 nucleoprotein - in
41 31 66.0 498 1 VHV334 nucleoprotein - in
42 31 66.0 498 1 VHV8H nucleoprotein - in
43 31 66.0 498 1 VHV33 nucleoprotein - in
44 31 66.0 498 1 VHVAK nucleoprotein - in
45 31 66.0 498 1 VHVCI nucleoprotein - in

ALIGNMENTS

RESULT 1
W6WLS
protein E6 - human papillomavirus type 16
C:Species: human papillomavirus type 16
C>Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A03682; T10427
R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A:Title: Human papillomavirus type 16 DNA sequence.
A:Reference number: A22355; MUID:85246220; PMID:2990099
A:Accession: A03682
A:Molecule type: DNA
A:Residues: 1-158 <SEE>
A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
J.Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A:Reference number: Z17014; MUID:91162763; PMID:1848319
A:Accession: T10427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-158 <KEN>
A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
C:Genetics:
A:Gene: E6
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:37-73/Region: zinc finger CCCC motif
P:110-146/Region: zinc finger CCCC motif

Query Match 100.0% Score 47; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELQTT 9
Db 21 QLCTELQTT 29

RESULT 2
AE0181
hypothetical protein YP01489 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AE0181
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; i
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, I
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AE0181

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-455 <KUR>
A;Cross-references: UNIPROT:Q8ZG30; GB:AL590842; PIDN:CAC90312.1; PID:gi51979531; GSPDB:G
C;Genetics:
A;Gene: YPO1489

Query Match 83.0%; Score 39; DB 2; Length 455;
Best Local Similarity 87.5%; Pred. No. 5.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELQOT 8
|||:||||
Db 141 QLCTQLQOT 148

RESULT 3
S30830
fumarate reductase (EC 1.3.99.1) - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: protein YEL047c
C;Species: *Saccharomyces cerevisiae*
C;Date: 28-May-1993 #sequence_revision 26-Jul-1996 #text_change 16-Aug-2004
C;Accession: S30830; S50497; JCS123; PC4235
R;Mulligan, J.T.; Dietrich, P.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, S.
submitted to the EMBL Data Library, February 1993
A;Reference number: S30812
A;Cross-references: UNIPROT:P32614; GB:U18779; EMBL:L10830; NID:G603625; PIDN:AAB64995.1
R;Dietrich, P.S.
submitted to the EMBL Data Library, December 1994
A;Description: The sequence of *S. cerevisiae* cosmids 8199, 8334, and 9871.
A;Reference number: S50429
A;Accession: S50497
A;Molecule type: DNA
A;Residues: 1-470 <MUL>
A;Cross-references: UNIPROT:P32614; GB:U18779; EMBL:L10830; NID:G603625; PIDN:AAB64995.1
R;Dietrich, P.S.
submitted to the EMBL Data Library, December 1994
A;Description: The sequence of *S. cerevisiae* cosmids 8199, 8334, and 9871.
A;Reference number: S50429
A;Accession: S50497
A;Molecule type: DNA
A;Residues: 1-470 <DIB>
A;Cross-references: EMBL:U18779; NID:G603625; PIDN:AAB64995.1; PID:G603632; GSPDB:GN0000
R;Enomoto, K.; Ohki, R.; Muratsubaki, H.
DNA Res. 3, 263-267, 1996
A;Title: Cloning and sequencing of the gene encoding the soluble fumarate reductase from
A;Reference number: JCS123; MUID:97101648; PMID:8946166
A;Accession: JCS123
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-32, 'RQ', 35-284, 'K', 286-470 <ENO>
A;Accession: PC4235
A;Status: preliminary
A;Molecule type: protein
A;Residues: 89-106;245-253;322-327;409-423 <EN2>
C;Genetics:
A;Gene: FRDS; MIPS:YEL047c
A;Cross-references: SGD:S00000773
A;Map position: 5L
C;Superfamily: Fumarate reductase flavoprotein subunit without the flavoprotein C-termin
C;Keywords: FAD; flavoprotein; oxidoreductase
F;5-292/Domain: fumarate reductase flavoprotein homology <PRF>
F;5-34/Region: beta-alpha-beta FAD nucleotide-binding fold
F;358-457/Domain: 3-oxosteroid 1-dehydrogenase homology <OXD>
F;401-448/Region: AMP-binding #status predicted
F;249,272/Active site: His, Arg #status predicted

Query Match 76.6%; Score 36; DB 1; Length 470;
Best Local Similarity 87.5%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLCTELQOT 8
|||:||||
Db 357 QLCEELQOT 364

RESULT 4
E99818

hypothetical protein folk [imported] - *Staphylococcus aureus* (strain N315)
C;Species: *Staphylococcus aureus*
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E99818
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E99818
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-158 <KUR>
A;Cross-references: UNIPROT:Q99W87; GB:BA000018; PID:gl3700406; PIDN:BA841704.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: folK
C;Superfamily: 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase; 2-am
Query Match 74.5%; Score 35; DB 2; Length 158;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LCTELQOTT 9
|||:||||
Db 57 LCVEIQOTT 64

RESULT 5
A90126
hypothetical protein orf187 [imported] - *Guillardia theta* nucleomorph
C;Species: nucleomorph *Guillardia theta*
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A90126
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reit
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
A;Accession: A90126
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-187 <DOU>
A;Cross-references: UNIPROT:Q98S81; GB:AF083031; NID:gl3794324; PIDN:AAK39701.1; GSPDB:G
C;Genetics:
A;Gene: orf187
A;Map position: 3
A;Genome: nucleomorph
C;Keywords: nucleomorph

Query Match 74.5%; Score 35; DB 2; Length 187;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELQOT 8
|||:||||
Db 3 RLCTELET 10

RESULT 6
LNMSWA
mannose-binding lectin A precursor - mouse
N;Alternate names: Ra-reactive factor P28b; serum mannan-binding protein
C;Species: *Mus musculus* (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 02-Jun-1994 #text_change 09-Jul-2004
C;Accession: A46466; B42574; I48650
R;Sastry, K.; Zahedi, K.; Lelias, J.M.; Whitehead, A.S.; Ezekowitz, R.A.
J. Immunol. 147, 692-697, 1991
A;Title: Molecular characterization of the mouse mannose-binding proteins. The mannose-b
A;Reference number: A46466; MUID:91302823; PMID:1712818
A;Accession: A46466
A;Molecule type: mRNA

A;Residues: 1-239 <SAS1>
A;Cross-references: UNIPROT:P39039; GB:S42292; NID:g220587; PIDN:BA02006.1; PID:g223301
A;Experimental source: inbred CBA/J, acute phase liver library, PTZ 19 vector
A;Note: sequence extracted from NCBI backbone (NCBIN:42292, NCBIP:42293)
R;Kuge, S.; Ihara, S.; Watanabe, E.; Watanabe, M.; Takishima, K.; Suga, T.; Mamiya, G.;
Biochemistry 31, 6943-6950, 1992
A;Title: cDNAs and deduced amino acid sequences of subunits in the binding component of
A;Reference number: A42574; MUID:92345256; PMID:1637828
A;Accession: B42574
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA; protein
A;Residues: 1-239 <KUG>
A;Cross-references: GB:D11441; NID:g220587; PIDN:BA02006.1; PID:g220588
A;Experimental source: BALB/c, liver
A;Note: sequence extracted from NCBI backbone (NCBIP:110142)
R;Sastri, R.; Wang, J.S.; Brown, D.C.; Ezekowitz, R.A.; Tauber, A.I.; Sastri, K.N.
Mamm. Genome 6, 103-110, 1995
A;Title: Characterization of murine mannose-binding protein genes Mb11 and Mb12 reveals
A;Reference number: 148650; MUID:95284466; PMID:7766991
A;Accession: I48650
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-239 <SAS2>
A;Cross-references: EMBL:U09010; NID:g773278; PIDN:AA02009.1; PID:g773280
C;Comment: Mannose-binding lectins are opsonins that are important in host defense against
C;Genetics:
A;Gene: Mb11
A;Introns: 52/1; 91/1; 116/1
C;Superfamily: mannose-binding lectin; C-type lectin homology
C;Keywords: acute phase; calcium; hydroxyproline; lectin; liver; plasma
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-238/Product: mannose-binding lectin A #status predicted <MAT>
F;36-88/Region: collagen-like
F;119-235/Domain: C-type lectin homology <LCH>

Query Match 74.5%; Score 35; DB 1; Length 239;
Best Local Similarity 87.5%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCTELQTT 9
| | | | |
DB 145 LCTELQGT 152

RESULT 7
A12373
hypothetical protein all4545 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: A12373
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: A12373
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-182 <KUR>
A;Cross-references: UNIPROT:Q8YNL9; GB:BA000019; PIDN:BA076244.1; PID:g17133681; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all4545

Query Match 72.3%; Score 34; DB 2; Length 182;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLCTELQTT 9
| | | | |
DB 136 QLCGEVET 144

RESULT 8
AB3116

transcription regulator, Laci family Atu4550 [imported] - Agrobacterium tumefaciens (str
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AB3116
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan,
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Rao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB3116
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-342 <KUR>
A;Cross-references: UNIPROT:Q8U7A4; GB:AE008689; PIDN:AA45344.1; PID:g17743037; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu4550
A;Map position: linear chromosome

Query Match 72.3%; Score 34; DB 2; Length 342;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLCTELQTT 9
| | | | |
DB 306 ELCTDLLTT 314

RESULT 9

C98171
hypothetical protein AGR_L_636 [imported] - Agrobacterium tumefaciens (strain C58, Cereor
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: C98171
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markela, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C98171
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-356 <KUR>
A;Cross-references: UNIPROT:Q8U7A4; GB:AE007870; PIDN:AAK88893.1; PID:g15158664; GSPDB:G
C;Genetics:
A;Gene: AGR_L_636
A;Map position: linear chromosome

Query Match 72.3%; Score 34; DB 2; Length 356;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLCTELQTT 9
| | | | |
DB 320 ELCTDLLTT 328

RESULT 10

T23189
hypothetical protein K01D12.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23189
R;Dobson, R.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19703
A;Accession: T23189

E6 protein - human papillomavirus type 45
C:Species: human papillomavirus type 45
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36561
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36561
A:Molecule type: DNA
A:Residues: 1-158
A:Cross-references: UNIPROT:P21735; EMBL:X74479; NID:G397022; PIDN:CAA52573.1; PID:G3970
C:Superfamily: Papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 70.2%; Score 33; DB 2; Length 158;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCTELQTT 9
Db 17 LCTELNTS 24

Search completed: June 28, 2005, 19:23:15
Job time : 13.2 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-29

Perfect score: 47

Sequence: 1 LTNTGLVNL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	158	1 VEG_HPV18	P06463 human papillomavirus type 18
2	47	100.0	158	2 Q9NPN8	Q9NPN8 human papillomavirus type 18
3	39	83.0	796	2 Q8IEN5	Q8IEN5 plasmid
4	38	80.9	686	2 Q6DHR6	Q6DHR6 brachydanio
5	37	78.7	158	1 VEG_HPV39	P24835 human papillomavirus type 39
6	37	78.7	158	1 VEG_HPV45	P21735 human papillomavirus type 45
7	37	78.7	158	1 VEG_HPV68	P54667 human papillomavirus type 68
8	37	78.7	158	1 VEG_HPV70	P50804 human papillomavirus type 70
9	37	78.7	158	2 Q9V4Y4	Q9V4Y4 homo sapien
10	37	78.7	158	2 O10608	O10608 human papillomavirus type 18
11	37	78.7	215	2 Q8JND2	Q8JND2 ovine herpesvirus 1
12	37	78.7	402	2 Q74M18	Q74M18 nanoarchaeum
13	37	78.7	467	2 Q9SJV9	Q9SJV9 arabidopsis
14	37	78.7	1110	2 Q7VCX4	Q7VCX4 prochlorococcus
15	37	78.7	1121	2 Q8T9D9	Q8T9D9 drosophila
16	37	78.7	1961	2 Q6NNE1	Q6NNE1 drosophila
17	37	78.7	1961	2 Q9VAG5	Q9VAG5 drosophila
18	36	76.6	176	2 Q6EED0	Q6EED0 biomphalari
19	36	76.6	176	2 Q6EKX2	Q6EKX2 biomphalari
20	36	76.6	176	2 Q6EKX4	Q6EKX4 biomphalari
21	36	76.6	177	2 Q6EKX0	Q6EKX0 biomphalari
22	36	76.6	189	2 Q9ZY62	Q9ZY62 agarcus su
23	36	76.6	189	2 Q9ZY67	Q9ZY67 agarcus cr
24	36	76.6	192	2 Q9ZY68	Q9ZY68 agarcus ca
25	36	76.6	192	2 Q9ZY69	Q9ZY69 agarcus be
26	36	76.6	192	2 Q9ZY70	Q9ZY70 leucosagarc
27	36	76.6	193	2 Q9ZY66	Q9ZY66 agarcus su
28	36	76.6	276	2 Q33658	Q33658 agarcus bi
29	36	76.6	387	2 Q38546	Q38546 biomphalari
30	36	76.6	431	2 Q86H05	Q86H05 biomphalari
31	36	76.6	509	2 Q9C9E6	Q9C9E6 arabidopsis

32 36 76.6 652 2 Q95PK3 Q95pk3 biomphalari
33 36 76.6 655 2 Q8WQX8 Q8wx8 biomphalari
34 36 76.6 670 2 Q95PK2 Q95pk2 biomphalari
35 36 76.6 689 2 Q8WQX7 Q8wx7 biomphalari
36 36 76.6 702 2 Q702B4 Q702b4 uncultured
37 36 76.6 1433 2 Q8A043 Q8a043 bacteroides
38 35 74.5 184 2 Q8A033 Q8a033 clostridium
39 35 74.5 255 2 Q6U7V4 Q6u7v4 crinipellis
40 35 74.5 264 2 Q45147 Q45147 bacteroides
41 35 74.5 270 2 Q84V41 Q84v41 physcomitre
42 35 74.5 278 2 Q798W5 Q798w5 synchococcc
43 35 74.5 300 2 Q44173 Q44173 synchococcc
44 35 74.5 310 1 YGLA_SYNP2 P28606 synchococcc
45 35 74.5 367 2 Q98VT9 Q98vt9 muscovy duc

ALIGNMENTS

RESULT 1
VE6_HPV18
ID_VEG_HPV18 STANDARD; PRT; 158 AA.
AC P06463;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87283882; PubMed=3039146;
RA Cole S.F., Danos O.;
RT "Nucleotide sequence and comparative analysis of the human papillomavirus type 18 genome. Phylogeny of papillomaviruses and repeated structure of the E6 and E7 gene products.";
RL J. Mol. Biol. 193:599-608(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86306665; PubMed=3018129;
RA Matlashewski G., Banks L., Wu-Liao J., Spence P., Pim D., Crawford L.;
RT "The expression of human papillomavirus type 18 E6 protein in bacteria and the production of anti-E6 antibodies.";
RL J. Gen. Virol. 67:1909-1916(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88188247; PubMed=2833614;
RA Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M., Sugimura T.;
RT "Nucleotide sequences of cDNAs for human papillomavirus type 18 transcripts in HeLa cells.";
RL J. Virol. 62:1640-1646(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=87053870; PubMed=3023067;
RA Schneider-Gaedcke A., Schwarz E.;
RT "Different human cervical carcinoma cell lines show similar transcription patterns of human papillomavirus type 18 early genes.";
RL EMBO J. 5:2285-2292(1986).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=87218459; PubMed=3034571;
RA Seedorf K., Oltersdorf T., Kraemer G., Roewekamp W.;
RT "Identification of early proteins of the human papilloma viruses type 16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells.";
RL EMBO J. 6:139-144(1987).
RN [6]
RP ZINC-BINDING.
RX MEDLINE=89385606; PubMed=2550872;
RA Grossman S.R., Laimins L.A.;

"E6 protein of human papillomavirus type 18 binds zinc.";
OncoGene 4:1089-1093(1989).
[7]
INTERACTION WITH FBLN1, AND INHIBITION OF E6-MEDIATED TRANSFORMATION.
MEDLINE=22188366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;
Du M., Fan X., Hong E., Chen J.J.;
"Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";
Biochem. Biophys. Res. Commun. 296:962-969(2002).
CC -!- FUNCTION: This protein has transforming activity in vitro.
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double
CC stranded DNA (in vitro).
CC -!- SUBUNIT: Interacts with FBLN1.
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -----
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CC -----
DR EMBL; X04354; CAA27879.1; -.
DR EMBL; X05015; CAA28664.1; -.
DR EMBL; M20325; AAA99514.1; -.
DR EMBL; M26798; AAA46946.1; -.
DR EMBL; X04773; CAA28466.1; -.
DR EMBL; A06324; CAA00539.1; -.
DR EMBL; A06328; CAA00542.1; -.
DR PIR; A26165; W6WL18.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW DNA-binding; Early protein; Nuclear protein; Oncogene; Zinc-finger.
FT ZN FING 32 68
FT ZN FING 105 141
FT ZN FING 105 141
FT CONFLICT 22 22 N -> S (in Ref. 4).
SQ SEQUENCE 158 AA; 18871 MW; 5BCF13CF43D157FA CRC64;
Query Match 100.0%; Score 47; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LTNTGLYNL 9
Db 93 LTNTGLYNL 101

RESULT 2
Q9QNP8 PRELIMINARY; PRT; 158 AA.
AC Q9QNP8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RA Laeser M., Gul'ko L., Vinokurova S., Kisseljova N., Veiko V.,
RA Kisseljev F.;
RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
RT Transformation Potential of E7 Gene and its Mutants.";
RL Virus Genes 182:139-149(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Veiko V.P.;
RA Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y18491; CAB53096.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.

DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 18886 MW; 5BCF13CF43D407AF CRC64;
Query Match 100.0%; Score 47; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LTNTGLYNL 9
Db 93 LTNTGLYNL 101

RESULT 3
Q8IENS PRELIMINARY; PRT; 796 AA.
AC Q8IENS;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein MAL13P1.38.
GN Name=MAL13P1.38;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
RA Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844509; CAD52214.1; -.
KW Hypothetical protein.
SQ SEQUENCE 796 AA; 95690 MW; 3EB26CAD3BA83F33 CRC64;
Query Match 83.0%; Score 39; DB 2; Length 796;
Best Local Similarity 77.8%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LTNTGLYNL 9
Db 501 VTNTGYNL 509

RESULT 4
Q6DHR6 PRELIMINARY; PRT; 686 AA.
AC Q6DHR6
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Zgc:92139.
GN Name=zgc:92139;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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KW  DNA-binding; Early protein; Nuclear protein; Oncogene; Zinc-finger.
FT  ZN FING 32 68 Potential.
FT  ZN FING 105 141 Potential.
SQ  SEQUENCE 158 AA; 18726 MW; 1B5E9D55BC1B662E CRC64;

Query Match 78.7%; Score 37; DB 1; Length 158;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNTNGLYNL 9
DB 93 ITNTKLYNL 101

RESULT 6
VE6 HPV45 STANDARD; PRT; 158 AA.
ID VE6 HPV45
AC P21735;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
DD E6 protein.
GN Name=E6;
OS Human papillomavirus type 45.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI TaxID=10593;
RN [1]_TaxID=10593;
RP SEQUENCE FROM N.A.
RX MEDLINE=94265501; PubMed=8205838;
RA Delius H., Hofmann B.;
RT 'Primer-directed sequencing of human papillomavirus types.';
RN [2] Curr. Top. Microbiol. Immunol. 186:13-31(1994).
RP SEQUENCE FROM N.A.
RA Kaplan J.B., Burk R.D.;
RT Submitted (AUG-1990) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This protein has transforming activity in vitro.
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double
CC stranded DNA (in vitro).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
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CC -----
CC EMBL; X74479; CAA52573.1; -
CC EMBL; M38198; AAM46973.1; -
CC PIR; S36561; S36561.
CC InterPro; IPR001334; E6.
CC Pfam; PF00518; E6; 1.
CC DNA-binding; Early protein; Nuclear protein; Oncogene; Zinc-finger.
FT ZN FING 32 68 Potential.
FT ZN FING 105 141 Potential.
FT CONFLICT 10 10 R -> P (in Ref. 2).
FT CONFLICT 30 30 I -> N (in Ref. 2).
FT CONFLICT 118 118 R -> A (in Ref. 2).
SQ SEQUENCE 158 AA; 18897 MW; F1CF10DD33AA4C3E CRC64;

Query Match 78.7%; Score 37; DB 1; Length 158;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNTNGLYNL 9
DB 93 ITNTKLYNL 101

RESULT 7

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V56 HPV68
ID V56 HPV68 STANDARD; PRT; 158 AA.
AC P54667;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 68.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=45240;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97060129; PubMed=8904450;
RA Longuet M., Beaudenon S., Orth G.;
RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70,
RT related to the potentially oncogenic HPV39."
RL J. Clin. Microbiol. 34:738-744(1996).
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double
CC stranded DNA (in vitro).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
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CC -----
DR EMBL; U21941; AAC54850.1; -.
DR EMBL; U22461; AAC54880.1; -.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW DNA-binding; Early protein; Nuclear protein; Zinc-finger.
FT ZN_FING 32 68
FT ZN_FING 105 141
FT CONFLICT 100 100 N -> D (in Ref. 2).
SQ SEQUENCE 158 AA; 18617 MW; 6B610800D923D6DE CRC64;

Query Match 78.7%; Score 37; DB 1; Length 158;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTNTGLYNL 9
DB 93 ITNTKLYNL 101

RESULT 9
QY4Y4
ID Q9Y4Y4 PRELIMINARY; PRT; 158 AA.
AC Q9Y4Y4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
GN Name=HPV45 E6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sastre-Garau X., Favre M., Couturier J., Orth G.;
RT "Distinct patterns of alteration of myc genes associated with
RT integration of human papillomavirus type 16 oe type 45 in two genital
RT tumours."
RL J. Gen. Virol. 81:198-199(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Favre M.G.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ242956; CAB44706.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 18914 MW; A61AEF98390AE83 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 158;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTNTGLYNL 9
DB 93 ITNTKLYNL 101

V56 HPV70
ID V56 HPV70 STANDARD; PRT; 158 AA.
AC P50804;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 70.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=39457;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96249586; PubMed=8815087;
RA Forslund O., Hansson B.G.;
RT "Human papillomavirus type 70 genome cloned from overlapping PCR
RT products: complete nucleotide sequence and genomic organization."
RL J. Clin. Microbiol. 34:802-809(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97060129; PubMed=8904450;
RA Longuet M., Beaudenon S., Orth G.;
RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70,

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RESULT 10

Q74MI8 PRELIMINARY; PRT; 158 AA.
 ID O10608
 AC O10608;
 DT 01-JUL-1997 (TRENBLrel. 04, Created)
 DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Oncoprotein E6.
 OS Human papillomavirus type 45.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Saxtre-Garau X., Favre M., Couturier J., Orth G.;
 RT "Distinct patterns of alteration of myc genes associated with
 RT integration of HPV16 or HPV45 DNA in two genital tumors.";
 RL J. Gen. Virol. 0:0-0(0).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Favre M.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y13218; CAA73660.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 158 AA; 18914 MW; A61AEF98390AEB3 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 158;
 Best Local Similarity 77.8%; Pred. No. 25;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LTNTGLYNL 9

Db 93 ITNTELYNL 101
 :|||||
 :|||||

RESULT 11

Q8JND2 PRELIMINARY; PRT; 215 AA.
 ID Q8JND2
 AC Q8JND2;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Putative M transactivator-like protein (Fragment).
 GN Name=ORF57;
 OS Ovine herpesvirus 2.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 OC NCBI_TaxID=10398;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stewart J.P., Rosbottom J.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY044855; AAK97788.1; -;
 DR GO; GO:0030528; F:transcription regulator activity; IEA.
 DR GO; GO:0045449; P:regulation of transcription; IEA.
 DR InterPro; IPR008648; Herpes_UL69.
 DR Pfam; PF05459; Herpes_UL69; 1.
 FT NON_TER 1
 FT NON_TER 215
 SQ SEQUENCE 215 AA; 24590 MW; DF52B9C0C30C9DE6 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 215;
 Best Local Similarity 77.8%; Pred. No. 35;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LTNTGLYNL 9

Db 102 ITNTELYNL 110
 :|||||
 :|||||

RESULT 12

Q74MI8 PRELIMINARY; PRT; 402 AA.
 ID Q74MI8
 AC Q74MI8;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE NEQ080.
 OS OrderedLocusNames=NEQ080;
 OC Nanoarchaeum equitans.
 OC Archaea; Nanoarchaeota; Nanoarchaeum.
 OC NCBI_TaxID=160232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Kin4-M;
 RX MEDLINE=22946215; PubMed=14566062; DOI=10.1073/pnas.1735403100;
 RA Waters E., Hohn M.J., Ahel I., Graham D.E., Adams M.D., Barnstead M.,
 RA Beeson K.Y., Bibbs L., Bolanos R., Keller M., Kretz K., Lin X.,
 RA Mathur E., Ni J., Podar M., Richardson T., Sutton G.G., Simon M.,
 RA Soell D., Stetter K.O., Short J.M., Noorderwier M.;
 RT "The genome of Nanoarchaeum equitans: insights into early archaeal
 RT evolution and derived parasitism";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:12984-12988(2003).
 DR EMBL; AE017199; AAR38936.1; -;
 KW Complete proteome.
 SQ SEQUENCE 402 AA; 45253 MW; A2EDA95381CF2B71 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 402;
 Best Local Similarity 87.5%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LTNTGLYN 8

Db 372 LTKTGLYN 379
 :|||||
 :|||||

RESULT 13

Q9SJV9 PRELIMINARY; PRT; 467 AA.
 ID Q9SJV9
 AC Q9SJV9;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Hypothetical protein At2g01070.
 GN Name=At2g01070;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Town C.D., Haas B.J., Wu D., Maiti R., Hannick L.I., Chan A.P.,
 RA Tallon L.J., Rooney T., Utterback T.R., VanAken S.E., Feidbiyum T.V.,
 RA White O., Fraser C.M.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Town C.D., Kaul S.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC006837; AAF18655.1; -;
 DR PIR; C84420; C84420.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR InterPro; IPR009637; Lung_7TM_recept.
 DR Pfam; PF06814; Lung_7-TM_R; 1.
 DR Hypothetical protein_

Query Match 78.7%; Score 37; DB 2; Length 467;
 Best Local Similarity 87.5%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LTNTGLYN 8

Db 372 LTKTGLYN 379
 :|||||
 :|||||

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Best Local Similarity 66.7%; Pred. No. 78;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNTGTGLYNL 9
Db 120 ITKTGIYNL 128
:|||||

RESULT 14
Q7VCX4 PRELIMINARY; PRT; 1110 AA.
AC Q7VCX4;
DT 01-OCT-2003 (TREMELrel. 25, Created)
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE AbtB family transcriptional regulator fused to LRR containing
DE domain.
GN OrderedLocusNames=Pro0616;
OS Prochlorococcus marinus.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1219;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SARG / CCMP 1375 / SS120;
RX MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;
RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,
RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,
RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
RA Wolf Y.I., Hess W.R.;
RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
RT a nearly minimal oxyphototrophic genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025 (2003).
DR EMBL; AE017162; AAP99660.1; -.
DR InterPro; IPR004830; LRV.
DR Pfam; PF01816; LRV; 7.
KW Complete proteome.
SQ SEQUENCE 1110 AA; 126870 MW; 42E4CC7C842467F2 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 1110;
Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNTGTGLYN 8
Db 199 LKNTGLYN 206
||||||

RESULT 15
Q8T9D9 PRELIMINARY; PRT; 1121 AA.
AC Q8T9D9;
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE SD04942p.
GN Name=CG18134; ORFNames=CG31037;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY069808; AAL39953.1; -.
DR FlyBase; FBgn0051037; CG31037.

```

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DR InterPro; IPR009091; RCI1/BLIP-II.
DR InterPro; IPR00408; Reg chr condens.
DR PROSITE; PS50012; RCI1_3; 3.
SQ SEQUENCE 1121 AA; 124395 MW; F897789742C1CF49 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 1121;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNTGTGLYNL 9
Db 1034 LTNGLYSL 1042
|||||

Search completed: June 28, 2005, 21:24:00
Job time : 57.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-29
Perfect score: 47
Sequence: 1 LTNTGLYNL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	158	1 W6WL18	E6 protein - human
2	39	83.0	178	2 S69767	flagellin fleC, 39
3	37	78.7	158	1 W6WL39	E6 protein - human
4	37	78.7	158	2 S36561	hypothetical prote
5	37	78.7	467	2 C84420	unknown protein T1
6	36	76.6	509	2 A96749	hypothetical prote
7	35	74.5	264	2 I40184	hypothetical prote
8	35	74.5	310	2 B47050	glnA 3'-region hyp
9	35	74.5	963	2 B70524	probable PPE prote
10	35	74.5	2204	2 A70524	probable PPE prote
11	35	74.5	3716	2 F70969	probable PPE prote
12	34	72.3	269	2 C60950	apolipoprotein B-1
13	34	72.3	274	2 B60950	apolipoprotein B-1
14	34	72.3	274	2 A60950	apolipoprotein B-1
15	34	72.3	341	2 T41450	hypothetical prote
16	34	72.3	447	2 AF1751	RNA polymerase sig
17	34	72.3	578	1 S06097	type I site-specif
18	34	72.3	582	2 F70675	probable PPE prote
19	34	72.3	687	2 S43250	thimet oligopeptid
20	34	72.3	689	1 HHVUTH	thimet oligopeptid
21	34	72.3	779	2 JH0102	apolipoprotein B -
22	34	72.3	784	2 JH0101	apolipoprotein B -
23	34	72.3	1315	2 T50262	probable nucleopor
24	34	72.3	1778	2 J70382	apolipoprotein B -
25	34	72.3	2629	2 I46569	apolipoprotein B -
26	33	70.2	141	2 E57811	hypothetical prote
27	33	70.2	206	2 A64339	hypothetical prote
28	33	70.2	441	2 F48327	COI intron 5 prote
29	33	70.2	461	2 S50864	avermectin-sensiti

hypothetical prote
Rac GTPase activat
probable outer mem
probable exonuclea
probable PPE prote
hypothetical prote
E6 protein - human
mannose-1-phosphat
dimethylsulfoxide
hypothetical prote
branched-chain ami
xylose operon regu
chitinase (EC 3.2.
hypothetical prote
major capsid prote

ALIGNMENTS

RESULT 1

W6WL18
E6 protein - human papillomavirus type 18
C:Species: human papillomavirus type 18
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: A26165; G26251
R:Seedorf, K.; Olterdsdorf, T.; Kraemmer, G.; Roewekamp, W.
EMBO J. 6, 139-144, 1987

A:Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)
A:Reference number: A91068; MUID:87218459; PMID:3034571
A:Accession: A26165
A:Molecule type: DNA

A:Residues: 1-158 <SSE>

A:Cross-references: UNIPROT:P06463; GB:X04773; NID:G60876; PIDN:CAA28466.1; PID:G60877

R:Colie, S.T.; Danos, O.

J. Mol. Biol. 193, 599-608, 1987

A:Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 18

A:Reference number: A92937; MUID:87283882; PMID:3039146

A:Accession: G26251

A:Molecule type: DNA

A:Residues: 1-158 <COL>

A:Cross-references: GB:X05015; NID:G60975; PIDN:CAA28664.1; PID:G60976

R:Matlashewski, G.; Banke, L.; Wu-Liao, J.; Spence, P.; Pim, D.; Crawford, L.

J. Gen. Virol. 67, 1909-1916, 1986

A:Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the p

A:Reference number: A92791; MUID:8630665; PMID:3018129

A:Contents: annotation; identification of the protein

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; transforming protein; zinc finger

F:32-68/Region: zinc finger CCCC motif

F:105-141/Region: zinc finger CCCC motif

Query Match 100.0%; Score 47; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.055;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTNTGLYNL 9

Db 93 LTNTGLYNL 101

RESULT 2

S69767

flagellin fleC, 39.6K - Yersinia enterocolitica

C:Species: Yersinia enterocolitica

C:Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 17-Apr-1998

C:Accession: S69767

R:Kaputral V.; Minnich, S.A.

Mol. Microbiol. 17, 49-56, 1995

A:Title: Co-ordinate, temperature-sensitive regulation of the three Yersinia enterocolit

A:Reference number: S69767; MUID:96020661; PMID:7476208

A:Accession: S69767

```
A:Molecule type: DNA
A:Residues: 1-378 <KAP>
A:Experimental source: strain 8081
C:Genetics:
A:Gene: fleC
C:Superfamily: flagellin
C:Keywords: flagellum

Query Match      83.0%; Score 39; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2  TNTGLYN 8
      |||||
Db      242 TNTGLYN 248

RESULT 3
W6ML39
E6 protein - human papillomavirus type 39
C:Species: human papillomavirus type 39
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: A38502
R:Volpers, C.; Strebeck, R.E.
Virology 181, 419-423, 1991
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
A:Reference number: A38502; MUID:91135017; PMID:1847266
A:Accession: A38502
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-158 <VOL>
A:CROSS-references: UNIPROT:P24835; GB:M62849; EMBL:M38185; NID:g333245; PIDN:AAA47050.1
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:32-68/Region: zinc finger CCCC motif
F:105-141/Region: zinc finger CCCC motif

Query Match      78.7%; Score 37; DB 1; Length 158;
Best Local Similarity 77.8%; Pred. No. 5.3;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy      1  LTNTGLYNL 9
      :|||:
Db      93  ITNTKLYNL 101

RESULT 4
S36561
E6 protein - human papillomavirus type 45
C:Species: human papillomavirus type 45
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36561
R:Dellius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36561
A:Molecule type: DNA
A:Residues: 1-158 <DEL>
A:CROSS-references: UNIPROT:P21735; EMBL:X74479; NID:g397022; PIDN:CAA52573.1; PID:g3970
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match      78.7%; Score 37; DB 2; Length 158;
Best Local Similarity 77.8%; Pred. No. 5.3;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy      1  LTNTGLYNL 9
      :|||:
Db      93  ITNTKLYNL 101
```

```
RESULT 5
C84420
hypothetical protein At2g01070 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: C84420
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
L.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: C84420
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-467 <STO>
A:CROSS-references: UNIPROT:Q9SJV9; GB:A8002093; NID:g6598622; PIDN:AAF18655.1; GSPDB:GN
C:Genetics:
A:Gene: At2g01070
A:Map position: 2

Query Match      78.7%; Score 37; DB 2; Length 467;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1  LTNTGLYNL 9
      :|||:
Db      120 ITKTGYNL 128

RESULT 6
A96749
unknown protein T10D10.5 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: A96749
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.-
C.A.; Li, J.H.; Li, X.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A96749
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-509 <STO>
A:CROSS-references: UNIPROT:Q9C9E6; GB:A8005173; NID:g6730753; PIDN:AAF27142.1; GSPDB:GN
C:Genetics:
A:Gene: T10D10.5
A:Map position: 1

Query Match      76.6%; Score 36; DB 2; Length 509;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1  LTNTGLYNL 9
      :|||:
Db      161 VTRTGMYNL 169

RESULT 7
I40184
hypothetical protein I169a - Bacteroides fragilis
C:Species: Bacteroides fragilis
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40184; S41294
R:Trinh, S.; Haggoud, A.; Reyssset, G.; Sebald, M.
Microbiology 141, 927-935, 1995
```

A:Title: Plasmids pIP419 and pIP421 from Bacteroides: 5-nitroimidazole resistance genes
A:Reference number: I40184; MUID:95291442; PMID:7773395
A:Accession: I40184
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-264 <RES>
A:Cross-references: UNIPROT:Q45147; EMBL:X76949; NID:g440303; PIDN:CAA54270.1; PID:g4403

Query Match 74.5%; Score 35; DB 2; Length 264;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTGGLYN 8
DB 123 LNTGGLYN 130
|||||:

RESULT 8
B47050
glnA 3'-region hypothetical protein - *Synechococcus* sp.
N:Alternate names: RPD3/acuC homolog
C:Species: *Synechococcus* sp.
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 31-Mar-2000
C:Accession: B47050; S23853
R:Wagner, S.J.; Thomas, S.P.; Kaufman, R.I.; Nixon, B.T.; Stevens Jr., S.E.
J. Bacteriol. 175, 604-612, 1993
A:Title: The glnA gene of the cyanobacterium *Agmenellum quadruplicatum* PR-6 is nonessential
A:Reference number: A47050; MUID:93139025; PMID:7678591
A:Accession: B47050
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-310 <WAG>
A:Cross-references: EMBL:Z13965; NID:g38960; PIDN:CAA78367.1; PID:g580726
A:Experimental source: PR-6
C:Superfamily: acetyl/polyamine aminohydrolase; RPD3/acuC homolog
F:15-296/Domain: RPD3/acuC homolog <RAH1>

Query Match 74.5%; Score 35; DB 2; Length 310;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTGGLY 7
DB 257 MTNTGLY 263
|||||:

RESULT 9
B70524
probable PPE protein - *Mycobacterium tuberculosis* (strain H37RV)
C:Species: *Mycobacterium tuberculosis*
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: B70524
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: B70524
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-963 <COL>
A:Cross-references: GB:Z96800; GB:AL123456; NID:g3261800; PIDN:CAB09593.1; PID:g2193926
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: PPE
C:Superfamily: elastin

Query Match 74.5%; Score 35; DB 2; Length 963;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNTGLYN 8
DB 760 TNTGLFN 766
|||||:

RESULT 10
A70524
probable PPE protein - *Mycobacterium tuberculosis* (strain H37RV)
C:Species: *Mycobacterium tuberculosis*
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: A70524
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: A70524
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-2204 <COL>
A:Cross-references: GB:Z96800; GB:AL123456; NID:g3261800; PIDN:CAB09611.1; PID:el1300013;
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: PPE

Query Match 74.5%; Score 35; DB 2; Length 2204;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNTGLYN 8
DB 242 TNTGLFN 248
|||||:

RESULT 11
E70969
probable PPE protein - *Mycobacterium tuberculosis* (strain H37RV)
C:Species: *Mycobacterium tuberculosis*
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: E70969
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: E70969
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-3716 <COL>
A:Cross-references: GB:AL009198; GB:AL123456; NID:g3242262; PIDN:CAA15735.1; PID:el20226;
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: PPE

Query Match 74.5%; Score 35; DB 2; Length 3716;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TNTGLYN 8
DB 2173 TNTGLFN 2179
|||||:

RESULT 12
C60950
apolipoprotein B-100 - golden hamster (fragment)
C:Species: *Mesocricetus auratus* (golden hamster)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: C60950

R;Law, A.; Scott, J.
 J. Lipid Res. 31, 1109-1120, 1990
 A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL
 A;Reference number: A60950; PMID:90324804; PMID:2373961
 A;Accession: C60950
 A;Molecule type: DNA
 A;Residues: 1-269 <LAW>
 A;Cross-references: UNIPROT:Q60537; UNIPROT:Q60536
 C;Superfamily: apolipoprotein B
 C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

Query Match 72.3%; Score 34; DB 2; Length 269;
 Best Local Similarity 85.7%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TNTGLYN 8
 || ||||
 Db 183 TNVGLYN 189

RESULT 13

B60950
 apolipoprotein B-100 - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 07-Oct-1994
 C;Accession: B60950
 R;Law, A.; Scott, J.
 J. Lipid Res. 31, 1109-1120, 1990
 A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL
 A;Reference number: A60950; PMID:90324804; PMID:2373961
 A;Accession: B60950
 A;Molecule type: mRNA
 A;Residues: 1-274 <LAW>
 A;Note: authors translated the codon ATA for residue 8 as Val
 C;Superfamily: apolipoprotein B
 C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

Query Match 72.3%; Score 34; DB 2; Length 274;
 Best Local Similarity 85.7%; Pred. No. 39;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TNTGLYN 8
 || ||||
 Db 188 TNAGLYN 194

RESULT 14

A60950
 apolipoprotein B-100 - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
 C;Accession: A60950
 R;Law, A.; Scott, J.
 J. Lipid Res. 31, 1109-1120, 1990
 A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL
 A;Reference number: A60950; PMID:90324804; PMID:2373961
 A;Accession: A60950
 A;Molecule type: mRNA
 A;Residues: 1-274 <LAW>
 A;Cross-references: UNIPROT:Q7M2U9
 A;Note: authors translated the codon GAT for residue 155 as His
 C;Superfamily: apolipoprotein B
 C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

Query Match 72.3%; Score 34; DB 2; Length 274;
 Best Local Similarity 85.7%; Pred. No. 39;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TNTGLYN 8
 || ||||
 Db 188 TNAGLYN 194

RESULT 15

T41450
 hypothetical protein SPCC594.06c - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: T41450
 R;Rieger, M.; Lyne, M.; Rajandream, M.A.; Batreil, B.G.
 submitted to the EMBL Data Library, September 1998
 A;Reference number: Z21994
 A;Accession: T41450
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-341 <RIB>
 A;Cross-references: UNIPROT:O74509; EMBL:AL031523; PIDN:CAA20665.1; GSPDB:GN00068; SPDB:
 A;Experimental source: strain 972h-; cosmid c594
 C;Genetics:
 A;Gene: SPDB:SPCC594.06c
 A;Map position: 3
 A;Introns: 12/3

Query Match 72.3%; Score 34; DB 2; Length 341;
 Best Local Similarity 66.7%; Pred. No. 49;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LNTNTGLYNL 9
 | | | | |
 Db 268 LDNVGLYNN 276

Search completed: June 28, 2005, 21:27:45
 Job time : 12.15 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)
78.367 Million cell updates/sec

Title: US-08-170-344-50
Perfect score: 57
Sequence: 1 RHYCVSLYG 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	158	1 W6WLS	protein E6 - human
2	45	78.9	148	2 A61237	E6 protein - human
3	45	78.9	148	2 S36573	E6 protein - human
4	45	78.9	149	1 W6WLS	E6 protein - human
5	45	78.9	153	2 S36503	E6 protein - human
6	42	73.7	149	1 W6WLS	E6 protein - human
7	41	71.9	1541	2 T02831	AAA protein L4171.
8	38	66.7	1914	2 T42635	tenascin Y precurs
9	38	66.7	2573	2 D71614	hypothetical prote
10	37	64.9	97	2 S59427	hypothetical prote
11	37	64.9	109	2 PH1668	Ig heavy chain V r
12	37	64.9	187	2 S32968	probable membrane
13	37	64.9	216	2 JX0265	platelet aggregati
14	37	64.9	323	2 T24836	hypothetical prote
15	37	64.9	383	2 D88633	protein F56B3.2 [i
16	37	64.9	403	2 G70038	conserved hypothet
17	37	64.9	493	2 S72196	X-Pro dipeptidase
18	37	64.9	522	2 E84833	hypothetical prote
19	37	64.9	571	2 S24789	jararagin C precu
20	37	64.9	759	2 S76989	sensory transducti
21	37	64.9	795	2 D64343	hypothetical prote
22	37	64.9	944	2 AC2073	two-component sens
23	37	64.9	1716	2 T14103	probable DNA-direc
24	37	64.9	1717	2 T13961	DNA-directed RNA p
25	36.5	64.0	307	2 D75143	udp-glucose 4-epim
26	36	63.2	155	1 W6WLS	E6 protein - human
27	36	63.2	155	2 A44890	E6 protein - human
28	36	63.2	209	2 JX0266	platelet aggregati
29	36	63.2	209	2 H97519	hypothetical prote

30	36	63.2	323	1 LUH03	annexin III - huma
31	36	63.2	335	2 JH0813	GTP-binding regula
32	36	63.2	376	2 S27015	GTP-binding regula
33	36	63.2	377	1 RQMSA1	GTP-binding regula
34	36	63.2	379	1 RQXLA	GTP-binding regula
35	36	63.2	379	2 A42964	guanine nucleotide
36	36	63.2	380	1 RGHUAI	GTP-binding regula
37	36	63.2	394	1 RGHYAE	GTP-binding regula
38	36	63.2	394	1 RQMSA2	GTP-binding regula
39	36	63.2	394	1 RQBOGA	GTP-binding regula
40	36	63.2	394	1 RGHYA2	GTP-binding regula
41	36	63.2	394	1 RQRTA2	GTP-binding regula
42	36	63.2	394	2 S33458	GTP-binding regula
43	36	63.2	395	1 RGHUA2	GTP-binding regula
44	36	63.2	397	1 RQPGA2	GTP-binding regula
45	36	63.2	406	2 F70632	probable metzZ prot

ALIGNMENTS

RESULT 1

W6WLS

protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Krammer, G.; Duret, M.; Suhai, S.; Rowe, W.G.

Virology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: 217014; MUID:91162763; PMID:1848319

A:Accession: T10427

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C:Genetics:

C:Gene: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 57; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.019;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy

1 RHYCVSLYG 9

|||||||

84 RHYCVSLYG 92

RESULT 2

A61237

E6 protein - human papillomavirus type 52

C:Species: human papillomavirus type 52

C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996

C:Accession: A61237

R:Takami, Y.; Kondoh, G.; Saito, K.; Sudiro, T.M.; Sjahruachman, A.; Warsa, U.

Int. J. Cancer 48, 516-522, 1991

A:Title: Cloning and characterization of human papillomavirus type 52 from cervical carci

A:Reference number: A61237; MUID:91258022; PMID:1646174

A:Accession: A61237

A>Status: preliminary

A:Molecule type: DNA

A;Residues: 1-148 <TAK>
C;Superfamily: papillomavirus E6 protein

Query Match 78.9%; Score 45; DB 2; Length 148;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RHYCVSLYG 9
||| |||||
Db 77 RHYQVSLYG 85

RESULT 3
S36573
E6 protein - human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36573
R;Delius, H.; Hofmann, B.
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36573
A;Molecule type: DNA
A;Residues: 1-148
A;Cross-references: UNIPROT:P36814; EMBL:X74481; NID:g397038; PIDN:CAAS2585.1; PID:g397038
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 78.9%; Score 45; DB 2; Length 148;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RHYCVSLYG 9
||| |||||
Db 77 RHYQVSLYG 85

RESULT 4
W6WL58
E6 protein - human papillomavirus type 58
C;Species: human papillomavirus type 58
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: E36779
R;Kirii, Y.; Iwamoto, S.; Matsukura, T.
A;Title: Human papillomavirus type 58 DNA sequence.
A;Reference number: A36779; MUID:92024102; PMID:1656594
A;Accession: E36779
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-149 <KIR>
A;Cross-references: UNIPROT:P26555; GB:D90400; NID:g222386; PIDN:BAAS31845.1; PID:g333709
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 78.9%; Score 45; DB 1; Length 149;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RHYCVSLYG 9
||| |||||
Db 77 RHYQVSLYG 85

RESULT 5
S36503
E6 protein - human papillomavirus type 30
C;Species: human papillomavirus type 30
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: S36503
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36503
A;Molecule type: DNA
A;Residues: 1-153
A;Cross-references: UNIPROT:P36809; EMBL:X74474; NID:g396973; PIDN:CAAS2543.1; PID:g396973
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 78.9%; Score 45; DB 2; Length 153;
Best Local Similarity 88.9%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RHYCVSLYG 9
||| |||||
Db 80 RHYNYSLYG 88

RESULT 6
W6WL33
E6 protein - human papillomavirus type 33
C;Species: human papillomavirus type 33
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A03683
R;Cole, S.T.; Strebeck, R.E.
J. Virol. 58, 991-995, 1986
A;Title: Genome organization and nucleotide sequence of human papillomavirus type 33, whi
A;Reference number: A93020; MUID:86200464; PMID:3009902
A;Accession: A03683
A;Molecule type: DNA
A;Residues: 1-149 <COL>
A;Cross-references: UNIPROT:P06427; GB:M12732; NID:g333049; PIDN:AAA46958.1; PID:g463177
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 73.7%; Score 42; DB 1; Length 149;
Best Local Similarity 77.8%; Pred. No. 5.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RHYCVSLYG 9
||| |||||
Db 77 RHYNYSLYG 85

RESULT 7
T02831
AAA protein L4171.3 [imported] - Leishmania major (strain Friedlin)
C;Species: Leishmania major
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: C81460; T02831
R;Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.; F
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A;Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-c
A;Reference number: A81455; MUID:99178987; PMID:10077609
A;Accession: C81460
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1541 <PYL>
A;Cross-references: UNIPROT:O15837; GB:A8001274; NID:g3264850; PIDN:AAC24654.1; PID:g226
C;Experimental source: strain MHOM/IL/81/Friedlin
C;Genetics:
A;Gene: L4171.3
A;Map position: 1

Query Match 71.9%; Score 41; DB 2; Length 1541;
Best Local Similarity 75.0%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RHYCYSLY 8
 ||||| :
 Db 1255 RHYCYSW 1262

RESULT 8

T42635
 tenascin Y precursor, variant 206.5K - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T42635
 R:Hagios, C.; Koch, M.; Chiquet, M.; Spring, J.; Chiquet-Ehrismann, R.
 J. Cell Biol. 134, 1499-1512, 1996
 A:Title: Tenascin-Y: a protein of novel domain structure is secreted by differentiated fibroblasts
 A:Reference number: Z2222; MUID:96427453; PMID:8830777
 A:Accession: T42635
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1914 <HAG>
 A:Cross-references: UNIPROT:Q91008; EMBL:X99062; NID:g1419545; PIDN:CAA67509.1; PID:g1419545
 C:Genes: tn-y
 C:Keywords: extracellular matrix; heparin binding; heptad repeat
 P:1-19/Domain: signal sequence #status predicted <SIG>
 F:2-1914/Product: tenascin Y, variant 206.5K #status predicted <MAT>

Query Match 66.7%; Score 38; DB 2; Length 1914;
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RHYCYSLYG 9
 ||||| :
 Db 614 RHYKFNLYG 622

RESULT 9

D71614
 hypothetical protein PFB0460c - malaria parasite (Plasmodium falciparum)
 C:Species: Plasmodium falciparum
 C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
 C:Accession: D71614
 R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
 ; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
 Science 282, 1126-1132, 1998
 A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
 A:Reference number: A71600; MUID:99021743; PMID:9804551
 A:Accession: D71614
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-2573 <GAR>
 A:Cross-references: UNIPROT:O96185; GB:AE001396; GB:AE001362; NID:g3845188; PIDN:AAC7188
 A:Experimental source: clone 3D7
 C:Genetics:
 A:Gene: PFB0460c

Query Match 66.7%; Score 38; DB 2; Length 2573;
 Best Local Similarity 71.4%; Pred. No. 2.7e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HCYCSLY 8
 ||||| :
 Db 2508 HCYCDLF 2514

RESULT 10

S59427
 hypothetical protein YDR220c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein YD9934.05c
 C:Species: Saccharomyces cerevisiae
 C:Date: 30-Nov-1995 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
 C:Accession: S59427
 R:Murphy, L.; Harris, D.
 submitted to the EMBL Data Library, March 1995

A:Reference number: S59423
 A:Accession: S59427
 A:Molecule type: DNA
 A:Residues: 1-97 <MUR>
 A:Cross-references: UNIPROT:Q04923; EMBL:Z48612; NID:g728671; PID:g728676; GSPDB:GN00004;
 A:Experimental source: strain AB972
 C:Genetics:
 A:Gene: MIPS:YDR220c
 A:Cross-references: SGD:S0002628
 A:Map position: 4R

Query Match 64.9%; Score 37; DB 2; Length 97;
 Best Local Similarity 75.0%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HCYCSLYG 9
 ||||| :
 Db 23 HYYSFYG 30

RESULT 11

PH1668
 Ig heavy chain V region (clone 3G5) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
 C:Accession: PH1668
 R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
 J. Exp. Med. 178, 331-336, 1993
 A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
 A:Reference number: PH1642; MUID:93301610; PMID:8315388
 A:Accession: PH1668
 A:Molecule type: mRNA
 A:Residues: 1-109 <HIL>
 A:Experimental source: B cell
 A:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 64.9%; Score 37; DB 2; Length 109;
 Best Local Similarity 75.0%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HCYCSLYG 9
 ||||| :
 Db 86 YYCASLYG 93

RESULT 12

S32968
 probable membrane protein YBR266c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein YBR1735
 C:Species: Saccharomyces cerevisiae
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C:Accession: S32968; S46147
 R:Doignon, F.; Biteau, N.; Crouzet, M.; Aigle, M.
 Yeast 9, 189-199, 1993
 A:Title: The complete sequence of a 19,482 bp segment located on the right arm of chromosome 1
 A:Reference number: S29348; MUID:93220397; PMID:8465606
 A:Accession: S32968
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-187 <DOI>

A:Cross-references: UNIPROT:P38343; EMBL:X70529
 R:Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.
 submitted to the Protein Sequence Database, August 1994
 A:Reference number: S45940
 A:Accession: S46147
 A:Molecule type: DNA
 A:Residues: 1-187 <ATG>
 A:Cross-references: EMBL:Z36135; NID:g536697; PID:g536698; MIPS:YBR266c
 C:Genetics:
 A:Cross-references: SGD:S0000470
 A:Map position: 2R

C:Superfamily: Saccharomyces cerevisiae probable membrane protein YBR266c
C:Keywords: transmembrane protein
F:24-40/Domain: transmembrane #status predicted <TM1>
F:72-91/Domain: transmembrane #status predicted <TM2>
F:109-128/Domain: transmembrane #status predicted <TM3>

Query Match 64.9%; Score 37; DB 2; Length 187;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RHVCSLYG 8
 :|:|:|:|
Db 178 KHHCYSSY 185

RESULT 13

JX0265
platelet aggregation inhibitor - red diamond rattlesnake (fragment)
N:Alternate names: disintegrin
C:Species: Crotales ruber (red diamond rattlesnake)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: JX0265
R:Takeya, H.; Nishida, S.; Nishino, N.; Makinose, Y.; Omori-Sato, T.; Nikai, T.; Sugihara, J. Biochem. 113, 473-483, 1993
A:Title: Primary structures of platelet aggregation inhibitors (disintegrins) autoproteolytically released from these enzymes.
A:Reference number: JX0265; MUID:93293798; PMID:8514736
A:Accession: JX0265
A:Molecule type: protein
A:Residues: 1-216 <TAK>
A:Cross-references: UNIPROT:Q9PSN7
A:Experimental source: venom
C:Superfamily: mouse meltrin alpha; disintegrin homology
F:7-89/Domain: disintegrin homology <DIS>

Query Match 64.9%; Score 37; DB 2; Length 216;
Best Local Similarity 62.5%; Pred. No. 52;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HVCYSLYG 9
 |:|:|:|
Db 115 HCVAFVG 122

RESULT 14

T24836
hypothetical protein T11F9.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24836
R:Lennard, N.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19941
A:Accession: T24836
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-323 <WIL>
A:Cross-references: UNIPROT:Q22396; EMBL:274042; PIDN:CAA98528.1; GSPDB:GN000023; CESP:TL11F9
A:Experimental source: clone T11F9
C:Genetics:
A:Gene: CESP:T11F9.3
A:Map position: 5
A:introns: 115/2; 229/3

Query Match 64.9%; Score 37; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CYSLYG 9
 |:|:|:|
Db 35 CYSLYG 40

RESULT 15

D88633
protein F56B3.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: D88633
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: D88633
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-383 <STO>
A:Cross-references: GB:chr_IV; PIDN:AAC02613.1; PID:g2854199; GSPDB:GN000022; CESP:F56B3.2
A>Note: contains similarity to tenascins
C:Genetics:
A:Gene: F56B3.2
A:Map position: 4

Query Match 64.9%; Score 37; DB 2; Length 383;
Best Local Similarity 75.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HVCYSLYG 9
 |:|:|:|
Db 177 HVCYFLSG 184

Search completed: June 28, 2005, 23:32:06
Job time : 12.05 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-50

Perfect score: 57

Sequence: 1 RHYCYSLYG 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	57	100.0	90	2	Q80883	Q80883	human papil
2	57	100.0	90	2	Q80884	Q80884	human papil
3	57	100.0	99	2	Q19B2	Q19B2	human papil
4	57	100.0	103	2	Q19D6	Q19D6	human papil
5	57	100.0	130	2	Q19B4	Q19B4	human papil
6	57	100.0	130	2	Q19D0	Q19D0	human papil
7	57	100.0	143	2	Q19B6	Q19B6	human papil
8	57	100.0	151	2	Q12336	Q12336	human papil
9	57	100.0	151	2	Q77816	Q77816	human papil
10	57	100.0	151	2	Q89640	Q89640	human papil
11	57	100.0	151	2	Q89755	Q89755	human papil
12	57	100.0	151	2	Q8B564	Q8B564	human papil
13	57	100.0	151	2	Q9W931	Q9W931	human papil
14	57	100.0	151	2	Q9WMP4	Q9WMP4	human papil
15	57	100.0	158	1	V26 HPV16	V26 HPV16	human papil
16	57	100.0	158	2	Q8CHP5	Q8CHP5	human papil
17	57	100.0	158	2	Q8QHT0	Q8QHT0	human papil
18	57	100.0	158	2	Q8QRD6	Q8QRD6	human papil
19	57	100.0	158	2	Q8QRD7	Q8QRD7	human papil
20	57	100.0	158	2	Q8QRD8	Q8QRD8	human papil
21	57	100.0	158	2	Q8QRD9	Q8QRD9	human papil
22	57	100.0	158	2	Q8QRE0	Q8QRE0	human papil
23	57	100.0	158	2	Q8QRE1	Q8QRE1	human papil
24	57	100.0	158	2	Q8QDH3	Q8QDH3	human papil
25	57	100.0	158	2	Q8QDH5	Q8QDH5	human papil
26	57	100.0	158	2	Q8QDH7	Q8QDH7	human papil
27	57	100.0	158	2	Q8QDH9	Q8QDH9	human papil
28	57	100.0	161	2	Q819B1	Q819B1	human papil
29	57	100.0	161	2	Q819C6	Q819C6	human papil
30	57	100.0	161	2	Q819D4	Q819D4	human papil
31	54	94.7	84	2	Q80882	Q80882	human papil

32 54 94.7 130 2 Q919B8 human papil
33 54 94.7 130 2 Q919C0 human papil
34 54 94.7 130 2 Q919C2 human papil
35 54 94.7 130 2 Q919C8 human papil
36 54 94.7 138 2 Q919D2 human papil
37 54 94.7 143 2 Q919C4 human papil
38 54 94.7 151 2 Q12335 human papil
39 54 94.7 151 2 Q77JC7 human papil
40 54 94.7 151 2 Q77ZJ5 human papil
41 54 94.7 151 2 Q80963 human papil
42 54 94.7 151 2 Q89648 human papil
43 54 94.7 151 2 Q89852 human papil
44 54 94.7 151 2 Q88B19 human papil
45 54 94.7 151 2 Q88B20 human papil

ALIGNMENTS

RESULT 1

Q80883 PRELIMINARY; PRT; 90 AA.
AC Q80883;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galuira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14512; AAB60566.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10904 MW; 5D3ADF843AD606B CRC64;

Query Match 100.0%; Score 57; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYCYSLYG 9
Db 36 RHYCYSLYG 44
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RESULT 2

Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galuira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

SQ SEQUENCE 130 AA; 15735 MW; 9EFB30BEDCA21AF3 CRC64;
 Query Match 100.0%; Score 57; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.093;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYCYSLYG 9
 |||||
 Db 56 RHYCYSLYG 64

RESULT 7
 Q91986 PRELIMINARY; PRT; 143 AA.
 ID Q91986
 AC Q91986
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874 (2002).
 DR EMBL; AF404702; AAL01361.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER
 SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3BEB2AC CRC64;

Query Match 100.0%; Score 57; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYCYSLYG 9
 |||||
 Db 69 RHYCYSLYG 77

RESULT 8
 O12336 PRELIMINARY; PRT; 151 AA.
 ID O12336
 AC O12336
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus
 type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208 (1997).
 DR EMBL; AF003016; AAB70733.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match 100.0%; Score 57; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYCYSLYG 9
 |||||
 Db 77 RHYCYSLYG 85

RESULT 9
 Q77816 PRELIMINARY; PRT; 151 AA.
 ID Q77816
 AC Q77816
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
 RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325 (2000).
 DR EMBL; AJ388056; CAB45104.1; -;
 DR EMBL; AJ388061; CAB45114.1; -;
 DR EMBL; AJ388066; CAB45124.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYCYSLYG 9
 |||||
 Db 77 RHYCYSLYG 85

RESULT 10
 Q89640 PRELIMINARY; PRT; 151 AA.
 ID Q89640
 AC Q89640
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Early transforming protein E6.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96079021; PubMed=7494284;
 RA Yanada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
 RA Jenison S.A.;
 RT "Human papillomavirus type 16 variant lineages in United States
 populations characterized by nucleotide sequence analysis of the E6,
 RT L2, and L1 coding segments.";
 RL J. Virol. 69:7743-7753 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Farmer A.D.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]

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RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34129; AAA91676.1; -.
DR EMBL; AF469198; AA015693.1; -.
DR EMBL; U34115; AAA91662.1; -.
DR EMBL; U34120; AAA91667.1; -.
DR EMBL; U34124; AAA91671.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18348 MW; FE3F2A2FCF0A6CB2 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYCYSLYG 9
Db 77 RHYCYSLYG 85

RESULT 11
Q89755 ID Q89755 PRELIMINARY; PRT; 151 AA.
AC Q89755;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RT J. Virol. 69:7743-7753 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34126; AAA91673.1; -.
DR EMBL; U34111; AAA91658.1; -.
DR EMBL; U34121; AAA91668.1; -.
DR EMBL; U34123; AAA91670.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; F8F82A2FCEBA6C02 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYCYSLYG 9
Db 77 RHYCYSLYG 85

RESULT 12
Q8B564 ID Q8B564 PRELIMINARY; PRT; 151 AA.
AC Q8B564;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF548023; AA016239.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18348 MW; FE3F2D5FCD7A69B2 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYCYSLYG 9
Db 77 RHYCYSLYG 85

RESULT 13
Q9W931 ID Q9W931 PRELIMINARY; PRT; 151 AA.
AC Q9W931;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OS Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325 (2000).
DR EMBL; AJ388059; CAB45110.1; -.
DR EMBL; AJ388058; CAB45108.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18306 MW; 6FB3D9E0F24A5300 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYCYSLYG 9
Db 77 RHYCYSLYG 85

RESULT 14
Q9WMP4 ID Q9WMP4 PRELIMINARY; PRT; 151 AA.
AC Q9WMP4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OS Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

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OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Weijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388060; CAB45112.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18387 MW; E2244784BBA6C02 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHVCYSLYG 9
| | | | |
DB 77 RHVCYSLYG 85

RESULT 15
VE6 HPV16
ID VE6 HPV16 STANDARD; PRT; 158 AA.
AC P03126;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85246220; PubMed=2990099;
RA Seedorf K., Krammer G., Durst M., Suhai S., Rowekamp W.G.;
RT "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185(1985).
RN [2]
RP SEQUENCE OF 31-50 FROM N.A.
RX MEDLINE=90218027; PubMed=2157796;
RA Schneider-Maunoury S., Pehau-Arnauudet G., Breitburd F., Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-v cells,
RT a line derived from a vulvar intraepithelial neoplasia.";
RL J. Gen. Virol. 71:809-817(1990).
RN [3]
RP INTERACTION WITH FBLN1, AND INHIBITION OF E6-MEDIATED TRANSFORMATION.
RX MEDLINE=22188366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;
RA Du M., Fan X., Hong E., Chen J.J.;
RT "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";
RL Biochem. Biophys. Res. Commun. 296:962-969(2002).
CC -!- FUNCTION: This protein has transforming activity in vitro.
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double
CC stranded DNA (in vitro).
CC -!- SUBUNIT: Interacts with FBLN1.
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -!- MISCELLANEOUS: HPV16, in comparison to HPV types 6 and 11, is more
CC often associated with malignant genital cancers in humans.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).

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CC EMBL; K02718; AAA46939.1; -
DR EMBL; D00735; BAA00632.1; -
DR PIR; A03682; W6WLHS.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW DNA-binding; Early protein; Nuclear protein; Oncogene; Zinc-finger.
FT ZN FING 37 73
FT ZN FING 110 146
SQ SEQUENCE 158 AA; 19187 MW; 01FEF5ADCFDB37EB CRC64;

Query Match 100.0%; Score 57; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHVCYSLYG 9
| | | | |
DB 84 RHVCYSLYG 92

Search completed: June 28, 2005, 23:28:11
Job time : 55.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-50

Perfect score: 57

Sequence: 1 RHYCVSLXG 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	15	16	US-10-476-570-32
2	57	100.0	15	16	US-10-476-570-33
3	57	100.0	15	16	US-10-476-570-34
4	57	100.0	20	16	US-10-476-570-12
5	57	100.0	23	17	US-10-751-845-66
6	57	100.0	29	16	US-10-476-570-55
7	57	100.0	29	17	US-10-858-384-8
8	57	100.0	117	17	US-10-751-845-126
9	57	100.0	158	17	US-10-858-384-2
10	57	100.0	158	17	US-10-367-057-16
11	57	100.0	171	16	US-10-472-724-2

12	57	100.0	236	17	US-10-751-845-157	Sequence 157, App
13	57	100.0	237	17	US-10-751-845-158	Sequence 158, App
14	57	100.0	261	17	US-10-751-845-160	Sequence 160, App
15	57	100.0	266	9	US-09-367-309A-1	Sequence 1, Appli
16	57	100.0	273	13	US-10-000-903-4	Sequence 4, Appli
17	57	100.0	273	17	US-10-899-771-4	Sequence 4, Appli
18	57	100.0	292	13	US-10-000-903-10	Sequence 10, Appli
19	57	100.0	292	17	US-10-899-771-10	Sequence 10, Appli
20	57	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
21	57	100.0	371	17	US-10-899-771-6	Sequence 6, Appli
22	57	100.0	390	13	US-10-000-903-14	Sequence 14, Appli
23	57	100.0	390	17	US-10-899-771-14	Sequence 14, Appli
24	54	94.7	151	14	US-10-177-390-6	Sequence 6, Appli
25	54	94.7	151	17	US-10-484-063-20	Sequence 20, Appli
26	54	94.7	151	17	US-10-484-063-27	Sequence 27, Appli
27	52	91.2	9	17	US-10-751-845-88	Sequence 88, Appli
28	52	91.2	10	17	US-10-751-845-91	Sequence 91, Appli
29	51	89.5	10	17	US-10-751-845-93	Sequence 93, Appli
30	44	77.2	9	14	US-10-239-313A-313	Sequence 313, App
31	44	77.2	9	17	US-10-751-845-86	Sequence 86, Appli
32	44	77.2	10	17	US-10-751-845-80	Sequence 80, Appli
33	44	77.2	15	16	US-10-476-570-31	Sequence 31, Appli
34	42	73.7	10	17	US-10-751-845-79	Sequence 79, Appli
35	41	71.9	141	9	US-09-755-100-12	Sequence 12, Appli
36	41	71.9	141	15	US-10-298-965-12	Sequence 12, Appli
37	41	71.9	141	16	US-10-800-665-12	Sequence 12, Appli
38	40	70.2	10	17	US-10-751-845-75	Sequence 75, Appli
39	40	70.2	18	14	US-10-094-401-212	Sequence 212, App
40	40	70.2	18	15	US-10-462-262-180	Sequence 180, App
41	38	66.7	438	17	US-10-732-923-23922	Sequence 23922, A
42	38	66.7	1233	15	US-10-343-710-85	Sequence 85, Appli
43	38	66.7	1234	15	US-10-343-710-83	Sequence 83, Appli
44	38	66.7	1965	15	US-10-359-012-6	Sequence 6, Appli
45	37	64.9	9	17	US-10-751-845-85	Sequence 85, Appli

ALIGNMENTS

RESULT 1

US-10-476-570-32
; Sequence 32, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 78-92

Query Match 100.0%; Score 57; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 RHVCYSLYG 9
Db      7 RHVCYSLYG 15

RESULT 2
US-10-476-570-33
; Sequence 33, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 81-95
US-10-476-570-33

Query Match      100.0%; Score 57; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RHVCYSLYG 9
Db      4 RHVCYSLYG 12

RESULT 3
US-10-476-570-34
; Sequence 34, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 84-98
US-10-476-570-34

Query Match      100.0%; Score 57; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RHVCYSLYG 9
Db      4 RHVCYSLYG 12

RESULT 4
US-10-476-570-12
; Sequence 12, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 76-95
US-10-476-570-12

Query Match      100.0%; Score 57; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RHVCYSLYG 9
Db      9 RHVCYSLYG 17

RESULT 5
US-10-751-845-66
; Sequence 66, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman W.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/10/751,845
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-66
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```
US-10-751-845-66
Query Match      100.0%; Score 57; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYCYSLYG 9
Db 6 RHYCYSLYG 14

RESULT 6
US-10-476-570-55
; Sequence 55, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 29
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 80-108
US-10-476-570-55

Query Match      100.0%; Score 57; DB 16; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYCYSLYG 9
Db 5 RHYCYSLYG 13

RESULT 7
US-10-858-384-8
; Sequence 8, Application US/10858384
; Publication No. US2005003025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 29
; TYPE: PRT

US-10-751-845-126
; Sequence 126, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-126

Query Match      100.0%; Score 57; DB 17; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYCYSLYG 9
Db 50 RHYCYSLYG 58

RESULT 9
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US2005003025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
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; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match      100.0%; Score 57; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYCYSLYG 9
Db 84 RHYCYSLYG 92

RESULT 10
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match      100.0%; Score 57; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYCYSLYG 9
Db 84 RHYCYSLYG 92

RESULT 11
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match      100.0%; Score 57; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYCYSLYG 9
Db 89 RHYCYSLYG 97

RESULT 12
US-10-751-845-157
; Sequence 157, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiccz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-157

Query Match      100.0%; Score 57; DB 17; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYCYSLYG 9
Db 50 RHYCYSLYG 58

RESULT 13
US-10-751-845-158
; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiccz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-158

Query Match      100.0%; Score 57; DB 17; Length 237;
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Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 84 RHYCYSLYG 92
Search completed: June 29, 2005, 05:18:13
Job time : 116.15 secs

QY 1 RHYCYSLYG 9
Db 51 RHYCYSLYG 59

RESULT 14
US-10-751-845-160
; Sequence 160, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160

Query Match 100.0%; Score 57; DB 17; Length 261;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYCYSLYG 9
Db 75 RHYCYSLYG 83

RESULT 15
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 57; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYCYSLYG 9

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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-50
Perfect score: 57
Sequence: 1 RHYCYSLVG 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/ECTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	57	100.0	20	2	US-08-934-915-44
2	57	100.0	20	2	US-08-934-915-163
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4	57	100.0	158	4	US-09-980-523A-2
5	57	100.0	162	1	US-08-316-239B-3
6	57	100.0	172	3	US-08-860-165-12
7	57	100.0	172	3	US-08-860-165-14
8	57	100.0	172	3	US-09-359-382-12
9	57	100.0	172	3	US-09-359-382-14
10	57	100.0	182	1	US-08-117-083-10
11	57	100.0	266	3	US-08-860-165-10
12	57	100.0	266	3	US-09-359-382-10
13	57	100.0	266	4	US-09-367-309A-1
14	57	100.0	273	3	US-09-485-885-4
15	57	100.0	292	3	US-09-485-885-10
16	57	100.0	371	3	US-09-485-885-6
17	57	100.0	390	3	US-09-485-885-14
18	54	94.7	162	1	US-08-316-239B-4
19	52	91.2	11	3	US-08-159-339A-1171
20	48	84.2	9	3	US-08-159-339A-235
21	44	77.2	63	4	US-09-248-796A-24718
22	44	77.2	99	4	US-09-248-796A-21392
23	43	75.4	9	3	US-08-159-339A-251
24	41	71.9	141	4	US-09-755-100A-121
25	40	70.2	115	4	US-09-107-532A-6191
26	40	70.2	950	4	US-09-409-604-2
27	38	66.7	128	4	US-09-107-532A-4132

28	38	66.7	457	4	US-09-270-767-45501	Sequence 45501, A
29	38	66.7	2584	3	US-08-936-135-4	Sequence 4, Appli
30	38	66.7	2588	3	US-08-936-135-2	Sequence 2, Appli
31	37	64.9	9	3	US-08-159-339A-563	Sequence 563, App
32	37	64.9	295	4	US-09-893-737-324	Sequence 324, App
33	37	64.9	571	4	US-09-460-235B-13	Sequence 13, Appl
34	37	64.9	1380	4	US-09-949-016-11688	Sequence 11688, A
35	36	63.2	9	3	US-08-159-339A-76	Sequence 76, Appl
36	36	63.2	36	4	US-09-601-729-277	Sequence 277, App
37	36	63.2	194	4	US-09-543-681A-5029	Sequence 5029, Ap
38	36	63.2	245	4	US-08-469-260A-42	Sequence 42, Appl
39	36	63.2	245	4	US-08-488-446-42	Sequence 42, Appl
40	36	63.2	245	4	US-08-467-344A-42	Sequence 42, Appl
41	36	63.2	245	4	US-08-424-550B-42	Sequence 42, Appl
42	36	63.2	323	4	US-08-948-276-5	Sequence 5, Appli
43	36	63.2	323	4	US-09-949-016-6593	Sequence 6593, Ap
44	36	63.2	334	4	US-09-949-016-7952	Sequence 7952, Ap
45	36	63.2	374	4	US-09-442-349A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-934-915-44
; Sequence 44, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-44
Query Match 100.0%; Score 57; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0073;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYCYSLYG 9
Db 8 RHYCYSLYG 16

RESULT 2
US-08-934-915-163
; Sequence 163, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Fouch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-163

Query Match 100.0%; Score 57; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYCYSLYG 9
Db 8 RHYCYSLYG 16

RESULT 3
US-09-980-523A-8
; Sequence 8, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: WO/91/001513
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; TYPE: PRT
; LENGTH: 158
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 57; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYCYSLYG 9
Db 84 RHYCYSLYG 92

RESULT 4
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: WO/91/001513
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 158
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 57; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYCYSLYG 9
Db 84 RHYCYSLYG 92

RESULT 5
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; APPLICANT: CONNAN, FRANCINE
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
```

;; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
;; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSER: Jagtiani & Associates
;; STREET: 6126 Rocky Way Court
;; CITY: Centreville
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 20120-3400
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/316,239B
;; FILING DATE: 30-SEP-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jagtiani, Ajay A.
;; REGISTRATION NUMBER: 35,205
;; REFERENCE/DOCKET NUMBER: UNNE-0001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 817-9453
;; TELEFAX: (703) 803-9387
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 162 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: protein
;; HYPOTHEetical: NO
US-08-316-239B-3

Query Match 100.0%; Score 57; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYCYSLYG 9
DB 84 RHYCYSLYG 92

RESULT 6
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; FILE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; CURRENT APPLICATION NUMBER: US/08/860,165A
; EARLIER FILING DATE: 1997-09-22
; EARLIER FILING DATE: 1995-12-20
; EARLIER FILING DATE: 1995-12-20
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match 100.0%; Score 57; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYCYSLYG 9
DB 22 RHYCYSLYG 30

RESULT 7
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; FILE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; CURRENT APPLICATION NUMBER: US/08/860,165A
; EARLIER FILING DATE: 1997-09-22
; EARLIER FILING DATE: 1995-12-20
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match 100.0%; Score 57; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYCYSLYG 9
DB 153 RHYCYSLYG 161

RESULT 8
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; FILE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; CURRENT APPLICATION NUMBER: US/09/359,382
; EARLIER FILING DATE: 1999-07-23
; EARLIER FILING DATE: 1997-09-22
; EARLIER FILING DATE: 1995-12-20
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-09-359-382-12

Query Match 100.0%; Score 57; DB 3; Length 172;

Best Local Similarity 100.0%; Pred. No. 0.061; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 RHVCYSLYG 9
Db 22 RHVCYSLYG 30

RESULT 9
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match 100.0%; Score 57; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.061; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 RHVCYSLYG 9
Db 153 RHVCYSLYG 161

RESULT 10
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Bournnell, Michael E.
; APPLICANT: Ingalls, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.

; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-10

Query Match 100.0%; Score 57; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.065; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 RHVCYSLYG 9
Db 65 RHVCYSLYG 73

RESULT 11
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 57; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.094; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 RHVCYSLYG 9
Db 84 RHVCYSLYG 92

RESULT 12
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann

; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; PRIOR FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PNO157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 57; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYCYSLYG 9
Db 84 RHYCYSLYG 92
|||||

RESULT 13
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 57; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYCYSLYG 9
Db 84 RHYCYSLYG 92
|||||

RESULT 14
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885

; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 57; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYCYSLYG 9
Db 190 RHYCYSLYG 198
|||||

RESULT 15
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match 100.0%; Score 57; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYCYSLYG 9
Db 209 RHYCYSLYG 217
|||||

Search completed: June 28, 2005, 23:37:50
Job time : 18.05 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-5
Perfect score: 46
Sequence: 1 ELQTTIHDI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_eprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	46	100.0	138	Q919D2	Q919D2 human papil
3	46	100.0	143	Q919B6	Q919B6 human papil
4	46	100.0	143	Q919C4	Q919C4 human papil
5	46	100.0	151	Q12335	Q12335 human papil
6	46	100.0	151	Q12336	Q12336 human papil
7	46	100.0	151	Q76TS0	Q76TS0 human papil
8	46	100.0	151	Q778I6	Q778I6 human papil
9	46	100.0	151	Q77E16	Q77E16 human papil
10	46	100.0	151	Q77JC7	Q77JC7 human papil
11	46	100.0	151	Q77ZJ5	Q77ZJ5 human papil
12	46	100.0	151	Q80963	Q80963 human papil
13	46	100.0	151	Q80966	Q80966 human papil
14	46	100.0	151	Q89648	Q89648 human papil
15	46	100.0	151	Q89708	Q89708 human papil
16	46	100.0	151	Q89755	Q89755 human papil
17	46	100.0	151	Q89852	Q89852 human papil
18	46	100.0	151	Q89887	Q89887 human papil
19	46	100.0	151	Q89887	Q89887 human papil
20	46	100.0	151	Q89887	Q89887 human papil
21	46	100.0	151	Q89887	Q89887 human papil
22	46	100.0	151	Q89887	Q89887 human papil
23	46	100.0	151	Q89887	Q89887 human papil
24	46	100.0	151	Q89887	Q89887 human papil
25	46	100.0	151	Q89887	Q89887 human papil
26	46	100.0	151	Q89887	Q89887 human papil
27	46	100.0	158	1 V66 HPV16	P03126 human papil
28	46	100.0	158	1 V66 HPV16	Q89887 human papil
29	46	100.0	158	2 Q80H08	Q80H08 human papil
30	46	100.0	158	2 Q80H08	Q80H08 human papil
31	46	100.0	158	2 Q80H08	Q80H08 human papil

32 46 100.0 158 2 Q8QRD6 Q8QRD6 human papil
33 46 100.0 158 2 Q8QRD7 Q8QRD7 human papil
34 46 100.0 158 2 Q8QRD8 Q8QRD8 human papil
35 46 100.0 158 2 Q71B17 Q71B17 human papil
36 46 100.0 158 2 Q9WH13 Q9WH13 human papil
37 46 100.0 161 2 Q919A9 Q919A9 human papil
38 46 100.0 161 2 Q919C6 Q919C6 human papil
39 44 95.7 248 2 Q9SL88 Q9SL88 equus cabal
40 44 95.7 248 2 Q9NOG1 Q9NOG1 equus cabal
41 42 91.3 151 2 Q89640 Q89640 human papil
42 42 91.3 151 2 Q8B564 Q8B564 human papil
43 42 91.3 158 2 Q8QHT0 Q8QHT0 human papil
44 42 91.3 158 2 Q8QRD9 Q8QRD9 human papil
45 42 91.3 158 2 Q8QRE0 Q8QRE0 human papil

ALIGNMENTS

RESULT 1
Q81956 PRELIMINARY; PRT; 26 AA.
AC Q81956;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6E7 (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SIHA;
RA Shippy R., Siwkowski A., Hampel A.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59900; AA03505.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER
SQ SEQUENCE 26 AA; 3208 MW; F06EBE995EB67D5 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELQTTIHDI 9
|||
Db 1 ELQTTIHDI 9

RESULT 2
Q919D2 PRELIMINARY; PRT; 138 AA.
ID Q919D2
AC Q919D2;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart V.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
Int. J. Cancer 97:868-874(2002)."
DR EMBL; AF404694; AAL01345.1; -.

```
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;
Query Match 100.0%; Score 46; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.25; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 ELQTTIHDI 9
Db 5 ELQTTIHDI 13

RESULT 3
ID Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cosart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874 (2002).
DR EMBL; AF404702; AAL01361.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;
Query Match 100.0%; Score 46; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.26; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 ELQTTIHDI 9
Db 10 ELQTTIHDI 18

RESULT 4
ID Q919C4 PRELIMINARY; PRT; 143 AA.
AC Q919C4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cosart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874 (2002).
DR EMBL; AF404698; AAL01353.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
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FT NON_TER 1
SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;
Query Match 100.0%; Score 46; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.26; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 ELQTTIHDI 9
Db 10 ELQTTIHDI 18

RESULT 5
ID O12335 PRELIMINARY; PRT; 151 AA.
AC O12335;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208 (1997).
DR EMBL; AF003015; AAB70732.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC8B8 CRC64;
Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.28; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 ELQTTIHDI 9
Db 18 ELQTTIHDI 26

RESULT 6
ID O12336 PRELIMINARY; PRT; 151 AA.
AC O12336;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208 (1997).
DR EMBL; AF003016; AAB70733.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
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SQ SEQUENCE 151 AA; 18206 MW; 51C12A9B149C6D8A CRC64;
Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELQTTIHD 9
Db 18 ELQTTIHD 26

RESULT 7
Q76TSO PRELIMINARY; PRT; 151 AA.
AC Q76TSO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT E2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34114; AAA91661.1; -
DR EMBL; U34125; AAA91672.1; -
DR EMBL; U34130; AAA91677.1; -
DR EMBL; U34131; AAA91678.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELQTTIHD 9
Db 18 ELQTTIHD 26

RESULT 8
Q778I6 PRELIMINARY; PRT; 151 AA.
AC Q778I6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT
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RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388056; CAB45104.1; -
DR EMBL; AJ388061; CAB45114.1; -
DR EMBL; AJ388066; CAB45124.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELQTTIHD 9
Db 18 ELQTTIHD 26

RESULT 9
Q77E16 PRELIMINARY; PRT; 151 AA.
AC Q77E16;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 oncoprotein (E6 protein).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AF469197; AAO15691.1; -
DR EMBL; AJ388063; CAB45118.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELQTTIHD 9
Db 18 ELQTTIHD 26

RESULT 10
Q77JC7 PRELIMINARY; PRT; 151 AA.
AC Q77JC7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6 variant (Transforming protein E6).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;

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RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Xinjiang;
 RA Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang F.;
 RT "Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma
 RT Biopsies in Xinjiang";
 RL Sheng Wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan 0:0-0(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
 RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis";
 RL J. Gen. Virol. 81:317-325(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22242222; PubMed=12355268; DOI=10.1007/s00239-002-2344-y;
 RA Defilippis V.R., Ayala F.J., Villarreal L.P.;
 RT "Evidence of diversifying selection in human papillomavirus type 16 E6
 RT but not E7 oncogenes";
 RL J. Mol. Evol. 55:491-499(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Cruz Mr., Cercueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
 RA Martins C.R.F.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Cruz M.R., Martins C.R.F.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF327851; AAG45940.1; -;
 DR EMBL; AJ388057; CAB45106.1; -;
 DR EMBL; AJ388069; CAB45130.1; -;
 DR EMBL; AY089951; AAM11875.1; -;
 DR EMBL; AY089954; AAM11881.1; -;
 DR EMBL; AY112663; AAM51854.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18320 MW; 617D2A2FDB4F8C17 CRC64;
 Query Match 100.0%; Score 46; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.28; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELQTTIHDI 9
 DB 18 ELQTTIHDI 26
 RESULT 11
 Q77ZJ5 PRELIMINARY; PRT; 151 AA.
 AC Q77ZJ5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Girardo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus
 RT type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 DR EMBL; AF003019; AAB70736.1; -;

DR EMBL; AF003018; AAB70735.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18221 MW; 60CD2A34DAF48CB7 CRC64;
 Query Match 100.0%; Score 46; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.28; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELQTTIHDI 9
 DB 18 ELQTTIHDI 26
 RESULT 12
 Q80963 PRELIMINARY; PRT; 151 AA.
 ID Q80963;
 AC Q80963;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Early transforming protein E6.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96079021; PubMed=7494284;
 RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
 RA Jenison S.A.;
 RT "Human papillomavirus type 16 variant lineages in United States
 RT populations characterized by nucleotide sequence analysis of the E6,
 RT L2, and L1 coding segments.";
 RL J. Virol. 69:7743-7753(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Farmer A.D.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U34122; AAA91669.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18291 MW; 97C7028D5169382D CRC64;
 Query Match 100.0%; Score 46; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.28; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELQTTIHDI 9
 DB 18 ELQTTIHDI 26
 RESULT 13
 Q80966 PRELIMINARY; PRT; 151 AA.
 ID Q80966;
 AC Q80966; O12650; O12651; O12652; O12925; O12926; O12927; Q80962;
 AC Q80964; Q80965;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;

RA Torneello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Girardo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Terai M., Ma Z., Burk R.D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
RN [2]
DR EMBL; AF003014; AAB70731.1; -;
DR EMBL; AF003017; AAB70734.1; -;
DR EMBL; AF472508; AAO15697.1; -;
DR EMBL; AJ388068; CAB45128.1; -;
DR EMBL; AF003013; AAB70730.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;
Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELQTTIHDI 9
Db 18 ELQTTIHDI 26
RESULT 14
Q89648 PRELIMINARY; PRT; 151 AA.
ID Q89648; O12653; O12654; O12928; O12929;
AC Q89648; O12653; O12654; O12928; O12929;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34128; AAA91675.1; -;
DR EMBL; U34117; AAA91664.1; -;
DR EMBL; U34116; AAA91665.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBAGCF1F CRC64;
Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELQTTIHDI 9
Db 18 ELQTTIHDI 26
Search completed: June 28, 2005, 19:19:21
Job time : 56.3 secs

Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELQTTIHDI 9
Db 18 ELQTTIHDI 26
RESULT 15
Q89708 PRELIMINARY; PRT; 151 AA.
ID Q89708
AC Q89708
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34128; AAA91675.1; -;
DR EMBL; U34117; AAA91664.1; -;
DR EMBL; U34116; AAA91665.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBAGCF1F CRC64;
Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELQTTIHDI 9
Db 18 ELQTTIHDI 26
Search completed: June 28, 2005, 19:19:21
Job time : 56.3 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 Seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-5
Perfect score: 46
Sequence: 1 ELQTTIHDI 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	46	100.0	158	1	W6WLHS	protein E6 - human
2	42	91.3	248	1	LNDGPS	pulmonary surfactant
3	36	78.3	377	2	T12042	cysteine proteinase
4	35	76.1	132	2	G84274	hypothetical prote
5	35	76.1	175	2	F82262	polysaccharide exp
6	35	76.1	248	1	LNHUP1	pulmonary surfacta
7	35	76.1	248	1	LNHUPS	pulmonary surfacta
8	35	76.1	248	1	LNHUP6	pulmonary surfacta
9	35	76.1	248	2	I51921	pulmonary surfacta
10	35	76.1	394	2	H82168	cytochrome c-type
11	34	73.9	252	2	A28445	tropomyosin, cytos
12	34	73.9	383	2	D89975	conserved hypothet
13	34	73.9	438	2	T51395	hypothetical prote
14	34	73.9	470	2	T49278	hypothetical prote
15	34	73.9	588	2	I37202	B-CAM protein - hu
16	34	73.9	617	2	T15104	hypothetical prote
17	34	73.9	628	2	I38000	Lutheran blood gro
18	34	73.9	795	2	D83149	probable two-compo
19	34	73.9	1894	2	JC4980	plexin 1 precursor
20	34	73.9	1905	2	I51553	Plexin - African c
21	33	71.7	32	2	S19906	E6-II protein - hu
22	33	71.7	35	2	S19909	E6-III protein - h
23	33	71.7	47	2	S23825	E6-I protein - hum
24	33	71.7	149	1	W6WL33	E6 protein - human
25	33	71.7	158	1	W6WLPR	E6 protein - human
26	33	71.7	212	2	B47698	hemagglutinin hag2
27	33	71.7	233	2	D59614	purine nucleoside
28	33	71.7	247	1	LNRRBS	pulmonary surfacta
29	33	71.7	341	2	B89798	hypothetical prote

30	33	71.7	455	2	C84133	glutamine syntheta
31	33	71.7	1015	2	C84918	probable ATP-depen
32	33	71.7	1132	2	T00259	hypothetical prote
33	33	71.7	1215	2	S60904	hypothetical prote
34	33	71.7	1317	2	F83310	conserved hypothet
35	33	71.7	1784	2	A49420	tuberos sclerosi
36	33	71.7	1809	2	S57329	tuberos sclerosi
37	33	71.7	1882	2	T00069	hypothetical prote
38	33	71.7	2331	2	T25410	hypothetical prote
39	32	69.6	259	2	T26298	hypothetical prote
40	32	69.6	379	2	T23392	hypothetical prote
41	32	69.6	381	2	H88028	protein P46F5.2 (l
42	32	69.6	422	2	T41888	IE-2 (IE-N) orf151
43	32	69.6	430	2	T37549	hypothetical prote
44	32	69.6	438	2	A70544	probable histidino
45	32	69.6	498	2	T03634	cytochrome P450 -

ALIGNMENTS

RESULT 1

W6WLHS
Protein E6 - human papillomavirus type 16
C:Species: human papillomavirus type 16
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A03682; T10427
R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; RoweKamp, W.G.
Virology 145, 181-185, 1985
A:Title: Human papillomavirus type 16 DNA sequence.
A:Reference number: A22355; MUID:85246220; PMID:2990099
A:Accession: A03682
A:Molecule type: DNA
A:Residues: 1-158 <SEE>
A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
J.Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A:Reference number: Z17014; MUID:91162763; PMID:1848319
A:Accession: T10427
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-158 <KEN>
A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
C:Genetics:
A:Gene: E6
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:37-73/Region: zinc finger CCCC motif
F:110-146/Region: zinc finger CCCC motif

Query Match 100.0% Score 46; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ELQTTIHDI 9
|||
Db 25 ELQTTIHDI 33

RESULT 2

LNDGPS
pulmonary surfactant protein A precursor - dog
N:Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated I
C:Species: Canis lupus familiaris (dog)
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
C:Accession: A25296; A61227; A60142
R:Benson, B.; Hawgood, S.; Schilling, J.; Clements, J.; Damm, D.; Cordell, B.; White, R.J.
Proc. Natl. Acad. Sci. U.S.A. 82, 6379-6383, 1985
A:Title: Structure of canine pulmonary surfactant apoprotein: cDNA and complete amino aci
A:Reference number: A25296; MUID:86016705; PMID:3863100
A:Accession: A25296
A:Molecule type: mRNA

A;Residues: 1-248 <BEN>
A;Note: the authors translated the codon TTG for residue 60 as Pro
R;Liau, D.F.; Ryan, S.F.
Chem. Phys. Lipids 59, 29-38, 1991
A;Title: Purification of surfactant protein A from dog lung by reconstitution with surfactant
A;Reference number: A61227; MUID:92163993; PMID:1790579
A;Accession: A61227
A;Molecule type: protein
A;Residues: 18-32 <LIA>
R;Ross, G.F.; Meuth, J.; Ohning, B.; Kim, Y.; Whitsett, J.A.
Biochim. Biophys. Acta 870, 267-278, 1986
A;Title: Purification of canine surfactant-associated glycoproteins A. Identification of
A;Reference number: A60142; MUID:86159848; PMID:3006781
A;Accession: A60142
A;Molecule type: protein
A;Residues: 24-34;95-101,'X',103-108 <ROS>
R;Patthy, L.
Nature 325, 490, 1987
A;Reference number: A93388; MUID:87115834; PMID:3808053
A;Contents: annotation; animal lectin domain homology
C;Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lowers surface tension. This protein is a sialoglycoprotein synthesized by alveolar type II cells. It is dependent on the presence of calcium ions.
C;Superfamily: mannose-binding lectin; C-type lectin homology
C;Keywords: alveolar proteinosis; calcium; disulfide bond; gaseous exchange; hydroxyproline
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-248/Product: pulmonary surfactant protein A #status experimental <MPT>
F;128-102/Region: collagen-like
F;127-246/Domain: C-type lectin homology <LCH>
F;20,207/Binding site: carboxydrate (Aen) (covalent) #status predicted
F;30/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 91.3%; Score 42; DB 1; Length 248;
Best Local Similarity 77.8%; Pred. No. 0.65;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIHD 9
|||:|:|:
DB 106 ELQTTIHD 114

RESULT 3
T12042
cysteine proteinase (EC 3.4.22.-) 4 precursor - kidney bean
C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12042
R;Senyuk, V.; Becker, C.; Muentz, K.
submitted to the EMBL Data Library, October 1997
A;Description: Isolation of cDNA clone encoding cysteine proteinase (CP4) from a cotyledon
A;Reference number: Z17388
A;Accession: T12042
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-377 <SEN>
A;Cross-references: UNIPROT:Q24324; EMBL:Z99955
A;Experimental source: cultivar Moldavian; cotyledon; clone cp4
C;Superfamily: papain
C;Keywords: cysteine proteinase; hydrolase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-137/Domain: propeptide #status predicted <PRO>
F;138-377/Product: cysteine proteinase 4 #status predicted <MAT>
F;162,305,332/Active site: Cys, His, Asn #status predicted

Query Match 78.3%; Score 36; DB 2; Length 377;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QTTIHD 9
|||:|:|:
DB 29 QTTVHD 35

A;Residues: 1-248 <BEN>
A;Note: the authors translated the codon TTG for residue 60 as Pro
R;Liau, D.F.; Ryan, S.F.
Chem. Phys. Lipids 59, 29-38, 1991
A;Title: Purification of surfactant protein A from dog lung by reconstitution with surfactant
A;Reference number: A61227; MUID:92163993; PMID:1790579
A;Accession: A61227
A;Molecule type: protein
A;Residues: 18-32 <LIA>
R;Ross, G.F.; Meuth, J.; Ohning, B.; Kim, Y.; Whitsett, J.A.
Biochim. Biophys. Acta 870, 267-278, 1986
A;Title: Purification of canine surfactant-associated glycoproteins A. Identification of
A;Reference number: A60142; MUID:86159848; PMID:3006781
A;Accession: A60142
A;Molecule type: protein
A;Residues: 24-34;95-101,'X',103-108 <ROS>
R;Patthy, L.
Nature 325, 490, 1987
A;Reference number: A93388; MUID:87115834; PMID:3808053
A;Contents: annotation; animal lectin domain homology
C;Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lowers surface tension. This protein is a sialoglycoprotein synthesized by alveolar type II cells. It is dependent on the presence of calcium ions.
C;Superfamily: mannose-binding lectin; C-type lectin homology
C;Keywords: alveolar proteinosis; calcium; disulfide bond; gaseous exchange; hydroxyproline
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-248/Product: pulmonary surfactant protein A #status experimental <MPT>
F;128-102/Region: collagen-like
F;127-246/Domain: C-type lectin homology <LCH>
F;20,207/Binding site: carboxydrate (Aen) (covalent) #status predicted
F;30/Modified site: 4-hydroxyproline (Pro) #status experimental

RESULT 4

G84274

hypochemical protein Vngl189h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: G84274

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: G84274

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-132 <STO>

A;Cross-references: UNIPROT:Q9HQF2; GB:AE004437; NID:g10580723; PIDN:AAG19563.1; GSPDB:G

C;Genetics:

A;Gene: VNG1189H

Query Match 76.1%; Score 35; DB 2; Length 132;

Best Local Similarity 66.7%; Pred. No. 8.4;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELQTTIHD 9

::|:|:|:|

DB 92 DVDTTIHD 100

::|:|:|:|

RESULT 5

F82262

polysaccharide export-related protein VC0936 [imported] - Vibrio cholerae (strain N16961

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: F82262

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.

L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: F82262

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-175 <HEI>

A;Cross-references: UNIPROT:Q9KTG6; GB:AE004176; GB:AE003852; NID:g9655385; PIDN:AAF9409

A;Experimental source: serogroup O1, strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC0936

A;Map position: 1

Query Match 76.1%; Score 35; DB 2; Length 175;

Best Local Similarity 75.0%; Pred. No. 12;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIHD 8

::|:|:|:|

DB 73 EVKTTIHD 80

::|:|:|:|

RESULT 6

LNHUP1

pulmonary surfactant protein A precursor (clone 1A) - human

N;Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated I

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999

C;Accession: B25720

R;Floros, J.; Steinbrink, R.; Jacobs, K.; Phelps, D.; Kriz, R.; Recny, M.; Sultzman, L.;

J. Biol. Chem. 261, 9029-9033, 1986

A;Title: Isolation and characterization of cDNA clones for the 35-kDa pulmonary surfactant

A;Reference number: A25720; MUID:86250832; PMID:3755136

Query Match 78.3%; Score 36; DB 2; Length 377;

Best Local Similarity 85.7%; Pred. No. 17;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QTTIHD 9

|||:|:|:

DB 29 QTTVHD 35

|||:|:|:

A:Accession: B25720
A:Molecule type: mRNA
A:Residues: 1-248 <FLO>
A:CROSS-references: GB:K03475
A:Note: part of the sequence was confirmed by protein sequencing
A:Note: the amino end of the mature protein, which was not identified, is partially acetylated
A:Note: clones corresponding to two different proteins were sequenced. Cotranslational maturation
C:Genetics:
A:Gene: GDB:SFTPAL; SFTPL; SP-A; SP-A1
A:CROSS-references: GDB:119593; OMIM:178630
A:Map position: 10q22-10q23
C:Superfamily: mannose-binding lectin; C-type lectin homology
C:Keywords: acetylated amino end; alveolar proteinosis; calcium; gaseous exchange; glycosylation
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-248/Product: pulmonary surfactant protein A #status predicted <MAT>
F:127-246/Domain: C-type lectin homology <LCH>
F:21/Modified site: acetylated amino end (Glu) (in mature form) #status predicted
F:30.33.36.42.54.57.63.76.79.82.91.97/Modified site: 4-hydroxyproline (Pro) #status predicted
F:207/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 76.1%; Score 35; DB 1; Length 248;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELQTTIHD 8
||| |||
Db 106 ELQATLHD 113

RESULT 7
LNHUPS
pulmonary surfactant protein A precursor (genomic clone) - human
N:Alternate names: alveolar proteinosis protein; pulmonary surfactant 32K apoprotein; pulmonary surfactant protein A
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C:Accession: A24622; A43628
R:White, R.T.; Damm, D.; Miller, J.; Spratt, K.; Schilling, J.; Hawgood, S.; Benson, B.; Nature 317, 361-363, 1985
A:Title: Isolation and characterization of the human pulmonary surfactant apoprotein gene
A:Reference number: A24622; MUID:86014366; PMID:2995821
A:Accession: A24622
A:Molecule type: DNA
A:Residues: 1-248 <WHI>
A:CROSS-references: GB:M30838; NID:gl90564; PIDN:AAA36510.1; PID:gl90565
A:Note: the sequence in GenBank entry HUMPSAP, release 109.0, (PID:gl90565) has the codon TGA at position 109, which codes for a stop codon.
A:Note: four nucleotide differences, producing amino acid differences at positions 45, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000

Query Match 76.1%; Score 35; DB 1; Length 248;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELQTTIHD 8
||| |||
Db 106 ELQATLHD 113

RESULT 8
LNHUPS
pulmonary surfactant protein A precursor (clone 6A) - human
N:Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated protein A
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: A25720
R:Floros, J.; Steinbrink, R.; Jacobs, K.; Phelps, D.; Kriz, R.; Recny, M.; Sultzman, L.; J. Biol. Chem. 261, 9029-9033, 1986
A:Title: Isolation and characterization of cDNA clones for the 35-kDa pulmonary surfactant protein A
A:Reference number: A25720; MUID:86250832; PMID:3755136
A:Accession: A25720
A:Molecule type: mRNA
A:Residues: 1-248 <FLO>
A:CROSS-references: UNIPROT:P07714; GB:M13686; NID:gl90669; PIDN:AAA60211.1; PID:gl90670
A:Note: part of the sequence was confirmed by protein sequencing
A:Note: the amino end of the mature protein, which was not identified, is partially acetylated
A:Note: clones corresponding to two different proteins were sequenced. Cotranslational maturation
C:Genetics:
A:Gene: GDB:SFTPAL; SFTPL; SP-A; SP-A1
A:CROSS-references: GDB:119593; OMIM:178630
A:Map position: 10q22-10q23
C:Superfamily: mannose-binding lectin; C-type lectin homology
C:Keywords: acetylated amino end; alveolar proteinosis; calcium; gaseous exchange; glycosylation
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-248/Product: pulmonary surfactant protein A #status predicted <MAT>
F:127-246/Domain: C-type lectin homology <LCH>
F:21/Modified site: acetylated amino end (Glu) (in mature form) #status predicted
F:30.33.36.42.54.57.63.76.79.82.91.97/Modified site: 4-hydroxyproline (Pro) #status predicted
F:207/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 76.1%; Score 35; DB 1; Length 248;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELQTTIHD 8
||| |||
Db 106 ELQATLHD 113

RESULT 9
LNHUPS
pulmonary surfactant-associated protein A1 - human
N:Alternate names: SP-A1
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C:Accession: I51921
R:Katyal, S.L.; Singh, G.; Locker, J.; Am. J. Respir. Cell Mol. Biol. 6, 446-452, 1992
A:Title: Characterization of a second human pulmonary surfactant-associated protein SP-A
A:Reference number: I51921; MUID:92198680; PMID:1372511
A:Accession: I51921
A:Molecule type: DNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-248 <RES>
A:CROSS-references: GB:M68519; NID:G338048; PIDN:AAA60319.1; PID:G338049
C:Genetics:
A:Gene: GDB:SFTPAL; SFTPL; SP-A; SP-A1
A:CROSS-references: GDB:119593; OMIM:178630
A:Map position: 10q22-10q23
A:Introns: 58/1, 98/1, 124/1
C:Superfamily: mannose-binding lectin; C-type lectin homology
F:127-246/Domain: C-type lectin homology <LCH>

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Query Match          76.1%; Score 35; DB 2; Length 248;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 ELQTTIHD 8
Db 106 ELQATLHD 113

RESULT 10
H82168
cytochrome c-type protein TorC VC1693 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 21-Jul-2003
C:Accession: H82168
R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: H82168
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-394 <HEI>
A:Cross-references: GB:AE004247; GB:AE003852; NID:g9656204; PIDN:AAF94843.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1693
A:Map position: 1
C:Superfamily: membrane-bound tetraheme cytochrome TorC/YecK; nirT homology

Query Match          76.1%; Score 35; DB 2; Length 394;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIH 7
Db 65 ELQTTIVH 71

RESULT 11
A28449
tropomyosin, cytoskeletal - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C:Accession: A28449
R:Hanke, P.D.; Lepinske, H.M.; Storti, R.V.
J. Biol. Chem. 262, 17370-17373, 1987
A:Title: Characterization of a Drosophila cDNA clone that encodes a 252-amino acid non-m
A:Reference number: A28449; MUID:88087013; PMID:3693358
A:Accession: A28449
A:Molecule type: mRNA
A:Residues: 1-252 <HAN>
A:Cross-references: GB:J03502; NID:gl58699; PIDN:AAA28972.1; PID:gl58700
A:Note: the authors translated the codon AAA for residue 136 as Leu and CTC for residue
C:Genetics:
A:Gene: FlyBase:Tm1
A:Cross-references: FlyBase:FBgn0003721
C:Superfamily: tropomyosin
C:Keywords: alternative splicing; coiled coil; muscle

Query Match          73.9%; Score 34; DB 2; Length 252;
Best Local Similarity 55.6%; Pred. No. 27;
Matches 5; Conservative 3; Mismatches 1; Indels 1; Gaps 0;

QY 1 ELQTTIHD 9
Db 241 EMEATLHD 249

RESULT 12
D89975

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conserved hypothetical protein SAL693 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D89975
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: D89975
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-383 <KUR>
A:Cross-references: UNIPROT:Q99704; GB:BA000018; PID:gl3701670; PIDN:BAR42963.1; GSPDB:GN
A:Experimental source: strain N315
C:Genetics:
A:Gene: SAL693

Query Match          73.9%; Score 34; DB 2; Length 383;
Best Local Similarity 66.7%; Pred. No. 43;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELQTTIHD 9
Db 237 EMKTIHDI 245

RESULT 13
T51395
hypothetical protein F14F8_40 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: T51395
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew
submitted to the Protein Sequence Database, August 2000
A:Reference number: 225394
A:Accession: T51395
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-438 <SAT>
A:Cross-references: UNIPROT:Q9LFW0; EMBL:AL391144
A:Experimental source: cultivar Columbia; BAC clone F14F8
C:Genetics:
A:Map position: 5
A:Introns: 382/3
A:Note: F14F8_40
C:Superfamily: Arabidopsis thaliana hypothetical protein At2g23160

Query Match          73.9%; Score 34; DB 2; Length 438;
Best Local Similarity 62.5%; Pred. No. 50;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIHD 8
Db 263 ELQSLHD 270

RESULT 14
T49278
hypothetical protein T21J18_90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T49278
R:Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Rudd, S.;
submitted to the Protein Sequence Database, April 2000
A:Reference number: 225021
A:Accession: T49278
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-470 <RIE>
A:Cross-references: UNIPROT:Q9M301; EMBL:AL132963; GSPDB:GN00061; ATSP:T21J18_90
A:Experimental source: cultivar Columbia; BAC clone T21J18

```

C:Genetics:
A:Gene: ATSP:T21J18.90
A:Map position: 3
A:Introns: 35/2; 71/3; 123/3; 157/2; 174/2; 238/3; 269/1; 290/3; 342/2; 369/3; 406/2

Query Match 73.9%; Score 34; DB 2; Length 470;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQTTIHD 9
Db 277 VKTTIHD 284

RESULT 15
I37202
B-CAM protein - human
C:Species: Homo sapiens (man)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: I37202; S47272
R:Campbell, I.G.; Foulkes, W.D.; Senger, G.; Trowsdale, J.; Garin-Chesa, P.; Rettig, W.J.
Cancer Res. 54, 5761-5765, 1994
A:Title: Molecular cloning of the B-CAM cell surface glycoprotein of epithelial cancers:
A:Reference number: I37202; MUID:95042297; PMID:7954395
A:Accession: I37202
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-588 <RES>
A:Cross-references: UNIPROT:P50895; EMBL:X80026; NID:G535178; PIDN:CAA56327.1; PID:G5351
C:Genetics:
A:Gene: B-CAM

Query Match 73.9%; Score 34; DB 2; Length 588;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELQTTIHD 8
Db 87 ELQTTIHD 94

Search completed: June 28, 2005, 19:23:18
Job time : 13.2 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 01:35:30 ; Search time 57.55 Seconds
(without alignments)
60.138 Million cell updates/sec

Title: US-08-170-344-5
Perfect score: 46
Sequence: 1 ELQTTIHDI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	46	100.0	10	17	US-10-484-063-2
2	46	100.0	15	16	US-10-476-570-21
3	46	100.0	15	16	US-10-476-570-22
4	46	100.0	21	16	US-10-476-570-8
5	46	100.0	30	16	US-10-476-570-53
6	46	100.0	30	17	US-10-858-384-4
7	46	100.0	32	16	US-10-476-570-9
8	46	100.0	33	16	US-10-476-570-19
9	46	100.0	151	14	US-10-177-390-6
10	46	100.0	151	17	US-10-484-063-20
11	46	100.0	151	17	US-10-484-063-27
					Sequence 2, Appli
					Sequence 21, Appl
					Sequence 22, Appl
					Sequence 8, Appli
					Sequence 53, Appl
					Sequence 4, Appli
					Sequence 9, Appli
					Sequence 19, Appl
					Sequence 6, Appli
					Sequence 20, Appl
					Sequence 27, Appl

12	46	100.0	158	17	US-10-858-384-2	Sequence 2, Appli
13	46	100.0	158	17	US-10-367-057-16	Sequence 16, Appl
14	46	100.0	171	16	US-10-472-724-2	Sequence 2, Appli
15	46	100.0	266	9	US-09-367-309A-1	Sequence 1, Appli
16	46	100.0	273	13	US-10-000-903-4	Sequence 4, Appli
17	46	100.0	273	17	US-10-899-771-4	Sequence 4, Appli
18	46	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
19	46	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
20	46	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
21	46	100.0	371	17	US-10-899-771-6	Sequence 6, Appli
22	46	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
23	46	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
24	46	100.0	536	15	US-10-367-095-10	Sequence 10, Appl
25	46	100.0	536	15	US-10-368-046-10	Sequence 10, Appl
26	46	100.0	536	16	US-10-367-367-10	Sequence 10, Appl
27	46	100.0	536	17	US-10-918-337-10	Sequence 10, Appl
28	41	89.1	9	9	US-09-909-460-102	Sequence 102, App
29	41	89.1	9	11	US-09-872-836-102	Sequence 102, App
30	41	89.1	9	14	US-10-133-210-279	Sequence 279, App
31	41	89.1	9	17	US-10-758-970-102	Sequence 102, App
32	41	89.1	9	17	US-10-751-845-56	Sequence 56, Appl
33	37	80.4	1198	15	US-10-452-024-95	Sequence 95, Appl
34	36	78.3	15	15	US-10-476-570-20	Sequence 20, Appl
35	36	78.3	151	16	US-10-425-115-237192	Sequence 237192, App
36	35	76.1	93	15	US-10-312-829-6	Sequence 6, Appli
37	35	76.1	145	9	US-09-925-302-845	Sequence 845, App
38	35	76.1	145	10	US-09-925-302-845	Sequence 845, App
39	35	76.1	148	15	US-10-312-829-5	Sequence 5, Appli
40	35	76.1	166	15	US-10-336-603A-98	Sequence 98, Appl
41	35	76.1	233	16	US-10-437-363-163049	Sequence 163049, App
42	35	76.1	243	15	US-10-336-603A-96	Sequence 96, Appl
43	35	76.1	248	15	US-10-312-829-4	Sequence 4, Appli
44	35	76.1	248	15	US-10-336-603A-100	Sequence 100, App
45	35	76.1	248	17	US-10-971-461-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-10-484-063-2
; Sequence 2, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: FOLLEN, MICHELE
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-2

Query Match 100.0%; Score 46; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELQTTIHDI 9
Db 1 ELQTTIHDI 9

```
RESULT 2
US-10-476-570-21
; Sequence 21, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 20-34
US-10-476-570-21

Query Match          100.0%; Score 46; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELQTTIHI 9
Db 6 ELQTTIHI 14

RESULT 3
US-10-476-570-22
; Sequence 22, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 24-38
US-10-476-570-22

Query Match          100.0%; Score 46; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELQTTIHI 9
Db 6 ELQTTIHI 14

RESULT 4
US-10-476-570-8
; Sequence 8, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-34
US-10-476-570-8

Query Match          100.0%; Score 46; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELQTTIHI 9
Db 12 ELQTTIHI 20

RESULT 5
US-10-476-570-53
; Sequence 53, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 30
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 15-44
US-10-476-570-53
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Qy 1 ELQTTIHI 9
Db 2 ELQTTIHI 10

RESULT 4
US-10-476-570-8
; Sequence 8, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-34
US-10-476-570-8

Query Match          100.0%; Score 46; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELQTTIHI 9
Db 12 ELQTTIHI 20

RESULT 5
US-10-476-570-53
; Sequence 53, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 30
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 15-44
US-10-476-570-53
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Query Match      100.0%; Score 46; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIHDI 9
Db 11 ELQTTIHDI 19

RESULT 6
US-10-858-384-4
; Sequence 4, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT-VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide, fragment
; OTHER INFORMATION: for E6 of HPV
US-10-858-384-4

Query Match      100.0%; Score 46; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIHDI 9
Db 11 ELQTTIHDI 19

RESULT 7
US-10-476-570-9
; Sequence 9, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: Papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match      100.0%; Score 46; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIHDI 9
Db 12 ELQTTIHDI 20

RESULT 9
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-45
US-10-476-570-9

Query Match      100.0%; Score 46; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIHDI 9
Db 12 ELQTTIHDI 20

RESULT 8
US-10-476-570-19
; Sequence 19, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-45
US-10-476-570-19

Query Match      100.0%; Score 46; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIHDI 9
Db 12 ELQTTIHDI 20

RESULT 9
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6
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Query Match 100.0%; Score 46; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.71; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELQTTIHI 9
Db 18 ELQTTIHI 26

RESULT 10
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match 100.0%; Score 46; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.71; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELQTTIHI 9
Db 18 ELQTTIHI 26

RESULT 11
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match 100.0%; Score 46; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.71; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELQTTIHI 9

Db 18 ELQTTIHI 26

RESULT 12
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; FILE REFERENCE: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 100.0%; Score 46; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.75; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELQTTIHI 9
Db 25 ELQTTIHI 33

RESULT 13
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 100.0%; Score 46; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.75; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELQTTIHI 9
Db 25 ELQTTIHI 33

RESULT 14
US-10-472-724-2

; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 100.0%; Score 46; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.82; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELQTTIHDI 9
|||
Db 30 ELQTTIHDI 38

RESULT 15

US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 46; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.3; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELQTTIHDI 9
|||
Db 25 ELQTTIHDI 33

Search completed: June 29, 2005, 03:24:06
Job time : 58.55 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)
39.174 Million cell updates/sec

Title: US-08-170-344-5
Perfect score: 46
Sequence: 1 ELQTTIHDI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/ECTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	100.0	14	1 US-07-909-122-3	Sequence 3, Appli
2	46	100.0	30	1 US-08-363-586-4	Sequence 4, Appli
3	46	100.0	30	1 US-09-980-523A-4	Sequence 4, Appli
4	46	100.0	158	4 US-09-980-523A-2	Sequence 2, Appli
5	46	100.0	162	1 US-08-316-239B-3	Sequence 3, Appli
6	46	100.0	162	1 US-08-316-239B-4	Sequence 4, Appli
7	46	100.0	172	3 US-08-860-185-14	Sequence 14, Appl
8	46	100.0	172	3 US-09-359-382-14	Sequence 14, Appl
9	46	100.0	182	1 US-08-117-083-10	Sequence 10, Appl
10	46	100.0	266	3 US-08-860-165-10	Sequence 10, Appl
11	46	100.0	266	3 US-09-359-382-10	Sequence 10, Appl
12	46	100.0	266	3 US-09-367-309A-1	Sequence 1, Appli
13	46	100.0	273	3 US-09-485-885-4	Sequence 4, Appli
14	46	100.0	292	3 US-09-485-885-10	Sequence 10, Appl
15	46	100.0	371	3 US-09-485-885-6	Sequence 6, Appli
16	46	100.0	390	3 US-09-485-885-14	Sequence 14, Appl
17	41	89.1	9	1 US-08-787-547-102	Sequence 102, App
18	41	89.1	9	3 US-08-159-339A-248	Sequence 248, App
19	41	89.1	20	2 US-08-934-915-159	Sequence 159, App
20	36	78.3	317	3 US-08-913-159-14	Sequence 14, Appl
21	35	76.1	248	4 US-09-600-932-28	Sequence 28, Appl
22	35	76.1	248	4 US-09-949-016-6612	Sequence 6612, Ap
23	35	76.1	251	4 US-09-949-016-8481	Sequence 8481, Ap
24	35	76.1	251	4 US-09-949-016-9058	Sequence 9058, Ap
25	35	76.1	259	4 US-09-949-016-9059	Sequence 9059, Ap
26	34	73.9	56	3 US-08-936-165A-297	Sequence 297, App
27	34	73.9	383	4 US-09-603-208A-62	Sequence 62, Appl

28	34	73.9	640	4	US-09-949-016-7565	Sequence 7565, Ap
29	34	73.9	695	4	US-09-248-796A-20895	Sequence 20895, A
30	34	73.9	811	4	US-09-252-991A-22216	Sequence 22216, A
31	33	71.7	59	1	US-08-118-270-256	Sequence 256, App
32	33	71.7	59	5	PCT-US93-08528-256	Sequence 256, App
33	33	71.7	166	4	US-09-270-767-33046	Sequence 33046, A
34	33	71.7	166	4	US-09-270-767-48263	Sequence 48263, A
35	33	71.7	198	3	US-09-134-001C-4050	Sequence 4050, Ap
36	33	71.7	500	4	US-09-354-123-6	Sequence 6, Appli
37	33	71.7	503	4	US-09-990-337-3	Sequence 3, Appli
38	33	71.7	738	4	US-09-543-681A-7528	Sequence 7528, Ap
39	33	71.7	933	4	US-09-248-796A-20513	Sequence 20513, A
40	33	71.7	1128	4	US-09-252-991A-31032	Sequence 31032, A
41	33	71.7	1769	4	US-09-949-016-8280	Sequence 8280, Ap
42	33	71.7	1769	4	US-09-949-016-8281	Sequence 8281, Ap
43	33	71.7	1769	4	US-09-949-016-8282	Sequence 8282, Ap
44	33	71.7	1784	3	US-09-040-738-2	Sequence 2, Appli
45	33	71.7	1784	3	US-08-652-426A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-07-909-122-3
; Sequence 3, Application US/07909122
; Patent No. 5415995
; GENERAL INFORMATION:
; APPLICANT: SCHOOLNIK, GARY K.
; APPLICANT: PALEFSKY, JOEL M.
; TITLE OF INVENTION: DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA
; TITLE OF INVENTION: VIRUS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/909,122
; FILING DATE: 19920706
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: BENZ, WILLIAM H.
; REGISTRATION NUMBER: 25,952
; REFERENCE/DOCKET NUMBER: 28600-20105.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-909-122-3

Query Match 100.0%; Score 46; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELQTTIHDI 9

Db 2 ELQTTIHDI 10

RESULT 2
US-08-363-586-4
; Sequence 4, Application US/08363586
; Patent No. 5629161
; GENERAL INFORMATION:
; APPLICANT: Mueller, Martin
; APPLICANT: Giesmann, Lutz
; TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
; TITLE OF INVENTION: Peptides for the Diagnostic Purpose
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Duner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,586
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/909,296
; FILING DATE: 09-JUL-1992
; APPLICATION NUMBER: EP 9111720.8
; FILING DATE: 13-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wadler, Linda A.
; REGISTRATION NUMBER: 33,218
; REFERENCE/DOCKET NUMBER: 02481-1195-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-363-586-4

Query Match 100.0%; Score 46; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIHDI 9
Db 18 ELQTTIHDI 26

RESULT 3
US-09-980-523A-4
; Sequence 4, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO91 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29

; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-4

Query Match 100.0%; Score 46; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIHDI 9
Db 11 ELQTTIHDI 19

RESULT 4
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO91 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 46; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIHDI 9
Db 25 ELQTTIHDI 33

RESULT 5
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court

; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNNE-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-316-239B-3

Query Match 100.0%; Score 46; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIHDI 9
DB 25 ELQTTIHDI 33

RESULT 6

US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; Distinguishing a Subset of HPV that is Associated with an
; Increased Risk of Developing Cervical Dysplasia and
; Cervical Cancer
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; Increased Risk of Developing Cervical Dysplasia and
; Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNNE-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453

; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-316-239B-4

Query Match 100.0%; Score 46; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIHDI 9
DB 25 ELQTTIHDI 33

RESULT 7

US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PNO157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
; US-08-860-165-14

Query Match 100.0%; Score 46; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIHDI 9
DB 94 ELQTTIHDI 102

RESULT 8

US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 01727/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20

; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match 100.0%; Score 46; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIHDI 9
DB 94 ELQTTIHDI 102

RESULT 9
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Bournnell, Michael E.
; APPLICANT: Inglie, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-10

Query Match 100.0%; Score 46; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIHDI 9

DB 26 ELQTTIHDI 34

RESULT 10
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 46; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIHDI 9
DB 25 ELQTTIHDI 33

RESULT 11
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 46; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELQTTIHDI 9


```
Db      25 ELQTTIHI 33

RESULT 12
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 46; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELQTTIHI 9
Db      25 ELQTTIHI 33

RESULT 13
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match      100.0%; Score 46; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELQTTIHI 9
Db      131 ELQTTIHI 139

RESULT 14
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match      100.0%; Score 46; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELQTTIHI 9
Db      131 ELQTTIHI 139

Search completed: June 28, 2005, 19:29:02
Job time : 18.15 secs
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-49
Perfect score: 56
Sequence: 1 ISEYRHYCY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	84	2 Q80882	Q80882 human papil
2	56	100.0	90	2 Q80883	Q80883 human papil
3	56	100.0	90	2 Q80884	Q80884 human papil
4	56	100.0	99	2 Q919B2	Q919B2 human papil
5	56	100.0	103	2 Q919D6	Q919D6 human papil
6	56	100.0	130	2 Q919B4	Q919B4 human papil
7	56	100.0	130	2 Q919B8	Q919B8 human papil
8	56	100.0	130	2 Q919C0	Q919C0 human papil
9	56	100.0	130	2 Q919C2	Q919C2 human papil
10	56	100.0	130	2 Q919C8	Q919C8 human papil
11	56	100.0	130	2 Q919D0	Q919D0 human papil
12	56	100.0	138	2 Q919D2	Q919D2 human papil
13	56	100.0	143	2 Q919B6	Q919B6 human papil
14	56	100.0	143	2 Q919C4	Q919C4 human papil
15	56	100.0	151	2 Q12335	O12335 human papil
16	56	100.0	151	2 Q12336	O12336 human papil
17	56	100.0	151	2 Q77816	Q77816 human papil
18	56	100.0	151	2 Q77JC7	Q77JC7 human papil
19	56	100.0	151	2 Q77ZJ5	Q77ZJ5 human papil
20	56	100.0	151	2 Q80963	Q80963 human papil
21	56	100.0	151	2 Q89640	Q89640 human papil
22	56	100.0	151	2 Q89648	Q89648 human papil
23	56	100.0	151	2 Q89755	Q89755 human papil
24	56	100.0	151	2 Q89852	Q89852 human papil
25	56	100.0	151	2 Q8B564	Q8B564 human papil
26	56	100.0	151	2 Q8BB19	Q8BB19 human papil
27	56	100.0	151	2 Q8BB20	Q8BB20 human papil
28	56	100.0	151	2 Q9W931	Q9W931 human papil
29	56	100.0	151	2 Q9WMP4	Q9WMP4 human papil
30	56	100.0	151	2 Q9WMP5	Q9WMP5 human papil
31	56	100.0	158	1 V66_HPV16	P03126 human papil

32 56 100.0 158 2 Q8QHP5 Q8qhp5 human papil
33 56 100.0 158 2 Q8QHT0 Q8qht0 human papil
34 56 100.0 158 2 Q8QRD6 Q8qrd6 human papil
35 56 100.0 158 2 Q8QRD7 Q8qrd7 human papil
36 56 100.0 158 2 Q8QRD8 Q8qrd8 human papil
37 56 100.0 158 2 Q8QRD9 Q8qrd9 human papil
38 56 100.0 158 2 Q8QRE0 Q8qre0 human papil
39 56 100.0 158 2 Q8QRE1 Q8qre1 human papil
40 56 100.0 158 2 Q71BI7 Q71bi7 human papil
41 56 100.0 158 2 Q9QDH3 Q9qdh3 human papil
42 56 100.0 158 2 Q9QDH5 Q9qdh5 human papil
43 56 100.0 158 2 Q9QDH7 Q9qdh7 human papil
44 56 100.0 158 2 Q9QDH9 Q9qdh9 human papil
45 56 100.0 158 2 Q9WH13 Q9wh13 human papil

ALIGNMENTS

RESULT 1
Q80882 PRELIMINARY; PRT; 84 AA.
AC Q80882;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical;
RA Haggert D.G., Galuira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14511; AAB60565.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 84
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;
Query Match 100.0%; Score 56; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
Qy 1 ISEYRHYCY 9
Db 29 ISEYRHYCY 37
RESULT 2
Q80883 PRELIMINARY; PRT; 90 AA.
AC Q80883;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haggert D.G., Galuira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14512; AAB60566.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

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DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10904 MW; 5D3ADF843AD6060B CRC64;

Query Match
Best Local Similarity 100.0%; Score 56; DB 2; Length 90;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEYRHYCY 9
Db 32 ISEYRHYCY 40

RESULT 3
Q80884
ID Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AA60567.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFAACCC01 CRC64;

Query Match
Best Local Similarity 100.0%; Score 56; DB 2; Length 90;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEYRHYCY 9
Db 32 ISEYRHYCY 40

RESULT 4
Q919B2
ID Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404704; AAL01365.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR GO:0003677; F:DNA binding; IEA.

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DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;

Query Match
Best Local Similarity 100.0%; Score 56; DB 2; Length 99;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEYRHYCY 9
Db 49 ISEYRHYCY 57

RESULT 5
Q919D6
ID Q919D6 PRELIMINARY; PRT; 103 AA.
AC Q919D6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404692; AAL01342.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 103
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;

Query Match
Best Local Similarity 100.0%; Score 56; DB 2; Length 103;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEYRHYCY 9
Db 25 ISEYRHYCY 33

RESULT 6
Q919B4
ID Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01363.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1

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SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EBDDC CRC64;
Query Match 100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEYRHXYC 9
DB 52 ISEYRHXYC 60

RESULT 7
Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01357.1;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match 100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEYRHXYC 9
DB 52 ISEYRHXYC 60

RESULT 8
Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEYRHXYC 9
DB 52 ISEYRHXYC 60

RESULT 9
Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01355.1;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEYRHXYC 9
DB 52 ISEYRHXYC 60

RESULT 10
Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404696; AAL01349.1;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ISEYRHYCY 9
 |||||
 Db 52 ISEYRHYCY 60

RESULT 11

Q919D0 PRELIMINARY; PRT; 130 AA.
 AC Q919D0; (Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404694; AAL01347.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15735 MW; 9EFB30BEDCA21AF3 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

QY 1 ISEYRHYCY 9
 |||||
 Db 52 ISEYRHYCY 60

RESULT 12

Q919D2 PRELIMINARY; PRT; 138 AA.
 AC Q919D2; (Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404694; AAL01345.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 138;

Best Local Similarity 100.0%; Pred. No. 0.16; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

QY 1 ISEYRHYCY 9
 |||||
 Db 60 ISEYRHYCY 68

RESULT 13

Q919B6 PRELIMINARY; PRT; 143 AA.
 AC Q919B6; (Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404702; AAL01361.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match 100.0%; Score 56; DB 2; Length 143;

Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

QY 1 ISEYRHYCY 9

|||||

Db 65 ISEYRHYCY 73

RESULT 14

Q919C4 PRELIMINARY; PRT; 143 AA.
 AC Q919C4; (Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404698; AAL01353.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 143;

Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

QY 1 ISEYRHYCY 9

|||||

Db 65 ISEYRHYCY 73

RESULT 15

O12335
ID O12335 PRELIMINARY; PRT; 151 AA.
AC O12335;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003015; AAB70732.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;

Query Match 100.0%; Score 56; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISEYRHVCY 9
Db 73 ISEYRHVCY 81

Search completed: June 28, 2005, 23:28:11
Job time : 55.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)
78.367 Million cell updates/sec

Title: US-08-170-344-49
Perfect score: 56
Sequence: 1 ISEYRHVCY 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	56	100.0	158	1 W6WLS	protein E6 - human
2	44	78.6	148	2 A61237	E6 protein - human
3	44	78.6	148	2 S36573	E6 protein - human
4	44	78.6	149	1 W6WLS3	E6 protein - human
5	44	78.6	149	1 W6WLS8	E6 protein - human
6	42	75.0	68	2 T17702	hypothetical prote
7	41	73.2	294	2 A40993	H+/K+-exchanging A
8	41	73.2	370	2 E42951	long-chain-fatty-a
9	40	71.4	275	2 T32010	hypothetical prote
10	40	71.4	291	2 A36051	H+/K+-exchanging A
11	40	71.4	777	2 T25761	hypothetical prote
12	40	71.4	1541	2 T02831	AAA protein L4171.
13	38	67.9	285	2 E70151	chemotaxis protein
14	38	67.9	3655	2 T38084	TRAP-like protein
15	37	66.1	155	1 W6WLS4	E6 protein - human
16	37	66.1	430	2 D83977	hypothetical prote
17	36	64.3	115	2 T31781	hypothetical prote
18	36	64.3	146	2 S42570	flavodoxin - Desul
19	36	64.3	211	2 B82901	hypothetical prote
20	36	64.3	335	2 JH0813	GTP-binding regula
21	36	64.3	376	2 S27015	GTP-binding regula
22	36	64.3	377	1 RGN5A1	GTP-binding regula
23	36	64.3	379	1 RGXLA	GTP-binding regula
24	36	64.3	379	2 A42964	guanine nucleotide
25	36	64.3	380	1 RGHUA1	GTP-binding regula
26	36	64.3	394	1 RGHYAE	GTP-binding regula
27	36	64.3	394	1 RGN5A2	GTP-binding regula
28	36	64.3	394	1 RBOGA	GTP-binding regula
29	36	64.3	394	1 RGHYA2	GTP-binding regula

30	36	64.3	394	1	RGRTA2	GTP-binding regula
31	36	64.3	394	2	S33458	GTP-binding regula
32	36	64.3	395	1	RGHUA2	GTP-binding regula
33	36	64.3	397	1	RGPGA2	GTP-binding regula
34	36	64.3	400	2	AE0508	hypothetical prote
35	36	64.3	419	2	S34421	GTP-binding regula
36	36	64.3	493	2	S72196	x-pro dipeptidase
37	36	64.3	551	2	B64005	hypothetical prote
38	36	64.3	846	2	S52418	GTP-binding regula
39	36	64.3	890	2	T21000	hypothetical prote
40	35	62.5	78	2	B71622	metal binding prote
41	35	62.5	177	2	A37408	betacellulin precu
42	35	62.5	178	2	JCI467	betacellulin precu
43	35	62.5	187	2	S32968	probable membrane
44	35	62.5	298	2	AC0838	probable transcrip
45	35	62.5	479	2	T01922	hypothetical prote

ALIGNMENTS

RESULT 1
W6WLS
protein E6 - human papillomavirus type 16
C:Species: human papillomavirus type 16
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A03682; T10427
R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A:Title: Human papillomavirus type 16 DNA sequence.
A:Reference number: A22355; MUID:85246220; PMID:2990099
A:Accession: A03682
A:Molecule type: DNA
A:Residues: 1-158 <SEE>
A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
R:Kennedy, I.M.; Haddock, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A:Reference number: Z17014; MUID:91162763; PMID:1848319
A:Accession: T10427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-158 <KEN>
A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
C:Genetics:
A:Gene: E6
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:37-73/Region: zinc finger CCCC motif
F:110-146/Region: zinc finger CCCC motif
Query Match 100.0%; Score 56; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ISEYRHVCY 9
|||
Db 80 ISEYRHVCY 88
RESULT 2
A61237
E6 protein - human papillomavirus type 52
C:Species: human papillomavirus type 52
C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996
C:Accession: A61237
R:Takami, Y.; Kondoh, G.; Saito, K.; Sudiro, T.M.; Sjahrurachman, A.; Warsa, U.
Int. J. Cancer 48, 516-522, 1991
A:Title: Cloning and characterization of human papillomavirus type 52 from cervical carci
A:Reference number: A61237; MUID:91258022; PMID:1646174
A:Accession: A61237
A:Status: preliminary
A:Molecule type: DNA

A;Residues: 1-148 <TAK>
C;Superfamily: papillomavirus E6 protein

Query Match 78.6%; Score 44; DB 2; Length 148;
Best Local Similarity 88.9%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISEYRHYCY 9
Db 73 ISEYRHYQY 81

RESULT 3

S36573

E6 protein - human papillomavirus type 52

C;Species: human papillomavirus type 52

A;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: S36573

R;Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A;Description: Primer-directed sequencing of human papillomavirus types.

A;Reference number: S36469

A;Accession: S36573

A;Molecule type: DNA

A;Residues: 1-148

A;Cross-references: UNIPROT:P36814; EMBL:X74481; NID:G397038; PIDN:CAAS2585.1; PID:G3970

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 78.6%; Score 44; DB 2; Length 148;

Best Local Similarity 88.9%; Pred. No. 2.3;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISEYRHYCY 9
Db 73 ISEYRHYQY 81

RESULT 4

W6WL33

E6 protein - human papillomavirus type 33

C;Species: human papillomavirus type 33

A;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004

C;Accession: A03683

R;Coile, S.T.; Strebeck, R.E.

J. Virol. 58, 991-995, 1986

A;Title: Genome organization and nucleotide sequence of human papillomavirus type 33, wh

A;Reference number: A93020; MUID:86200464; PMID:3009902

A;Accession: A03683

A;Molecule type: DNA

A;Residues: 1-149 <COL>

A;Cross-references: UNIPROT:P06427; GB:M12732; NID:G333049; PIDN:AAA46958.1; PID:G463177

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

F;30-66/Region: zinc finger CCCC motif

F;103-139/Region: zinc finger CCCC motif

Query Match 78.6%; Score 44; DB 1; Length 149;

Best Local Similarity 88.9%; Pred. No. 2.3;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISEYRHYCY 9
Db 73 ISEYRHYNY 81

RESULT 5

W6WL58

E6 protein - human papillomavirus type 58

C;Species: human papillomavirus type 58

A;Note: host Homo sapiens (man)

A;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C;Accession: E36779

R;Kirii, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
A;Title: Human papillomavirus type 58 DNA sequence.
A;Reference number: A36779; MUID:92024102; PMID:1656594
A;Accession: E36779
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-149 <KIR>
A;Cross-references: UNIPROT:P26555; GB:D90400; NID:G222386; PIDN:BAA31845.1; PID:G3337096
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 78.6%; Score 44; DB 1; Length 149;

Best Local Similarity 88.9%; Pred. No. 2.3;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISEYRHYCY 9
Db 73 ISEYRHYNY 81

RESULT 6

T17702

hypothetical protein a212R - Chlorella virus PBCV-1

C;Species: Chlorella virus PBCV-1

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T17702

R;Graves, M.V.; Van Etten, J.L.

submitted to the EMBL Data Library, May 1999

A;Reference number: Z18806

A;Accession: T17702

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: DNA

A;Residues: 1-68 <GRA>

A;Cross-references: UNIPROT:Q84532; EMBL:U42580; NID:G4028896; PIDN:AAC96580.1

A;Experimental source: specific host Chlorella strain NC64A

C;Genetics:

A;Note: a212R

Query Match 75.0%; Score 42; DB 2; Length 68;

Best Local Similarity 85.7%; Pred. No. 2.6;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYRHYCY 9
Db 62 EYRYCY 68

RESULT 7

A40993

H+/K+-exchanging ATPase (EC 3.6.3.10) beta chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 09-Jul-2004

C;Accession: A40993; A41777; I49512

R;Canfield, V.A.; Levenson, R.

Proc. Natl. Acad. Sci. U.S.A. 88, 8247-8251, 1991

A;Title: Structural organization and transcription of the mouse gastric H(+),K(+)-ATPase

A;Reference number: A40993; MUID:91376121; PMID:1654563

A;Accession: A40993

A;Molecule type: DNA

A;Residues: 1-294 <CAN>

A;Cross-references: UNIPROT:P50992; GB:M64688; NID:G192079; PIDN:AAA37269.1; PID:G192081

R;Morley, G.P.; Callaghan, J.M.; Rose, J.B.; Toh, B.H.; Gleeson, P.A.; van Driel, I.R.

J. Biol. Chem. 267, 1165-1174, 1992

A;Title: The mouse gastric H,K-ATPase beta subunit. Gene structure and co-ordinate expres

A;Reference number: A41777; MUID:92112757; PMID:1370459

A;Accession: A41777

A;Molecule type: DNA

A;Residues: 1-294 <MOR>

A;Cross-references: GB:M80251; NID:G192086; PIDN:AAA37270.1; PID:G192088

A;Experimental source: gastric mucosal parietal cells

A>Note: sequence extracted from NCBI backbone (NCBIN:76277, NCBIN:76281, NCBIN:76285, NC
 C:Genetics:
 A:Introns: 38/1; 81/1; 119/1; 185/3; 204/3; 241/3
 C:Superfamily: Na+/K+-exchanging ATPase beta-3 chain
 C:Keywords: hydrolase; membrane protein

Query Match 73.2%; Score 41; DB 2; Length 294;
 Best Local Similarity 55.6%; Pred. No. 13;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEYRHYCY 9
 ::|||::
 Db 14 MAEFRHYCW 22

RESULT 8
 E42951
 long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) luxE - Xenorhabdus lumine
 N:Alternate names: fatty acid reductase complex synthetase
 C:Species: Xenorhabdus luminescens
 C:Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: E42951; E38448; D35411; D37898
 R:Meighen, E.A.; Szittner, R.B.
 J. Bacteriol. 174, 5371-5381, 1992
 A:Title: Multiple repetitive elements and organization of the lux operons of luminescent
 A:Reference number: A42951; MUID:92355513; PMID:1644764
 A:Accession: E42951
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-370 <MEI>
 A:Cross-references: UNIPROT:Q56823; GB:M90092; NID:gl55411; PIDN:AA05359.1; PID:gl55416
 A:Experimental source: strain Hw
 A:Note: sequence extracted from NCBI backbone (NCBIN:110516, NCBITP:110525)
 R:Xi, L.; Cho, K.W.; Tu, S.C.
 J. Bacteriol. 173, 1399-1405, 1991
 A:Title: Cloning and nucleotide sequences of lux genes and characterization of luciferase
 A:Reference number: A38448; MUID:91139581; PMID:1995589
 A:Accession: E38448
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-27, 'CA', 30-116 <XTA>
 A:Cross-references: GB:M62917; GB:M38525; NID:gl55427; PIDN:AAA63567.1; PID:gl55432
 R:Johnston, T.C.; Rucker, E.B.; Cochrum, L.; Hruska, K.S.; Vandegriff, V.
 Biochem. Biophys. Res. Commun. 170, 407-415, 1990
 A:Title: The nucleotide sequence of the luxA and luxB genes of Xenorhabdus luminescens H
 A:Reference number: A35411; MUID:90343746; PMID:2383248
 A:Accession: D35411
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-27, 'CA', 30-37 <JOH>
 A:Cross-references: GB:M55977; NID:gl55422; PIDN:AAA27628.1; PID:gl55426
 R:Szittner, R.; Meighen, E.
 J. Biol. Chem. 265, 16581-16587, 1990
 A:Title: Nucleotide sequence, expression, and properties of luciferase coded by lux gene
 A:Reference number: A37898; MUID:90375532; PMID:2204626
 A:Accession: D37898
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-4 <SZI>
 A:Cross-references: GB:M57416; GB:J05625; NID:gl55417
 A:Note: this translation is not annotated in GenBank entry XENLUXAB, release 113.0
 C:Genetics:
 A:Gene: luxE
 C:Keywords: acid-thiol ligase
 F:360/Active site: Cys (covalent substrate-binding) #status predicted

Query Match 73.2%; Score 41; DB 2; Length 370;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYRHYC 8
 |||||
 Db 54 EYRHYC 59

RESULT 9

T32010
 hypothetical protein K10G6.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T32010
 R:Davidson, S.; Wohldmann, P.; Mullen, G.
 submitted to the EMBL Data Library, July 1997
 A:Description: The sequence of C. elegans cosmid K10G6.
 A:Reference number: 221111
 A:Accession: T32010
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-275 <DAV>
 A:Cross-references: UNIPROT:O16627; EMBL:AF016669; PIDN:AAB66097.1; GSPDB:GN00020; CESP:
 A:Experimental source: strain Bristol N2; clone K10G6
 C:Genetics:
 A:Gene: CESP:K10G6.2
 A:Map position: 2
 A:Introns: 22/1; 66/2; 102/3; 136/2; 208/1

Query Match 71.4%; Score 40; DB 2; Length 275;
 Best Local Similarity 62.5%; Pred. No. 18;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISEYRHYC 8
 ::|||::
 Db 62 VNYRHYC 69

RESULT 10

A36051
 H+/K+-exchanging ATPase (EC 3.6.3.10) beta chain - rabbit
 N:Alternate names: H+/K+-transporting ATPase beta chain
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 09-Jul-2004
 C:Accession: A36051
 R:Reuben, M.A.; Lasater, L.S.; Sachs, G.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6767-6771, 1990
 A:Title: Characterization of a beta subunit of the gastric H+/K+-transporting ATPase.
 A:Reference number: A36051; MUID:90370865; PMID:2168558
 A:Accession: A36051
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-291 <REU>
 A:Cross-references: UNIPROT:P18597; GB:M35544; NID:gl65031; PIDN:AAA31256.1; PID:gl65032
 A:Superfamily: Na+/K+-exchanging ATPase beta-3 chain
 C:Keywords: hydrolase; transmembrane protein

Query Match 71.4%; Score 40; DB 2; Length 291;
 Best Local Similarity 55.6%; Pred. No. 19;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISEYRHYCY 9
 :|||::
 Db 14 MEFRHYCW 22

RESULT 11

T25761
 hypothetical protein F45E4.10 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
 C:Accession: T25761
 R:Wilson, R.
 submitted to the EMBL Data Library, September 1996
 A:Description: The sequence of C. elegans cosmid F45E4.
 A:Reference number: 220082
 A:Accession: T25761
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A;Residues: 1-777 <WIL>
A;Cross-references: EMBL:U70852; PIDN:AAB09141.1; GSPDB:GN00022; CESP:F45E4.10
A;Experimental source: strain Bristol N2; clone F45E4
C;Genetics:
A;Gene: CESP:F45E4.10
A;Map position: 4
A;Introns: 14/3; 39/2; 165/3; 268/3; 292/3; 335/1; 374/3; 487/3; 546/2; 576/1; 673/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F45E4.10

Query Match 71.4%; Score 40; DB 2; Length 777;
Best Local Similarity 71.4%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYRHYCY 9
:|||||
DB 368 QYRHWY 374

RESULT 12
T02831
AAA protein L4171.3 [imported] - Leishmania major (strain Friedlin)
C;Species: Leishmania major
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: C81460; T02831
R;Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.;
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A;Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-c
A;Reference number: A81455; MUID:99178987; PMID:10077609
A;Accession: C81460
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1541 <PVL>
A;Cross-references: UNIPROT:O15837; GB:AE001274; NID:g3264850; PIDN:AAC24654.1; PID:g226
A;Experimental source: strain MHOM/IL/81/Friedlin
C;Genetics:
A;Gene: L4171.3
A;Map position: 1

Query Match 71.4%; Score 40; DB 2; Length 1541;
Best Local Similarity 71.4%; Pred. No. 76;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYRHYCY 9
:|||||
DB 1253 DHRHYCY 1259

RESULT 13
E70151
chemotaxis protein methyltransferase (cher-2) homolog - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: E70151
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kervage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: E70151
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-285 <KLE>
A;Cross-references: UNIPROT:O51375; GB:AE001146; GB:AE000783; NID:g2688312; PIDN:AAC6678
A;Experimental source: strain B31
C;Superfamily: protein-glutamate O-methyltransferase; protein-glutamate O-methyltransferase
F.2-254/Domain: protein-glutamate O-methyltransferase homology <PGM>

Query Match 67.9%; Score 38; DB 2; Length 285;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 EYRHYCY 9
:|||||
DB 167 EYRHYI 173

RESULT 14
T38084
TRAP-like protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38084
R;Gentles, S.; Odell, C.; Churchet, C.M.; Barrell, B.G.; Rajandream, M.A.; Waish, S.V.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z21768
A;Accession: T38084
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-3655 <GEN>
A;Cross-references: UNIPROT:Q10064; EMBL:Z68136; PIDN:CAA92239.1; GSPDB:GN00066; SPDB:SP7
A;Experimental source: strain 972h-; cosmid c1f5
C;Genetics:
A;Gene: SPDB:SPAC1F5.11c
A;Map position: 1
A;Introns: 22/1

Query Match 67.9%; Score 38; DB 2; Length 3655;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISEYRHYCY 9
:|||||
DB 1110 LSDFRHKY 1118

RESULT 15
W6WL43
E6 protein - human papillomavirus type 43
C;Species: human papillomavirus type 43
A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Accession: A34144
R;Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; Schmidt, B.J.; Temple, G.F.
J. Virol. 63, 2829-2834, 1989
A;Title: Cloning and partial DNA sequencing of two new human papillomavirus types associ
A;Reference number: A34144; MUID:89259065; PMID:2542593
A;Accession: A34144
A;Molecule type: DNA
A;Residues: 1-155 <LOB>
A;Cross-references: UNIPROT:P19709; GB:M27022; NID:g341596; PIDN:AAA63453.1; PID:g703247
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;31-67/Region: zinc finger CCCC motif
F;104-140/Region: zinc finger CCCC motif

Query Match 66.1%; Score 37; DB 1; Length 155;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISEYRHYCY 9
:|||||
DB 74 ISQYRHFY 82

Search completed: June 28, 2005, 23:32:05
Job time : 12.05 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-49

Perfect score: 56

Sequence: 1 ISEYRHYCY 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	56	100.0	9	17	US-10-751-845-70
2	56	100.0	10	17	US-10-751-845-75
3	56	100.0	10	17	US-10-751-845-76
4	56	100.0	15	16	US-10-476-570-31
5	56	100.0	15	16	US-10-476-570-32
6	56	100.0	20	16	US-10-476-570-12
7	56	100.0	23	17	US-10-751-845-66
8	56	100.0	29	16	US-10-476-570-55
9	56	100.0	29	17	US-10-858-384-8
10	56	100.0	117	17	US-10-751-845-126
11	56	100.0	151	14	US-10-177-390-6

12	56	100.0	151	17	US-10-484-063-20	Sequence 20, Appl
13	56	100.0	151	17	US-10-484-063-27	Sequence 27, Appl
14	56	100.0	158	17	US-10-858-384-2	Sequence 2, Appl
15	56	100.0	158	17	US-10-367-057-16	Sequence 16, Appl
16	56	100.0	171	16	US-10-472-724-2	Sequence 2, Appl
17	56	100.0	236	17	US-10-751-845-157	Sequence 157, App
18	56	100.0	237	17	US-10-751-845-158	Sequence 158, App
19	56	100.0	261	17	US-10-751-845-160	Sequence 160, App
20	56	100.0	266	9	US-09-367-309A-1	Sequence 1, Appl
21	56	100.0	273	13	US-10-000-903-4	Sequence 4, Appl
22	56	100.0	273	17	US-10-899-771-4	Sequence 4, Appl
23	56	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
24	56	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
25	56	100.0	371	13	US-10-000-903-6	Sequence 6, Appl
26	56	100.0	371	17	US-10-899-771-6	Sequence 6, Appl
27	56	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
28	56	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
29	52	92.9	10	17	US-10-751-845-80	Sequence 80, Appl
30	52	92.9	15	16	US-10-476-570-33	Sequence 33, Appl
31	49	87.5	9	17	US-10-751-845-78	Sequence 78, Appl
32	48	85.7	9	14	US-10-239-313A-313	Sequence 313, App
33	48	85.7	9	17	US-10-751-845-86	Sequence 86, Appl
34	48	85.7	10	17	US-10-751-845-93	Sequence 93, Appl
35	41	73.2	113	16	US-10-425-115-195167	Sequence 195167, Sequence 249267, Sequence 308652, Sequence 640, App
36	39	69.6	112	16	US-10-425-115-249267	Sequence 249267, Sequence 308652, Sequence 640, App
37	39	69.6	147	16	US-10-425-115-308652	Sequence 308652, Sequence 640, App
38	38	67.9	28	10	US-09-809-391-640	Sequence 640, App
39	38	67.9	28	10	US-09-882-171-640	Sequence 640, App
40	38	67.9	28	15	US-10-164-861-640	Sequence 640, App
41	38	67.9	180	16	US-10-408-765A-1288	Sequence 1288, App
42	38	67.9	198	13	US-10-001-054-40	Sequence 40, Appl
43	38	67.9	198	14	US-10-028-072-550	Sequence 550, App
44	38	67.9	198	14	US-10-140-808-550	Sequence 550, App
45	38	67.9	198	14	US-10-121-049-550	Sequence 550, App

ALIGNMENTS

RESULT 1
US-10-751-845-70
; Sequence 70, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiccz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751.845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-70

Query Match 100.0%; Score 56; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ISEYRHYCY 9

|||||||

Db 1 ISEYRHYCY 9

RESULT 2
 US-10-751-845-75
 ; Sequence 75, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiciz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 75
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Human Papilloma virus
 US-10-751-845-75

Query Match 100.0%; Score 56; DB 17; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISEYRHYCY 9
 |||||
 Db 1 ISEYRHYCY 9

RESULT 3
 US-10-751-845-76
 ; Sequence 76, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiciz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 76
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Human Papilloma virus
 US-10-751-845-76

Query Match 100.0%; Score 56; DB 17; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISEYRHYCY 9
 |||||
 Db 2 ISEYRHYCY 10

RESULT 4
 US-10-476-570-31

; Sequence 31, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 31
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 76-90
 US-10-476-570-31

Query Match 100.0%; Score 56; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISEYRHYCY 9
 |||||
 Db 5 ISEYRHYCY 13

RESULT 5
 US-10-476-570-32
 ; Sequence 32, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: POUVELLE-MORATILLE, Sandra
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 32
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 78-92
 US-10-476-570-32

Query Match 100.0%; Score 56; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISEYRHYCY 9
 |||||

Db 3 ISEYRHYCY 11

RESULT 6

US-10-476-570-12
; Sequence 12, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 76-95
US-10-476-570-12

Query Match 100.0%; Score 56; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.022; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 ISEYRHYCY 9

Db 5 ISEYRHYCY 13

RESULT 7

US-10-751-845-66
; Sequence 66, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-66

Query Match 100.0%; Score 56; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.025; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 ISEYRHYCY 9

Db 2 ISEYRHYCY 10

RESULT 8

US-10-476-570-55
; Sequence 55, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 29
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 80-108
US-10-476-570-55

Query Match 100.0%; Score 56; DB 16; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.031; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 ISEYRHYCY 9

Db 1 ISEYRHYCY 9

RESULT 9

US-10-858-384-8
; Sequence 8, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E6 of HPV
US-10-858-384-8

Query Match 100.0%; Score 56; DB 17; Length 29;

Best Local Similarity 100.0%; Pred. No. 0.031; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 ISEYRHYCY 9
| | | | |
Db 1 ISEYRHYCY 9

RESULT 10

US-10-751-845-126
; Sequence 126, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-126

Query Match 100.0%; Score 56; DB 17; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 ISEYRHYCY 9
| | | | |
Db 46 ISEYRHYCY 54

RESULT 11

US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match 100.0%; Score 56; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 ISEYRHYCY 9
| | | | |
Db 73 ISEYRHYCY 81

RESULT 12
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match 100.0%; Score 56; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 ISEYRHYCY 9
| | | | |
Db 73 ISEYRHYCY 81

RESULT 13

US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match 100.0%; Score 56; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 ISEYRHYCY 9
| | | | |
Db 73 ISEYRHYCY 81

RESULT 14

US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1


```
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE B6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match      100.0%; Score 56; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ISEYRHYCY 9
Db      80 ISEYRHYCY 88
|||||||

RESULT 15
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-359
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match      100.0%; Score 56; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ISEYRHYCY 9
Db      80 ISEYRHYCY 88
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Search completed: June 29, 2005, 05:18:13
Job time : 117.15 secs
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-49
Perfect score: 56
Sequence: 1 ISEYHICY 9

Scoring table: BLASUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	9	3	US-08-159-339A-76
2	56	100.0	9	4	US-09-601-723-277
3	56	100.0	20	2	US-08-934-915-44
4	56	100.0	20	2	US-08-934-915-163
5	56	100.0	29	4	US-09-980-523A-8
6	56	100.0	158	4	US-09-980-523A-2
7	56	100.0	162	1	US-08-316-239B-3
8	56	100.0	162	1	US-08-316-239B-4
9	56	100.0	172	3	US-08-860-165-12
10	56	100.0	172	3	US-08-860-165-14
11	56	100.0	172	3	US-09-359-382-12
12	56	100.0	172	3	US-09-359-382-14
13	56	100.0	182	1	US-08-117-083-10
14	56	100.0	266	3	US-08-860-165-10
15	56	100.0	266	3	US-09-359-382-10
16	56	100.0	266	4	US-09-367-309A-1
17	56	100.0	273	3	US-09-485-885-4
18	56	100.0	292	3	US-09-485-885-10
19	56	100.0	371	3	US-09-485-885-6
20	56	100.0	390	3	US-09-485-885-14
21	47	83.9	9	3	US-08-159-339A-134
22	41	73.2	370	4	US-09-454-071-6
23	40	71.4	9	3	US-08-159-339A-234
24	40	71.4	10	3	US-08-159-339A-75
25	39	69.6	9	3	US-08-159-339A-247
26	38	67.9	28	4	US-09-149-476-640
27	38	67.9	143	4	US-09-583-110-4238

28	37	66.1	124	4	US-09-270-767-33888	Sequence 33888, A
29	36	64.3	63	4	US-09-248-796A-24718	Sequence 24718, A
30	36	64.3	75	4	US-09-248-796A-22612	Sequence 22612, A
31	36	64.3	169	4	US-09-489-039A-13995	Sequence 13995, A
32	36	64.3	200	3	US-09-099-041A-11	Sequence 11, Appl
33	36	64.3	200	3	US-09-245-281-11	Sequence 11, Appl
34	36	64.3	200	4	US-09-207-359B-11	Sequence 11, Appl
35	36	64.3	200	4	US-09-340-620A-11	Sequence 11, Appl
36	36	64.3	200	4	US-09-865-364-11	Sequence 11, Appl
37	36	64.3	212	4	US-09-388-221B-20	Sequence 20, Appl
38	36	64.3	238	4	US-09-134-000C-3467	Sequence 3467, Ap
39	36	64.3	245	4	US-08-469-260A-42	Sequence 42, Appl
40	36	64.3	245	4	US-08-488-446-42	Sequence 42, Appl
41	36	64.3	245	4	US-08-467-344A-42	Sequence 42, Appl
42	36	64.3	245	4	US-08-424-550B-42	Sequence 42, Appl
43	36	64.3	320	4	US-10-014-269-30	Sequence 30, Appl
44	36	64.3	374	4	US-09-442-349A-4	Sequence 4, Appli
45	36	64.3	374	4	US-09-442-349A-64	Sequence 64, Appl

ALIGNMENTS

RESULT 1
US-08-159-339A-76
; Sequence 76, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-76

Query Match 100.0%; Score 56; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISEYRHYCY 9
|||||
Db 1 ISEYRHYCY 9

RESULT 2

US-09-601-729-277
; Sequence 277, Application US/09601729
; Patent No. 6683052
; GENERAL INFORMATION:
; APPLICANT: THIAM, KADER
; APPLICANT: AURIAULT, CLAUDE
; APPLICANT: GRAS-MASSE, HELENE
; APPLICANT: LOING, ESTELLE
; APPLICANT: VERWAERDE, CLAUDIE
; APPLICANT: GUILLET, JEAN GERARD
; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
; TITLE OF INVENTION: THEROF IN PHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: USB-97-AU-IN
; CURRENT APPLICATION NUMBER: US/09/601,729
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: PCT/FR99/00259
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 98 01439
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 277
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide

US-09-601-729-277

Query Match 100.0%; Score 56; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISEYRHYCY 9
|||||
Db 1 ISEYRHYCY 9

RESULT 3

US-08-934-915-44
; Sequence 44, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-44

Query Match 100.0%; Score 56; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISEYRHYCY 9
|||||
Db 4 ISEYRHYCY 12

RESULT 4

US-08-934-915-163
; Sequence 163, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800

; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-163

Query Match 100.0%; Score 56; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEYRHYCY 9
Db 4 ISEYRHYCY 12

RESULT 5

US-09-980-523A-8
; Sequence 8, Application US/09980523A
; Patent No. 6783763

GENERAL INFORMATION:

; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WOBI AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Human Papillomavirus

US-09-980-523A-8

Query Match 100.0%; Score 56; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEYRHYCY 9
Db 1 ISEYRHYCY 9

RESULT 6

US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763

GENERAL INFORMATION:

; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WOBI AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513

; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
; US-09-980-523A-2

Query Match 100.0%; Score 56; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEYRHYCY 9
Db 80 ISEYRHYCY 88

RESULT 7

US-08-316-239B-3

; Sequence 3, Application US/08316239B
; Patent No. 5679509

GENERAL INFORMATION:

; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400

COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316.239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-316-239B-3

Query Match 100.0%; Score 56; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEYRHYCY 9
Db 80 ISEYRHYCY 88

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RESULT 8
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 604557
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Colette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNNE-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4
Query Match 100.0%; Score 56; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISEYRHYCY 9
Db 80 ISEYRHYCY 88

RESULT 9
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
US-08-860-165-12
Query Match 100.0%; Score 56; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISEYRHYCY 9
Db 149 ISEYRHYCY 157

RESULT 10
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
US-08-860-165-14
Query Match 100.0%; Score 56; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISEYRHYCY 9
Db 18 ISEYRHYCY 26

RESULT 11
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12
Query Match 100.0%; Score 56; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISEYRHYCY 9
Db 18 ISEYRHYCY 26

RESULT 10
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
US-08-860-165-14
Query Match 100.0%; Score 56; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISEYRHYCY 9
Db 149 ISEYRHYCY 157

RESULT 11
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match      100.0%; Score 56; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ISEYRHVCY 9
DB      18 ISEYRHVCY 26

RESULT 12
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match      100.0%; Score 56; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ISEYRHVCY 9
DB      149 ISEYRHVCY 157

RESULT 13
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Bournell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58783
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note= "xaa refers to stop codon in
; the open reading frame."
US-08-117-083-10

Query Match      100.0%; Score 56; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ISEYRHVCY 9
DB      61 ISEYRHVCY 69

RESULT 14
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match      100.0%; Score 56; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ISEYRHVCY 9
DB      80 ISEYRHVCY 88
```

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RESULT 15
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10
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Query Match      100.0%; Score 56; DB 3; Length 266;
Best Local Similarity 100.0%; Pred.No. 0.098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 ISEYRHYCY 9
        |||||
Db      80 ISEYRHYCY 88
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Search completed: June 28, 2005, 23:37:49
Job time : 17.05 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-48
Perfect score: 47
Sequence: 1 KFYSKISEY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	81	2 Q80886	Q80886 human papil
2	47	100.0	84	2 Q80882	Q80882 human papil
3	47	100.0	90	2 Q80884	Q80884 human papil
4	47	100.0	90	2 Q80885	Q80885 human papil
5	47	100.0	91	2 Q80887	Q80887 human papil
6	47	100.0	99	2 Q91982	Q91982 human papil
7	47	100.0	103	2 Q919D6	Q919D6 human papil
8	47	100.0	130	2 Q919B4	Q919B4 human papil
9	47	100.0	130	2 Q919B8	Q919B8 human papil
10	47	100.0	130	2 Q919C0	Q919C0 human papil
11	47	100.0	130	2 Q919C2	Q919C2 human papil
12	47	100.0	130	2 Q919C8	Q919C8 human papil
13	47	100.0	130	2 Q919D0	Q919D0 human papil
14	47	100.0	138	2 Q919D2	Q919D2 human papil
15	47	100.0	143	2 Q919B6	Q919B6 human papil
16	47	100.0	143	2 Q919C4	Q919C4 human papil
17	47	100.0	149	1 VEG_HPV35	P27228 human papil
18	47	100.0	149	2 Q84298	Q84298 human papil
19	47	100.0	151	2 Q12335	Q12335 human papil
20	47	100.0	151	2 Q12336	Q12336 human papil
21	47	100.0	151	2 Q76TS0	Q76TS0 human papil
22	47	100.0	151	2 Q778I6	Q778I6 human papil
23	47	100.0	151	2 Q778I6	Q778I6 human papil
24	47	100.0	151	2 Q77JC7	Q77JC7 human papil
25	47	100.0	151	2 Q77ZJ5	Q77ZJ5 human papil
26	47	100.0	151	2 Q80963	Q80963 human papil
27	47	100.0	151	2 Q80966	Q80966 human papil
28	47	100.0	151	2 Q89640	Q89640 human papil
29	47	100.0	151	2 Q89648	Q89648 human papil
30	47	100.0	151	2 Q89708	Q89708 human papil
31	47	100.0	151	2 Q89755	Q89755 human papil

32 47 100.0 151 2 Q89852 human papil
33 47 100.0 151 2 Q89887 human papil
34 47 100.0 151 2 Q88564 human papil
35 47 100.0 151 2 Q88B19 human papil
36 47 100.0 151 2 Q88B20 human papil
37 47 100.0 151 2 Q88B21 human papil
38 47 100.0 151 2 Q88B21 human papil
39 47 100.0 151 2 Q9W8C3 human papil
40 47 100.0 151 2 Q9W931 human papil
41 47 100.0 151 2 Q9WMP2 human papil
42 47 100.0 151 2 Q9WMP3 human papil
43 47 100.0 151 2 Q9WMP4 human papil
44 47 100.0 151 2 Q9WMP5 human papil
45 47 100.0 158 1 VEG_HPV16 human papil
46 47 100.0 158 2 Q8JMU8 human papil

ALIGNMENTS

RESULT 1
Q80886 PRELIMINARY; PRT; 81 AA.
AC Q80886;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Hager D.G., Galutira D.F., Youngusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14515; AAB60569.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 81 81
SQ SEQUENCE 81 AA; 9784 MW; DD5FEDBC9F845B97 CRC64;

Query Match Similarity 100.0%; Score 47; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.2; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 KFYSKISEY 9
Db 27 KFYSKISEY 35
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RESULT 2
Q80882 PRELIMINARY; PRT; 84 AA.
AC Q80882;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical;
RA Hager D.G., Galutira D.F., Youngusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14511; AAB60565.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

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DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 84
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;
Query Match 100.0%; Score 47; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFYISKISEY 9
Db 24 KFYISKISEY 32

RESULT 3
Q08084 PRELIMINARY; PRT; 90 AA.
AC Q08084;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFACCC01 CRC64;
Query Match 100.0%; Score 47; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFYISKISEY 9
Db 27 KFYISKISEY 35

RESULT 4
Q08085 PRELIMINARY; PRT; 90 AA.
AC Q08085;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14514; AAB60568.2; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.

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```

FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10964 MW; BC2531643ACBA76C CRC64;
Query Match 100.0%; Score 47; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFYISKISEY 9
Db 27 KFYISKISEY 35

RESULT 5
Q08087 PRELIMINARY; PRT; 91 AA.
AC Q08087;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14516; AAB60570.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 11136 MW; 22PDF3EA185ACBA7 CRC64;
Query Match 100.0%; Score 47; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFYISKISEY 9
Db 27 KFYISKISEY 35

RESULT 6
Q019B2 PRELIMINARY; PRT; 99 AA.
AC Q019B2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
   Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404704; AAL01365.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 99

```

```

SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;
Query Match 100.0%; Score 47; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
DB 44 KFYISKISEY 52

RESULT 7
Q919D6 PRELIMINARY; PRT; 103 AA.
AC Q919D6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404692; AAL01342.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 103 AA; 12422 MW; 6P90CBAP1E25449B CRC64;

Query Match 100.0%; Score 47; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
DB 20 KFYISKISEY 28

RESULT 8
Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;

Query Match 100.0%; Score 47; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
DB 47 KFYISKISEY 55

RESULT 9
Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01359.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF968092F CRC64;

Query Match 100.0%; Score 47; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
DB 47 KFYISKISEY 55

RESULT 10
Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 KFYISKISEY 9
|||||

Db 47 KFYISKISEY 55

RESULT 11

Q919C2 ID Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2; 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01355.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
SQ

Query Match 100.0%; Score 47; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
|||||

Db 47 KFYISKISEY 55

RESULT 12

Q919C8 ID Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8; 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404696; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;
SQ

Query Match 100.0%; Score 47; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
|||||

Db 47 KFYISKISEY 55

RESULT 13

Q919D0 ID Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0; 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404695; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT SEQUENCE 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;
SQ

Query Match 100.0%; Score 47; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
|||||

Db 47 KFYISKISEY 55

RESULT 14

Q919D2 ID Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2; 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404694; AAL01345.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT SEQUENCE 138 AA; 16696 MW; 481ESAEA90895FC2 CRC64;
SQ

Query Match 100.0%; Score 47; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
|||||

Db 55 KFYISKISEY 63

RESULT 15

```
Q919B6
ID Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404702; AAL01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match 100.0%; Score 47; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFYSKISEY 9
Db 60 KFYSKISEY 68
```

Search completed: June 28, 2005, 23:28:11
Job time : 56.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)
78.367 Million cell updates/sec

Title: US-08-170-344-48

Perfect score: 47

Sequence: 1 KFYISKISEY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	149	1 W6WLJ35	E6 protein - human
2	47	100.0	158	1 W6WLHS	protein E6 - human
3	39	83.0	149	1 W6WLJ31	E6 protein - human
4	39	83.0	150	2 S36544	E6 protein - human
5	37	78.7	151	1 W6WL51	E6 protein - human
6	37	78.7	413	2 T12533	hypothetical prote
7	37	78.7	818	2 A59433	KIAA0672 protein l
8	36	76.6	148	2 A61237	E6 protein - human
9	36	76.6	148	2 S36573	E6 protein - human
10	36	76.6	149	1 W6WL33	E6 protein - human
11	36	76.6	260	2 B64367	hypothetical prote
12	36	76.6	480	2 S22701	mannosyltransferas
13	35	74.5	191	1 W6WLR1	E6 protein - rhesu
14	35	74.5	688	1 JCI469	beta-adrenergic-re
15	35	74.5	688	1 A39336	beta-adrenergic-re
16	35	74.5	688	1 I73628	interferon beta-1
17	34	72.3	186	1 IVHOBI	interferon beta-1
18	34	72.3	218	2 D72227	hypothetical prote
19	34	72.3	221	2 F75211	hypothetical prote
20	34	72.3	298	2 T22538	hypothetical prote
21	34	72.3	534	2 G89924	protein R02C2.1 li
22	34	72.3	548	2 B97026	probable Fe-S oxid
23	34	72.3	1234	2 C84465	hypothetical prote
24	33	70.2	120	2 D90546	proline dipeptidas
25	33	70.2	136	2 T40693	hypothetical prote
26	33	70.2	143	2 T33576	hypothetical prote
27	33	70.2	148	2 S36515	E6 protein - human
28	33	70.2	151	1 S66580	hypothetical prote
29	33	70.2	151	1 S66587	hypothetical prote

30	33	70.2	151	2 H90830	hypothetical prote
31	33	70.2	151	2 H90830	unknown protein en
32	33	70.2	218	2 H64230	hypothetical prote
33	33	70.2	251	2 T25121	hypothetical prote
34	33	70.2	254	2 T33575	hypothetical prote
35	33	70.2	290	2 G84930	H+-transporting tw
36	33	70.2	308	2 D89429	hypothetical prote
37	33	70.2	325	2 C95182	conserved hypotnet
38	33	70.2	325	2 F98049	conserved hypotnet
39	33	70.2	331	2 A99179	conserved hypotnet
40	33	70.2	350	2 A80277	probable phage pro
41	33	70.2	381	2 B97182	acyl-protein synth
42	33	70.2	400	2 H69009	hypothetical prote
43	33	70.2	572	2 T40856	probable nucleotid
44	33	70.2	727	2 T26096	hypothetical prote
45	33	70.2	846	2 T19179	hypothetical prote

ALIGNMENTS

RESULT 1

W6WLJ35

E6 protein - human papillomavirus type 35

C:Species: human papillomavirus type 35

A:Note: host Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: E40824; S36521

R:Marich, J.E.; Pontaler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.

R:Virology 186, 770-776, 1992

A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillon

A:Reference number: A40824; MUID:92124753; PMID:1310198

A:Accession: E40824

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-149 <MAR>

A:Cross-references: UNIPROT:P27228; GB:M74117; NID:g333050; PIDN:AAA46966.1; PID:g333051

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36521

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-149

A:Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52561.1; PID:g396998

A:Experimental source: strain 35H

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F;30-66/Region: zinc finger CCCC motif

F;103-139/Region: zinc finger CCCC motif

Query Match 100.0%; Score 47; DB 1; Length 149;

Best Local Similarity 100.0%; Pred. No. 0.073;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFYISKISEY 9

Db 68 KFYISKISEY 76

RESULT 2

W6WLHS

protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

R:Virology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A;Residues: 1-158 <SEE>
A;Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
R;Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A;Title: A negative element in the human papillomavirus type 16 genome acts at the level of transcriptional activation
A;Reference number: Z17014; MUID:91162763; PMID:1848319
A;Accession: T10427
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-158 <KEN>
A;Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
C;Genetics:
A;Gene: E6
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;77-73/Region: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 47; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.077; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0

Qy 1 KFYISKISEY 9
| | | | | | | |
Db 75 KFYISKISEY 83

RESULT 3
W6WL31
E6 protein - human papillomavirus type 31
C;Species: human papillomavirus type 31
A;Note: host Homo sapiens (man)
C;Accession: A32444
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
R;Goldsbrough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated virus
A;Reference number: A94398; MUID:89299478; PMID:2545036
A;Accession: A32444
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-149 <GOL>
A;Cross-references: UNIPROT:P17386; GB:J04353; NID:G333048; PIDN:AAA46950.1; PID:G459916
C;Comment: This protein may be involved in the oncogenic potential of this virus.
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 83.0%; Score 39; DB 1; Length 149;
Best Local Similarity 66.7%; Pred. No. 2.7; Indels 0; Gaps 0;
Matches 6; Conservative 3; Mismatches 0

Qy 1 KFYISKISEY 9
| | | | | | | |
Db 68 RPYSKVSEF 76

RESULT 4
S36544
E6 protein - human papillomavirus type 26
C;Species: human papillomavirus type 26
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36544
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36544
A;Molecule type: DNA
A;Residues: 1-150
A;Cross-references: UNIPROT:P36807; EMBL:X74472; NID:G396956; PIDN:CAA52530.1; PID:G396959
C;Superfamily: papillomavirus E6 protein

C;Keywords: early protein; zinc finger

Query Match 83.0%; Score 39; DB 2; Length 150;
Best Local Similarity 87.5%; Pred. No. 2.7; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 0

Qy 2 FYSKISEY 9
| | | | | | | |
Db 69 FYSKITEY 76

RESULT 5
W6WL51
E6 protein - human papillomavirus type 51
C;Species: human papillomavirus type 51
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: E40415
R;Lungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991
A;Title: Biologic properties and nucleotide sequence analysis of human papillomavirus type 51
A;Reference number: A40415; MUID:91303675; PMID:1649326
A;Accession: E40415
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-151 <LUN>
A;Cross-references: UNIPROT:P26554; GB:M62877
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 78.7%; Score 37; DB 1; Length 151;
Best Local Similarity 87.5%; Pred. No. 6.6; Indels 1; Gaps 0;
Matches 7; Conservative 0; Mismatches 1

Qy 2 FYSKISEY 9
| | | | | | | |
Db 69 FYSKIREY 76

RESULT 6
T12533
hypothetical protein DKFZp434B034.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12533
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z17524
A;Accession: T12533
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-413 <WAM>
A;Cross-references: UNIPROT:Q9Y4Q4; EMBL:AL096728
A;Experimental source: adult testis; clone DKFZp434B034
C;Genetics:
A;Note: DKFZp434B034.1

Query Match 78.7%; Score 37; DB 2; Length 413;
Best Local Similarity 77.8%; Pred. No. 18; Indels 1; Gaps 0;
Matches 7; Conservative 1; Mismatches 1

Qy 1 KFYISKISEY 9
| | | | | | | |
Db 28 KFLSKLSEY 36

RESULT 7
A59433
K1AA0672 protein [imported] - human
C;Species: Homo sapiens (man)
C;Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004

C:Accession: A59433
C:Species: human papillomavirus type 33
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
A:Title: Prediction of the coding sequences of unidentified human genes. X. The complete
A:Reference number: A59433; MUID:98403880; PMID:9734811
A:Accession: A59433
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-818 <ISH>
A:Cross-references: UNIPROT:O75160; GB:NP_055674; PID:g7662242; PIDN:NP_055674.1

Query Match 78.6%; Score 37; DB 2; Length 818;
Best Local Similarity 77.8%; Pred. No. 34;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
|||:||||
Db 383 KPLSKLSEY 391

RESULT 8
A61237
E6 protein - human papillomavirus type 52
C:Species: human papillomavirus type 52
C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996
C:Accession: A61237
R:Takami, Y.; Kondoh, G.; Saito, J.; Noda, K.; Sudiro, T.M.; Sjahrurachman, A.; Warsa, U.
Int. J. Cancer 48, 516-522, 1991
A:Title: Cloning and characterization of human papillomavirus type 52 from cervical car
A:Reference number: A61237; MUID:91258022; PMID:1646174
A:Accession: A61237
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <TAK>
C:Superfamily: papillomavirus E6 protein

Query Match 76.6%; Score 36; DB 2; Length 148;
Best Local Similarity 77.8%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
:|||:||||
Db 68 RPLSKLSEY 76

RESULT 9
S36573
E6 protein - human papillomavirus type 52
C:Species: human papillomavirus type 52
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36573
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36573
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148
A:Cross-references: UNIPROT:P36814; EMBL:X74481; NID:g397038; PIDN:CAAS2585.1; PID:g3970
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 76.6%; Score 36; DB 2; Length 148;
Best Local Similarity 77.8%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
:|||:||||
Db 68 RPLSKLSEY 76

RESULT 10
W6WL33

E6 protein - human papillomavirus type 33
C:Species: human papillomavirus type 33
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A03683
R:Cole, S.T.; Strebeck, R.E.
J. Virol. 58, 991-995, 1986
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 33, whi
A:Reference number: A93020; MUID:86200464; PMID:3009902
A:Accession: A03683
A:Molecule type: DNA
A:Residues: 1-149 <COL>
A:Cross-references: UNIPROT:P06427; GB:M12732; NID:g333049; PIDN:AAA46958.1; PID:g463177
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 76.6%; Score 36; DB 1; Length 149;
Best Local Similarity 77.8%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
:|||:||||
Db 68 RPLSKLSEY 76

RESULT 11
B64367
Hypoetical protein MJ0538 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: B64367
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.
Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
reson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: B64367
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-260 <BUL>
A:Cross-references: UNIPROT:Q57958; GB:U67503; GB:L77117; NID:g1591239; PIDN:AAB98536.1;
C:Genetics:
A:Map position: REV474807-474025

Query Match 76.6%; Score 36; DB 2; Length 260;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
:|||:||||
Db 51 KFYTKIGEF 59

RESULT 12
S22701
mannosyltransferase (EC 2.4.1.1.) - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein G3626; protein YGL038c
C:Species: Saccharomyces cerevisiae
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C:Accession: S22701; S64040
R:Nakayama, K.I.; Nagasu, T.; Shima, Y.; Kuromitsu, J.; Jigami, Y.
EMBO J. 11, 2511-2519, 1992
A:Title: OCH1 encodes a novel membrane bound mannosyltransferase: outer chain elongation
A:Reference number: S22701; MUID:92331603; PMID:1628616
A:Accession: S22701
A:Molecule type: DNA
A:Residues: 1-480 <NAK>
A:Cross-references: UNIPROT:P31755; EMBL:D11095; NID:g218450; PIDN:BAA01869.1; PID:g2184;
R:Hebling, U.; Hofmann, B.; Delius, H.
submitted to the Protein Sequence Database, May 1996

A;Reference number: S64003
A;Accession: S64040
A;Molecule type: DNA
A;Residues: 1-480 <HEB>
A;Cross-references: EMBL:272560; NID:g1322519; PID:e243938; PID:g1322520; MIPS:YGL038c
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:OCHI
A;Cross-references: SGD:S0003006; MIPS:YGL038c
A;Map position: 7L
C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase; transmembrane protein
F:16-32/Domain: transmembrane #status predicted <TM>
F:203,281,341,393/Binding site: carbonylrate (Asn) (covalent) #status predicted

Query Match 76.6%; Score 36; DB 2; Length 480;
Best Local Similarity 87.5%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KFYKISE 8
||| ||||
Db 402 KFYKISE 409

RESULT 13
W6WLR1
E6 protein - rhesus papillomavirus (type 1)
C;Species: rhesus papillomavirus
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A38503
R;Ostrow, R.S.; LaBresh, K.V.; Faras, A.J.
Virology 181, 424-429, 1991
A;Title: Characterization of the complete RHPV 1 genomic sequence and an integration loc
A;Reference number: A38503; MUID:91135018; PMID:1847267
A;Accession: A38503
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-191 <OST>
A;Cross-references: UNIPROT:P22159; EMBL:M37717
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F:60-96/Region: zinc finger CCCC motif
F:133-169/Region: zinc finger CCCC motif

Query Match 74.5%; Score 35; DB 1; Length 191;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KFYKIRY 9
:|||||:
Db 98 RFYKIRY 106

RESULT 14
JC1469
beta-adrenergic-receptor kinase (EC 2.7.1.126) 2 - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Jun-1999
C;Accession: JC1469
R;Parrotti, G.; Ambrosini, G.; Salliese, M.; De Blasi, A.
Biochem. Biophys. Res. Commun. 190, 475-481, 1993
A;Title: Molecular cloning, functional expression and mRNA analysis of human beta-adre
A;Reference number: JC1469; MUID:93151031; PMID:8427589
A;Accession: JC1469
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-688 <PAR>
A;Cross-references: GB:X69117; NID:g312394; PIDN:CAA48870.1; PID:g312395
A;Experimental source: pituitary
C;Comment: This enzyme plays a role in the regulation of receptor-mediated immune functi
C;Genetics:
A;Gene: GDB:ADRBK2
A;Cross-references: GDB:131716; OMIM:109636
A;Map position: 22q11-22q11

C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A;Pathway: desensitization of beta-adrenergic receptor
A;Note: phosphorylation inactivates the agonist-occupied receptor
C;Superfamily: beta-adrenergic-receptor kinase; pleckstrin repeat
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F:189-453/Domain: protein kinase homology <KIN>
F:197-205/Region: protein kinase ATP-binding motif
F:557-650/Domain: pleckstrin repeat homology <PLK>
F:220,239,317,319/Active site: Lys, Glu, Asp, Lys #status predicted
F:322,326/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 74.5%; Score 35; DB 1; Length 688;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KFYSKISEY 9
||| :|||
Db 84 KFYBEIKY 92

RESULT 15
A39336
beta-adrenergic-receptor kinase (EC 2.7.1.126) 2 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C;Accession: A39336
R;Benovic, J.L.; Onorato, J.J.; Arriza, J.L.; Stone, W.C.; Lohse, M.; Jenkins, N.A.; Gil
J. Biol. Chem. 266, 14939-14946, 1991
A;Title: Cloning, expression, and chromosomal localization of beta-adrenergic receptor k
A;Reference number: A39336; MUID:91332005; PMID:1869533
A;Accession: A39336
A;Molecule type: mRNA
A;Residues: 1-688 <BEN>
A;Cross-references: UNIPROT:P26818; GB:M73216; NID:g162734; PIDN:AAA30406.1; PID:g162735
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A;Pathway: desensitization of beta-adrenergic receptor
A;Note: phosphorylation inactivates the agonist-occupied receptor
C;Superfamily: beta-adrenergic-receptor kinase; pleckstrin repeat
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F:189-453/Domain: protein kinase homology <KIN>
F:197-205/Region: protein kinase ATP-binding motif
F:557-650/Domain: pleckstrin repeat homology <PLK>
F:220,239,317,319/Active site: Lys, Glu, Asp, Lys #status predicted
F:322,326/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 74.5%; Score 35; DB 1; Length 688;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KFYSKISEY 9
||| :|||
Db 84 KFYBEIKY 92

Search completed: June 28, 2005, 23:32:04
Job time : 12.05 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-48

Perfect score: 47

Sequence: 1 KFYSKISEY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/ECT_NEW_PUB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/ECTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	47	100.0	22	16	US-10-612-818-4
2	47	100.0	151	14	US-10-177-390-6
3	47	100.0	151	17	US-10-484-063-20
4	47	100.0	151	17	US-10-484-063-27
5	47	100.0	158	17	US-10-858-384-2
6	47	100.0	158	17	US-10-367-057-16
7	47	100.0	171	16	US-10-472-724-2
8	47	100.0	266	9	US-09-367-309A-1
9	47	100.0	273	13	US-10-000-903-4
10	47	100.0	273	17	US-10-899-771-4
11	47	100.0	292	13	US-10-000-903-10

12	47	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
13	47	100.0	371	13	US-10-000-903-6	Sequence 6, Appl
14	47	100.0	371	17	US-10-899-771-6	Sequence 6, Appl
15	47	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
16	47	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
17	42	89.4	15	16	US-10-476-570-31	Sequence 31, Appl
18	42	89.4	20	16	US-10-476-570-12	Sequence 12, Appl
19	37	78.7	818	10	US-09-918-715-246	Sequence 246, App
20	37	78.7	818	16	US-10-474-794-246	Sequence 246, App
21	36	76.6	353	16	US-10-437-963-140423	Sequence 140423,
22	36	76.6	480	15	US-10-369-493-21946	Sequence 21946, A
23	35	74.5	43	16	US-10-437-963-194869	Sequence 194869,
24	35	74.5	229	16	US-10-425-115-194792	Sequence 194792,
25	35	74.5	237	16	US-10-425-115-194796	Sequence 194796,
26	35	74.5	688	14	US-10-038-010-50	Sequence 50, Appl
27	35	74.5	688	15	US-10-029-020-45	Sequence 45, Appl
28	35	74.5	688	15	US-10-029-020-48	Sequence 48, Appl
29	35	74.5	688	15	US-10-029-020-49	Sequence 49, Appl
30	35	74.5	688	17	US-10-788-197-25	Sequence 25, Appl
31	35	74.5	688	17	US-10-788-197-27	Sequence 27, Appl
32	35	74.5	1521	13	US-10-087-192-1071	Sequence 1071, Ap
33	35	74.5	1651	16	US-10-467-909-5	Sequence 5, Appl
34	34	72.3	59	16	US-10-425-115-238474	Sequence 238474,
35	34	72.3	88	16	US-10-767-701-57456	Sequence 57456, A
36	34	72.3	186	14	US-10-096-373-16	Sequence 16, Appl
37	34	72.3	534	15	US-10-369-493-6248	Sequence 6248, Ap
38	33	70.2	56	15	US-10-424-599-153695	Sequence 153695,
39	33	70.2	325	9	US-09-815-242-13562	Sequence 13562, A
40	33	70.2	325	10	US-09-769-787-141	Sequence 141, App
41	33	70.2	325	15	US-10-282-122A-74092	Sequence 74092, A
42	33	70.2	325	15	US-10-472-928-3204	Sequence 3204, Ap
43	33	70.2	478	15	US-10-424-599-166133	Sequence 166133,
44	33	70.2	535	17	US-10-741-849-7181	Sequence 7181, Ap
45	33	70.2	572	15	US-10-369-493-22722	Sequence 22722, A

ALIGNMENTS

RESULT 1

US-10-612-818-4
; Sequence 4, Application US/10612818
; Publication No. US20040110925A1
; GENERAL INFORMATION:
; APPLICANT: Impact Diagnostics
; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus
; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papillomavirus
; FILE REFERENCE: 3352-2-2
; CURRENT APPLICATION NUMBER: US/10/612,818
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/394,172
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/828,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E6 early coding region of HPV 16

Query Match 100.0%; Score 47; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYSKISEY 9

DB 14 KFYSKISEY 22

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RESULT 2
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; FILE REFERENCE: Polynucleotides by Electroporation
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6
Query Match 100.0%; Score 47; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
DB 68 KFYISKISEY 76

RESULT 3
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20
Query Match 100.0%; Score 47; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
DB 68 KFYISKISEY 76

RESULT 4
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-27
Query Match 100.0%; Score 47; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
DB 75 KFYISKISEY 83

RESULT 5
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; FILE REFERENCE: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2
Query Match 100.0%; Score 47; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
DB 75 KFYISKISEY 83

RESULT 6
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057

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; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuroSeqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match      100.0%; Score 47; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
DB 75 KFYISKISEY 83

RESULT 7
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match      100.0%; Score 47; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
DB 80 KFYISKISEY 88

RESULT 8
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
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; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 47; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
DB 75 KFYISKISEY 83

RESULT 9
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match      100.0%; Score 47; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
DB 181 KFYISKISEY 189

RESULT 10
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

Query Match 100.0%; Score 47; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KFYISKISEY 9
Db 181 KFYISKISEY 189
|||||

RESULT 11
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match 100.0%; Score 47; DB 13; Length 292;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KFYISKISEY 9
Db 200 KFYISKISEY 208
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RESULT 12
US-10-899-771-10
; Sequence 10, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus
; OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-10

Query Match 100.0%; Score 47; DB 17; Length 292;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KFYISKISEY 9
Db 200 KFYISKISEY 208
|||||

RESULT 13
US-10-000-903-6
; Sequence 6, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-6

Query Match 100.0%; Score 47; DB 13; Length 371;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KFYISKISEY 9
Db 181 KFYISKISEY 189
|||||

RESULT 14
US-10-899-771-6
; Sequence 6, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 16)
US-10-899-771-6

Query Match      100.0%; Score 47; DB 17; Length 371;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KEYSKISEY 9
Db      181 KEYSKISEY 189

RESULT 15
US-10-000-903-14
; Sequence 14, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-14

Query Match      100.0%; Score 47; DB 13; Length 390;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KEYSKISEY 9
Db      200 KEYSKISEY 208

Search completed: June 29, 2005, 05:18:12
Job time : 116.15 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-48
Perfect score: 47
Sequence: 1 KFYSKISBY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	9	3	US-08-159-339A-229
2	47	100.0	158	4	US-09-980-523A-2
3	47	100.0	162	1	US-08-316-239B-3
4	47	100.0	162	1	US-08-316-239B-4
5	47	100.0	172	3	US-08-860-165-12
6	47	100.0	172	3	US-08-860-165-14
7	47	100.0	172	3	US-09-359-382-12
8	47	100.0	172	3	US-09-359-382-14
9	47	100.0	266	3	US-08-860-165-10
10	47	100.0	266	3	US-09-382-10
11	47	100.0	266	4	US-09-367-309A-1
12	47	100.0	273	3	US-09-485-885-4
13	47	100.0	292	3	US-09-485-885-10
14	47	100.0	371	3	US-09-485-885-6
15	47	100.0	390	3	US-09-485-885-14
16	36	76.6	10	3	US-08-159-339A-75
17	36	76.6	20	2	US-08-934-915-44
18	36	76.6	20	2	US-08-934-915-163
19	35	74.5	20	2	US-08-934-915-162
20	35	74.5	54	4	US-09-270-767-33745
21	35	74.5	54	4	US-09-270-767-54962
22	35	74.5	604	4	US-09-134-000C-5828
23	35	74.5	688	1	US-08-221-817-19
24	35	74.5	688	1	US-08-454-439-19
25	35	74.5	688	5	PCT-US94-10487-19
26	35	74.5	698	4	US-09-949-016-10644
27	34	72.3	112	4	US-09-107-532A-4977

Sequence 23345, A
Sequence 21349, A
Sequence 3778, Ap
Sequence 4716, Ap
Sequence 3313, Ap
Sequence 43778, A
Sequence 4173, Ap
Sequence 5, Appli
Sequence 6133, Ap
Sequence 2, Appli
Sequence 28037, A
Sequence 18661, A
Sequence 4349, Ap
Sequence 18642, A
Sequence 5186, Ap
Sequence 31878, A
Sequence 1, Appli
Sequence 137, App

28 33 70.2 97 4 US-09-248-796A-23345
29 33 70.2 206 4 US-09-248-796A-21349
30 33 70.2 215 4 US-09-134-000C-3778
31 33 70.2 236 4 US-09-134-000C-4716
32 33 70.2 325 4 US-09-583-110-3313
33 33 70.2 340 4 US-09-270-767-43778
34 33 70.2 340 4 US-09-107-433-4173
35 33 70.2 1183 4 US-09-532-310B-5
36 33 70.2 1439 4 US-09-134-000C-6133
37 32 68.1 51 1 US-08-418-893D-2
38 32 68.1 132 4 US-09-248-796A-28037
39 32 68.1 289 4 US-09-248-796A-18661
40 32 68.1 338 4 US-09-107-532A-4349
41 32 68.1 421 4 US-09-248-796A-18642
42 32 68.1 478 4 US-09-543-681A-5186
43 32 68.1 529 4 US-09-252-991A-31878
44 32 68.1 2237 1 US-08-354-973-1
45 31 66.0 9 3 US-08-159-339A-137

ALIGNMENTS

RESULT 1
US-08-159-339A-229
; Sequence 229, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 229:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-229

Query Match 100.0%; Score 47; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFYISKISEY 9
| | | | | | | | | |
Db 1 KFYISKISEY 9

RESULT 2

US-09-980-523A-2

; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 47; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFYISKISEY 9
| | | | | | | | | |
Db 75 KFYISKISEY 83

RESULT 3

US-08-316-239B-3

; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/316,239B

; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 47; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFYISKISEY 9
| | | | | | | | | |
Db 75 KFYISKISEY 83

RESULT 4

US-08-316-239B-4

; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Cancer
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 47; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
Db 75 KFYISKISEY 83

RESULT 5
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match 100.0%; Score 47; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
Db 13 KFYISKISEY 21

RESULT 6
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match 100.0%; Score 47; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
Db 144 KFYISKISEY 152

RESULT 7
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match 100.0%; Score 47; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFYISKISEY 9
Db 13 KFYISKISEY 21

RESULT 8
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match 100.0%; Score 47; DB 3; Length 172;

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Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFYISKISEY 9
Db 144 KFYISKISEY 152

RESULT 9
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 47; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFYISKISEY 9
Db 75 KFYISKISEY 83

RESULT 10
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 47; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.35;

Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFYISKISEY 9
Db 75 KFYISKISEY 83

RESULT 11
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 47; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFYISKISEY 9
Db 75 KFYISKISEY 83

RESULT 12
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 47; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFYISKISEY 9
Db 181 KFYISKISEY 189
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RESULT 13

US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match 100.0%; Score 47; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFYISKISEY 9
Db 200 KFYISKISEY 208
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RESULT 14

US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match 100.0%; Score 47; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFYISKISEY 9
Db 181 KFYISKISEY 189
|||||

RESULT 15

US-09-485-885-14

; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match 100.0%; Score 47; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFYISKISEY 9
Db 200 KFYISKISEY 208
|||||

Search completed: June 28, 2005, 23:37:49
Job time : 18.05 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-47
Perfect score: 55
Sequence: 1 VCDKCLAFY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	55	100.0	81	2	Q80886	Q80886 human papil
2	55	100.0	84	2	Q80882	Q80882 human papil
3	55	100.0	90	2	Q80884	Q80884 human papil
4	55	100.0	90	2	Q80885	Q80885 human papil
5	55	100.0	91	2	Q80887	Q80887 human papil
6	55	100.0	99	2	Q819B2	Q819B2 human papil
7	55	100.0	103	2	Q819D6	Q819D6 human papil
8	55	100.0	130	2	Q819B4	Q819B4 human papil
9	55	100.0	130	2	Q819B8	Q819B8 human papil
10	55	100.0	130	2	Q819C0	Q819C0 human papil
11	55	100.0	130	2	Q819C2	Q819C2 human papil
12	55	100.0	130	2	Q819C8	Q819C8 human papil
13	55	100.0	130	2	Q819D0	Q819D0 human papil
14	55	100.0	138	2	Q819D2	Q819D2 human papil
15	55	100.0	143	2	Q819B6	Q819B6 human papil
16	55	100.0	143	2	Q819C4	Q819C4 human papil
17	55	100.0	151	2	Q819C4	Q819C4 human papil
18	55	100.0	151	2	Q819C4	Q819C4 human papil
19	55	100.0	151	2	Q819C4	Q819C4 human papil
20	55	100.0	151	2	Q819C4	Q819C4 human papil
21	55	100.0	151	2	Q819C4	Q819C4 human papil
22	55	100.0	151	2	Q819C4	Q819C4 human papil
23	55	100.0	151	2	Q819C4	Q819C4 human papil
24	55	100.0	151	2	Q819C4	Q819C4 human papil
25	55	100.0	151	2	Q819C4	Q819C4 human papil
26	55	100.0	151	2	Q819C4	Q819C4 human papil
27	55	100.0	151	2	Q819C4	Q819C4 human papil
28	55	100.0	151	2	Q819C4	Q819C4 human papil
29	55	100.0	151	2	Q819C4	Q819C4 human papil
30	55	100.0	151	2	Q819C4	Q819C4 human papil
31	55	100.0	151	2	Q819C4	Q819C4 human papil

32 55 100.0 151 2 Q8B564 human papil
33 55 100.0 151 2 Q8BB19 human papil
34 55 100.0 151 2 Q8BB20 human papil
35 55 100.0 151 2 Q8BB21 human papil
36 55 100.0 151 2 Q8W8C3 human papil
37 55 100.0 151 2 Q8W931 human papil
38 55 100.0 151 2 Q8WMP2 human papil
39 55 100.0 151 2 Q8WMP4 human papil
40 55 100.0 151 2 Q8WMP5 human papil
41 55 100.0 158 1 V86 HPV16 human papil
42 55 100.0 158 2 Q8JMU8 human papil
43 55 100.0 158 2 Q8QHN0 human papil
44 55 100.0 158 2 Q8QHP5 human papil
45 55 100.0 158 2 Q8QHT0 human papil

ALIGNMENTS

RESULT 1
Q80886 PRELIMINARY; PRT; 81 AA.
AC Q80886;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14515; AAB60565.2; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.1
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9784 MW; DD5FEDBC9F845B97 CRC64;
Query Match 100.0%; Score 55; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.079; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Indels 0; Gaps 0;
Qy 1 VCDKCLAFY 9
Db 21 VCDKCLAFY 29
RESULT 2
Q80882 PRELIMINARY; PRT; 84 AA.
AC Q80882;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14511; AAB60565.2; -
DR GO; GO:0042025; C:host cell nucleus; IEA.

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DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 84
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;
Query Match 100.0%; Score 55; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCDKCLKFY 9
Db 18 VCDKCLKFY 26

RESULT 3
Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFAACCC01 CRC64;
Query Match 100.0%; Score 55; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCDKCLKFY 9
Db 21 VCDKCLKFY 29

RESULT 4
Q80885 PRELIMINARY; PRT; 90 AA.
AC Q80885;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14514; AAB60568.2; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.

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FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10964 MW; BC2531643ACBA76C CRC64;
Query Match 100.0%; Score 55; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCDKCLKFY 9
Db 21 VCDKCLKFY 29

RESULT 5
Q80887 PRELIMINARY; PRT; 91 AA.
AC Q80887;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14516; AAB60570.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 11136 MW; 22FDF3EA185ACBA7 CRC64;
Query Match 100.0%; Score 55; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCDKCLKFY 9
Db 21 VCDKCLKFY 29

RESULT 6
Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
   cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404704; AAL01365.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6; 1.
FT NON_TER 1
FT NON_TER 99

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SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;
Query Match 100.0%; Score 55; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
DB 38 VCDKCLKFY 46

RESULT 7
Q919D6 PRELIMINARY; PRT; 103 AA.
AC Q919D6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404692; AAL01342.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBFAF1F25449B CRC64;

Query Match 100.0%; Score 55; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
DB 14 VCDKCLKFY 22

RESULT 8
Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D27EEDDC CRC64;

Query Match 100.0%; Score 55; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
DB 41 VCDKCLKFY 49

RESULT 9
Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01359.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match 100.0%; Score 55; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
DB 41 VCDKCLKFY 49

RESULT 10
Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 VCDKCLKFY 9
 |||||
 Db 41 VCDKCLKFY 49

RESULT 11

Q919C2 PRELIMINARY; PRT; 130 AA.
 AC Q919C2; (TREMELrel. 19, Created)
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874 (2002).
 DR EMBL; AF404699; AAL01355.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
 |||||
 Db 41 VCDKCLKFY 49

RESULT 12

Q919C8 PRELIMINARY; PRT; 130 AA.
 AC Q919C8; (TREMELrel. 19, Created)
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874 (2002).
 DR EMBL; AF404699; AAL01349.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
 |||||
 Db 41 VCDKCLKFY 49

RESULT 13

Q919D0 PRELIMINARY; PRT; 130 AA.
 AC Q919D0; (TREMELrel. 19, Created)
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874 (2002).
 DR EMBL; AF404699; AAL01347.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 SQ SEQUENCE 130 AA; 15735 MW; 9EBF30EEDCA21AF3 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
 |||||
 Db 41 VCDKCLKFY 49

RESULT 14

Q919D2 PRELIMINARY; PRT; 138 AA.
 AC Q919D2; (TREMELrel. 19, Created)
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874 (2002).
 DR EMBL; AF404699; AAL01345.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
 |||||
 Db 49 VCDKCLKFY 57

RESULT 15

Q919B6
ID Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:869-874(2002).
DR EMBL; AF404702; AAL01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match 100.0%; Score 55; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCDKCLKFY 9
Db 54 VCDKCLKFY 62

Search completed: June 28, 2005, 23:28:10
Job time : 55.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)
78.367 Million cell updates/sec

Title: US-08-170-344-47
Perfect score: 55
Sequence: 1 VCDKCLKFY 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	158	1 W6WL35	protein E6 - human
2	46	83.6	149	1 W6WL35	E6 protein - human
3	45	81.8	149	1 W6WL31	E6 protein - human
4	44	80.0	242	2 E88250	protein T21B10.5 (
5	44	80.0	272	2 T25044	hypothetical prote
6	42	76.4	72	2 B82047	ribosomal protein
7	41	74.5	402	2 T01082	probable zinc fing
8	39	70.9	270	2 T22151	hypothetical prote
9	39	70.9	397	2 G84461	hypothetical prote
10	39	70.9	761	2 E64449	hypothetical prote
11	39	70.9	918	2 S45872	hypothetical prote
12	38	69.1	154	2 S36584	E6 protein - human
13	38	69.1	158	1 W6WL39	E6 protein - human
14	38	69.1	158	1 W6WLPR	E6 protein - human
15	38	69.1	680	2 T29204	hypothetical prote
16	38	69.1	725	2 T26688	hypothetical prote
17	38	69.1	740	2 E69420	hydrogenase expres
18	38	69.1	1613	2 G64488	reverse gyrase (in
19	38	69.1	3078	2 T28432	variant-specific s
20	37	67.3	151	1 W6WL51	E6 protein - human
21	37	67.3	191	1 W6WLRI	E6 protein - rhesu
22	37	67.3	249	2 T46184	hypothetical prote
23	37	67.3	303	2 B45067	laminin B1 chain -
24	37	67.3	378	2 A57488	proteinase inhibit
25	37	67.3	443	2 T08905	hypothetical prote
26	37	67.3	1168	2 I56985	kalinin B1 - mouse
27	37	67.3	1607	1 MMH5B2	laminin gamma-1 ch
28	37	67.3	1609	1 MMHUB2	laminin gamma-1 ch
29	37	67.3	2440	2 S39162	transcription coac

30	37	67.3	2441	2 S39161	CREB-binding prote
31	37	67.3	3190	2 T13828	CREB-binding prote
32	36	65.5	148	2 S36515	E6 protein - human
33	36	65.5	158	1 W6WL18	E6 protein - human
34	36	65.5	158	2 S36561	E6 protein - human
35	36	65.5	159	2 A85022	probable actin pol
36	36	65.5	409	2 S48352	DNA primase (EC 2.
37	36	65.5	452	2 T46147	zinc finger protei
38	36	65.5	453	2 T47466	zinc finger protei
39	36	65.5	602	2 F84432	probable C2H2-type
40	36	65.5	604	1 S00726	protein kinase A-r
41	36	65.5	606	1 TVHUAP	protein kinase A-r
42	36	65.5	833	2 T28385	ORF MSV224 probabl
43	36	65.5	1557	2 T28811	hypothetical prote
44	36	65.5	1639	1 MMFFB2	laminin gamma-1 ch
45	36	65.5	1787	2 F84528	probable retroelem

ALIGNMENTS

RESULT 1
W6WL35
Protein E6 - human papillomavirus type 16
C:Species: human papillomavirus type 16
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A03682; T10427
R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virolgy 145, 181-185, 1985
A:Title: Human papillomavirus type 16 DNA sequence.
A:Reference number: A22355; MUID:85246220; PMID:2990099
A:Accession: A03682
A:Molecule type: DNA
A:Residues: 1-158 <SEE>
A:Cross-references: UNIPROT:P03126; GB:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032
R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A:Reference number: Z17014; MUID:91162763; PMID:1848319
A:Accession: T10427
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-158 <KEN>
A:Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032
C:Genetics:
A:Gene: E6
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:37-73/Region: zinc finger CCCC motif
F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 55; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCDKCLKFY 9
|||||||
Db 69 VCDKCLKFY 77

RESULT 2
W6WL35
E6 protein - human papillomavirus type 35
C:Species: human papillomavirus type 35
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: E40824; S36521
R:Marich, J.E.; Pontaler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virolgy 186, 770-776, 1992
A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillon
A:Reference number: A40824; MUID:92124753; PMID:1310198
A:Accession: E40824
A>Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-149 <MAR>
A:Cross-references: UNIPROT:P27228; GB:M74117; NID:G333050; PIDN:AAA46966.1; PID:G333051
R:Delius, H.; Hofmann, B.
A:Description: The EMBL Data Library, August 1993
A:Reference number: S36469
A:Accession: S36521
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149
A:Cross-references: EMBL:X74477; NID:G396997; PIDN:CAA52561.1; PID:G396998
A:Experimental source: strain 35H
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 83.6%; Score 46; DB 1; Length 149;
Best Local Similarity 88.9%; Pred. No. 2; Mismatches 1; Indels 0; Gaps 0;
Matches 8; Conservative 0

Qy 1 VCDKCLKFY 9
Db 62 VCMKCLKFY 70

RESULT 3
W6WL31
A:Title: E6 protein - human papillomavirus type 31
C:Species: human papillomavirus type 31
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: A32444
R:Goldsbrough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated virus
A:Reference number: A94398; MUID:89299478; PMID:2545036
A:Accession: A32444
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-149 <GOL>
A:Cross-references: UNIPROT:P17386; GB:J04353; NID:G333048; PIDN:AAA46950.1; PID:G459916
C:Comment: This protein may be involved in the oncogenic potential of this virus.
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 81.8%; Score 45; DB 1; Length 149;
Best Local Similarity 77.8%; Pred. No. 2.9; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1

Qy 1 VCDKCLKFY 9
Db 62 VCTKCLKFY 70

RESULT 4
E88250
A:Title: T21B10.5 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: E88250
R:anonymous, The C. elegans Sequencing Consortium.
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 282, 2012-2018, 1998
A:Accession: E88250
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-242 <STO>
A:Cross-references: UNIPROT:Q22626; GB:chr_II; PIDN:CAA92695.1; PID:G3879989; GSPDB:GN000
C:Genetics:
A:Gene: T21B10.5
A:Map position: 2

Query Match 80.0%; Score 44; DB 2; Length 242;
Best Local Similarity 87.5%; Pred. No. 6.1; Mismatches 0; Gaps 0;
Matches 7; Conservative 0

Qy 2 CDKCLKFY 9
Db 62 CDKCNKFY 69

RESULT 5
T25044
A:Title: hypothetical protein T21B10.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25044
R:Baynes, C.
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Accession: T25044
A:Reference number: Z19973
A:Residues: 1-272 <WIL>
A:Cross-references: UNIPROT:Q22626; EMBL:Z68318; PIDN:CAA92695.2; GSPDB:GN000020; CESP:T21
A:Experimental source: clone T21B10
C:Genetics:
A:Gene: CESP:T21B10.5
A:Map position: 2
A:Introns: 34/3; 69/1; 91/1; 212/1; 243/1

Query Match 80.0%; Score 44; DB 2; Length 272;
Best Local Similarity 87.5%; Pred. No. 6.6; Mismatches 0; Gaps 0;
Matches 7; Conservative 0

Qy 2 CDKCLKFY 9
Db 92 CDKCNKFY 99

RESULT 6
B82047
A:Title: ribosomal protein L31 VC2679 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: B82047
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: B82047
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-72 <HEI>
A:Cross-references: UNIPROT:Q9KNO2; GB:AE003852; NID:G9657266; PIDN:AAF95821
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2679
A:Map position: 1
A:Superfamily: Escherichia coli ribosomal protein L31

Query Match 76.4%; Score 42; DB 2; Length 72;
Best Local Similarity 77.8%; Pred. No. 5.1; Mismatches 0; Gaps 0;
Matches 7; Conservative 0

Qy 1 VCDKCLKFY 9
Db 11

Db 37 VCDKCHPFY 45

RESULT 7
T01082
probable zinc finger protein T10P11.4 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01082
R:Kaplan, N.; Johnson, D.; Schutz, K.; Gnoj, L.; Hoffman, J.; Till, S.; de la Bastide, M.
hi, M.; Martienssen, R.; Chen, E.Y.; Wilson, R.; McCombie, W.R.
submitted to the EMBL Data Library, November 1998
A:Description: Sequence of A. thaliana BAC T10P11 from chromosome IV.
A:Reference number: Z14248
A:Accession: T01082
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-402 <KAP>
A:Cross-references: UNIPROT:O22759; EMBL:AC002330; NID:G2262135; PID:G3892045
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Introns: 63/1; 196/2
A:Note: T10P11.4
C:Keywords: zinc finger

Query Match 74.5%; Score 41; DB 2; Length 402;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CDKCLKFY 9
Db 161 CBKCKSKFY 168
|:|:|:|:|

RESULT 8
T22151
Hypothetical protein F43G9.11 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22151
R:Kershaw, J.
submitted to the EMBL Data Library, September 1996
A:Reference number: Z19523
A:Accession: T22151
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-270 <WIL>
A:Cross-references: UNIPROT:Q93721; EMBL:Z79755; PIDN:CAB02113.1; GSPDB:GN00019; CESP:F43G9
A:Experimental source: clone F43G9
C:Genetics:
A:Gene: CESP:F43G9.11
A:Map position: 1
A:Introns: 26/1; 127/2; 154/3; 181/2; 243/1

Query Match 70.9%; Score 39; DB 2; Length 270;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
Db 135 VCDKCKSKY 143
|:|:|:|:|

RESULT 9
G84461
Hypothetical protein At2G04810 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: G84461
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84461
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-397 <STO>
A:Cross-references: UNIPROT:Q9SU78; GB:AE002093; NID:G4544416; PIDN:AAD22325.1; GSPDB:GN00019
C:Genetics:
A:Gene: At2G04810
A:Map position: 2
C:Superfamily: Arabidopsis thaliana hypothetical protein T12H17.50

Query Match 70.9%; Score 39; DB 2; Length 397;
Best Local Similarity 85.7%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DKCLKFY 9
Db 107 DRCLKFY 113
|:|:|:|:|

RESULT 10
E84449
Hypothetical protein MJ1198 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: E84449
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, L.;
Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
reson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: E84449
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-761 <BUL>
A:Cross-references: UNIPROT:Q58598; GB:U67561; GB:L77117; NID:G2826373; PIDN:AAB99202.1;
C:Genetics:
A:Map position: FOR1142325-1144610
C:Superfamily: conserved hypothetical protein MJ1198

Query Match 70.9%; Score 39; DB 2; Length 761;
Best Local Similarity 85.7%; Pred. No. 87;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLK 7
Db 102 LCDKCLK 108
|:|:|:|:|

RESULT 11
S45872
Hypothetical protein YBR017c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YBR0224
C:Species: Saccharomyces cerevisiae
C>Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: S45872; S50812; S50321
R:Entian, K.D.; Koetter, P.; Rose, M.; Li, Z.; Thermann, R.; Brendel, M.; Baur, A.; Boles
submitted to the Protein Sequence Database, August 1994
A:Reference number: S45862
A:Accession: S45872
A:Molecule type: DNA
A:Residues: 1-318 <ENT>
A:Cross-references: UNIPROT:P38217; EMBL:Z35886; NID:G536217; PIDN:CAA84959.1; PID:G53621
A:Experimental source: strain S288C
R:Schaff-Gerstenachlaeger, I.; Schindewolf, T.; Lehnert, W.; Rose, M.; Zimmermann, P.K.
Yeast 11, 79-83, 1995
A:Title: Sequence and functional analysis of a 7.2 kb fragment of Saccharomyces cerevisiae
A:Reference number: S50812; MUID:95282516; PMID:7762304
A:Accession: S50812

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-918 <SCW>

A:Cross-references: EMBL:X81324; NID:G587572; PIDN:CAA57104.1; PID:G587573

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:KAP104

A:Cross-references: SGD:S0000221; MIPS:YBR017C

A:Map position: 2R

Query Match 70.9%; Score 39; DB 2; Length 918;

Best Local Similarity 85.7%; Pred. No. 1e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DKCLKFY 9

Db 552 DKCLKFY 558

RESULT 12

E6 protein - human papillomavirus type 7

C:Species: human papillomavirus type 7

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S36584

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36584

A:Molecule type: DNA

A:Residues: 1-154

A:Cross-references: UNIPROT:P36800; EMBL:X74463; NID:G397060; PIDN:CAA52476.1; PID:G3970

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match

Best Local Similarity 69.1%; Score 38; DB 2; Length 154;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CDKCLKFY 9

Db 63 CVKCLEFY 70

RESULT 13

W6WL39

E6 protein - human papillomavirus type 39

C:Species: human papillomavirus type 39

A:Note: host Homo sapiens (man)

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C:Accession: A38502

R:Volpers, C.; Streeck, R.E.

Virology 181, 419-423, 1991

A:Title: Genome organization and nucleotide sequence of human papillomavirus type 39.

A:Reference number: A38502; MUID:91135017; PMID:1847266

A:Accession: A38502

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-158 <VOL>

A:Cross-references: UNIPROT:P24835; GB:M62849; EMBL:M38185; NID:G333245; PIDN:AAA47050.1

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; transforming protein; zinc finger

F:32-68/Region: zinc finger CCCC motif

F:105-141/Region: zinc finger CCCC motif

Query Match

Best Local Similarity 69.1%; Score 38; DB 1; Length 158;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CDKCLKFY 9

Db 65 CQSCIKFY 72

RESULT 14

W6WLPR

E6 protein - human papillomavirus type ME180 (provirus)

C:Species: human papillomavirus type ME180

A:Note: host Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: C40509

R:Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.

J. Virol. 65, 5564-5568, 1991

A:Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma (

A:Reference number: A40509; MUID:91374616; PMID:1716694

A:Accession: C40509

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-158 <REU>

A:Cross-references: UNIPROT:P27962; GB:M73258

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:32-68/Region: zinc finger CCCC motif

F:105-141/Region: zinc finger CCCC motif

Query Match

Best Local Similarity 69.1%; Score 38; DB 1; Length 158;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CDKCLKFY 9

Db 65 CQSCIKFY 72

RESULT 15

T29204

hypothetical protein F28F9.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T29204

R:Nelson, J.; Wohldmann, P.

submitted to the EMBL Data Library, September 1996

A:Description: The sequence of C. elegans cosmid F28F9.

A:Reference number: Z20587

A:Accession: T29204

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-680 <NEL>

A:Cross-references: UNIPROT:Q94196; EMBL:U70850; PIDN:AAB09122.1; GSPDB:GN00022; CESP:F2E

A:Experimental source: strain Bristol N2; clone F28F9

C:Genetics:

A:Gene: CESP:F28F9.1

A:Map position: 4

A:Introns: 53/3; 234/3; 268/3; 331/3; 485/2; 531/3; 589/1

Query Match

Best Local Similarity 69.1%; Score 38; DB 2; Length 680;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CDKCLK 7

Db 623 CDKCLK 628

Search completed: June 28, 2005, 23:32:03

Job time : 11.05 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-47
Perfect score: 55
Sequence: 1 VCDKCLKEY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	20	16	US-10-476-570-11
2	55	100.0	22	16	US-10-612-818-4
3	55	100.0	151	14	US-10-177-390-6
4	55	100.0	151	17	US-10-484-063-20
5	55	100.0	151	17	US-10-484-063-27
6	55	100.0	158	17	US-10-858-384-2
7	55	100.0	158	17	US-10-367-057-16
8	55	100.0	171	16	US-10-472-724-2
9	55	100.0	266	9	US-09-367-309A-1
10	55	100.0	273	13	US-10-000-903-4
11	55	100.0	273	17	US-10-899-771-4

12	55	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
13	55	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
14	55	100.0	371	13	US-10-000-903-6	Sequence 6, Appl
15	55	100.0	371	17	US-10-899-771-6	Sequence 6, Appl
16	55	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
17	55	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
18	41	74.5	188	15	US-10-424-599-252455	Sequence 252455,
19	40	72.7	451	15	US-10-424-599-246501	Sequence 246501, A
20	40	72.7	458	15	US-10-425-114-38721	Sequence 38721, A
21	39	70.9	152	15	US-10-424-599-199555	Sequence 199555,
22	39	70.9	610	15	US-10-094-749-2604	Sequence 2604, Ap
23	39	70.9	610	15	US-10-108-260A-3772	Sequence 3772, Ap
24	39	70.9	738	16	US-10-408-765A-740	Sequence 740, App
25	38	69.1	109	14	US-10-029-386-30645	Sequence 30645, A
26	38	69.1	161	15	US-10-377-079-64	Sequence 64, Appl
27	38	69.1	241	15	US-10-425-114-53267	Sequence 53267, A
28	38	69.1	256	15	US-10-424-599-197309	Sequence 197309,
29	38	69.1	692	15	US-10-211-462-227	Sequence 227, App
30	38	69.1	796	15	US-10-377-079-2	Sequence 2, Appl
31	38	69.1	2710	13	US-10-153-273-12	Sequence 12, Appl
32	37	67.3	9	17	US-10-484-063-6	Sequence 6, Appl
33	37	67.3	10	8	US-08-344-824-237	Sequence 237, App
34	37	67.3	181	15	US-10-220-120-302	Sequence 302, App
35	37	67.3	218	16	US-10-767-701-36133	Sequence 36133, A
36	37	67.3	264	16	US-10-363-829-384	Sequence 384, App
37	37	67.3	264	16	US-10-363-829-479	Sequence 479, App
38	37	67.3	276	16	US-10-739-930-9885	Sequence 9885, Ap
39	37	67.3	420	15	US-10-424-599-265648	Sequence 265648,
40	37	67.3	497	15	US-10-416-316-8	Sequence 8, Appl
41	37	67.3	530	16	US-10-655-799-32	Sequence 32, Appl
42	37	67.3	595	15	US-10-416-316-6	Sequence 6, Appl
43	37	67.3	1066	16	US-10-437-963-157156	Sequence 157156,
44	37	67.3	1572	14	US-10-037-182-20	Sequence 20, Appl
45	37	67.3	1576	14	US-10-037-182-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-10-476-570-11
; Sequence 11, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial sequence
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 61-80
US-10-476-570-11

Query Match 100.0%; Score 55; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCDKCLKFY 9
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 Db 9 VCDKCLKFY 17

RESULT 2

US-10-612-818-4
 ; Sequence 4, Application US/10612818
 ; Publication No. US20040110925A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Impact Diagnostics
 ; APPLICANT: Impact Diagnostics
 ; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus
 ; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papi
 ; TITLE OF INVENTION: Associated Cancers
 ; FILE REFERENCE: 3352-2-2
 ; CURRENT APPLICATION NUMBER: US/10/612,818
 ; CURRENT FILING DATE: 2003-07-01
 ; PRIOR APPLICATION NUMBER: US 60/394,172
 ; PRIOR FILING DATE: 2002-07-02
 ; PRIOR APPLICATION NUMBER: US 09/828,645
 ; PRIOR FILING DATE: 2001-04-05
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 22
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Derived from the E6 early coding region of HPV 16
 US-10-612-818-4

Query Match 100.0%; Score 55; DB 16; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.061;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCDKCLKFY 9
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 Db 8 VCDKCLKFY 16

RESULT 3

US-10-177-390-6
 ; Sequence 6, Application US/10177390
 ; Publication No. US20030143743A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schuler, Gerold
 ; APPLICANT: N.V. Antwerp Innovatiecentrum
 ; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
 ; TITLE OF INVENTION: Polynucleotides by Electroporation
 ; FILE REFERENCE: 021505wo/JH/ml
 ; CURRENT APPLICATION NUMBER: US/10/177,390
 ; CURRENT FILING DATE: 2002-06-20
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus type 16
 US-10-177-390-6

Query Match 100.0%; Score 55; DB 14; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCDKCLKFY 9
 |||||
 Db 62 VCDKCLKFY 70

RESULT 4

US-10-484-063-20
 ; Sequence 20, Application US/10484063

; Publication No. US20050048467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SASTRY, K. JAGANNADHA
 ; APPLICANT: TORTOLERO-LUNA, GUILLERMO
 ; APPLICANT: FOLLEN, MICHELE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
 ; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
 ; FILE REFERENCE: UTSC:560US
 ; CURRENT APPLICATION NUMBER: US/10/484,063
 ; CURRENT FILING DATE: 2004-01-16
 ; PRIOR APPLICATION NUMBER: PCT/US02/23198
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 60/306,809
 ; PRIOR FILING DATE: 2001-07-20
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus
 US-10-484-063-20

Query Match 100.0%; Score 55; DB 17; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCDKCLKFY 9
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 Db 62 VCDKCLKFY 70

RESULT 5

US-10-484-063-27
 ; Sequence 27, Application US/10484063
 ; Publication No. US20050048467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SASTRY, K. JAGANNADHA
 ; APPLICANT: TORTOLERO-LUNA, GUILLERMO
 ; APPLICANT: FOLLEN, MICHELE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
 ; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
 ; FILE REFERENCE: UTSC:560US
 ; CURRENT APPLICATION NUMBER: US/10/484,063
 ; CURRENT FILING DATE: 2004-01-16
 ; PRIOR APPLICATION NUMBER: PCT/US02/23198
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 60/306,809
 ; PRIOR FILING DATE: 2001-07-20
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 27
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus type 16
 US-10-484-063-27

Query Match 100.0%; Score 55; DB 17; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCDKCLKFY 9
 |||||
 Db 62 VCDKCLKFY 70

RESULT 6

US-10-858-384-2
 ; Sequence 2, Application US/10858384
 ; Publication No. US20050033025A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHOPPIN, JEANNINE
 ; APPLICANT: BOURGAULT VILLADA, ISABELLE
 ; APPLICANT: GUILLET, JEAN-GERARD

```
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match      100.0%; Score 55; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCDKCLKFY 9
Db 69 VCDKCLKFY 77

RESULT 7
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US2005010054A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chuan Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match      100.0%; Score 55; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCDKCLKFY 9
Db 69 VCDKCLKFY 77

RESULT 8
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
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; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match      100.0%; Score 55; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCDKCLKFY 9
Db 74 VCDKCLKFY 82

RESULT 9
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 55; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCDKCLKFY 9
Db 69 VCDKCLKFY 77

RESULT 10
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
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; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match      100.0%; Score 55; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
Db 175 VCDKCLKFY 183

RESULT 11
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

Query Match      100.0%; Score 55; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
Db 175 VCDKCLKFY 183

RESULT 12
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match      100.0%; Score 55; DB 13; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
Db 194 VCDKCLKFY 202

RESULT 13
US-10-899-771-10
; Sequence 10, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus
; OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-10

Query Match      100.0%; Score 55; DB 17; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
Db 194 VCDKCLKFY 202

RESULT 14
US-10-000-903-6
; Sequence 6, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-6

Query Match      100.0%; Score 55; DB 13; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
DB 175 VCDKCLKFY 183

RESULT 15
US-10-899-771-6
; Sequence 6, Application US/10899771
; Publication NO. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 16)
US-10-899-771-6

Query Match      100.0%; Score 55; DB 17; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
DB 175 VCDKCLKFY 183

Search completed: June 29, 2005, 05:18:12
Job time : 117.15 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-47
Perfect score: 55
Sequence: 1 VCDKCLKPY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	9	3	US-08-159-339A-74
2	55	100.0	10	3	US-08-159-339A-561
3	55	100.0	158	4	US-09-980-523A-2
4	55	100.0	162	1	US-08-316-239B-3
5	55	100.0	162	1	US-08-316-239B-4
6	55	100.0	172	3	US-08-860-165-12
7	55	100.0	172	3	US-08-860-165-14
8	55	100.0	172	3	US-09-359-382-12
9	55	100.0	172	3	US-09-359-382-14
10	55	100.0	266	3	US-08-860-165-10
11	55	100.0	266	3	US-09-359-382-10
12	55	100.0	266	4	US-09-367-309A-1
13	55	100.0	273	3	US-09-485-885-4
14	55	100.0	292	3	US-09-485-885-10
15	55	100.0	371	3	US-09-485-885-6
16	55	100.0	390	3	US-09-485-885-14
17	50	90.9	20	2	US-08-934-915-162
18	48	87.3	11	3	US-08-159-339A-1170
19	42	76.4	8	3	US-08-159-339A-1169
20	42	76.4	74	4	US-09-543-681A-8341
21	38	69.1	161	4	US-09-389-956-64
22	38	69.1	796	4	US-09-389-956-2
23	38	69.1	801	4	US-09-949-016-6836
24	38	69.1	819	4	US-09-949-016-11155
25	38	69.1	2710	2	US-08-568-459A-12
26	38	69.1	2710	2	US-08-487-826B-12
27	38	69.1	2710	3	US-09-210-288-12

28 69.1 3060 2 US-08-487-826B-14 Sequence 14, Appl
29 37 67.3 9 3 US-08-159-339A-136 Sequence 136, Appl
30 37 67.3 219 1 US-08-152-019A-31 Sequence 31, Appl
31 37 67.3 219 1 US-08-152-019A-32 Sequence 32, Appl
32 37 67.3 219 2 US-08-460-309-18 Sequence 18, Appl
33 37 67.3 219 2 US-08-125-077-18 Sequence 18, Appl
34 37 67.3 1572 4 US-09-562-702A-32 Sequence 32, Appl
35 37 67.3 1572 4 US-09-561-818A-28 Sequence 28, Appl
36 37 67.3 1576 4 US-09-562-702A-24 Sequence 24, Appl
37 37 67.3 1576 4 US-09-561-818A-24 Sequence 24, Appl
38 37 67.3 1584 4 US-09-562-702A-28 Sequence 28, Appl
39 37 67.3 1605 4 US-09-562-702A-30 Sequence 30, Appl
40 37 67.3 1609 4 US-09-561-818A-26 Sequence 26, Appl
41 37 67.3 1609 4 US-09-562-702A-22 Sequence 22, Appl
42 37 67.3 1609 4 US-09-561-818A-22 Sequence 22, Appl
43 37 67.3 1609 4 US-09-538-092-900 Sequence 900, Appl
44 37 67.3 1617 4 US-09-562-702A-26 Sequence 26, Appl
45 37 67.3 2441 1 US-08-194-468-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-159-339A-74
; Sequence 74, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cellis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-74

Query Match 100.0%; Score 55; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCDKCLKFY 9
Db 1 VCDKCLKFY 9

RESULT 2

US-08-159-339A-561
; Sequence 561, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Eteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 561:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-561

Query Match 100.0%; Score 55; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCDKCLKFY 9
Db 2 VCDKCLKFY 10

, RESULT 3

US-09-980-523A-2

; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/1 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus

US-09-980-523A-2

Query Match 100.0%; Score 55; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCDKCLKFY 9
Db 69 VCDKCLKFY 77

RESULT 4

US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:


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; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match      100.0%; Score 55; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
DB 69 VCDKCLKFY 77

RESULT 5
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match      100.0%; Score 55; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
DB 69 VCDKCLKFY 77

RESULT 6
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match      100.0%; Score 55; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
DB 7 VCDKCLKFY 15

RESULT 7
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match      100.0%; Score 55; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKFY 9
DB 138 VCDKCLKFY 146

RESULT 8
US-09-359-382-12
; Sequence 12, Application US/09359382
```

; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match 100.0%; Score 55; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.082; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 VCDKCLKFY 9
| | | | |
DB 7 VCDKCLKFY 15

RESULT 9
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match 100.0%; Score 55; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.082; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 VCDKCLKFY 9
| | | | |
DB 138 VCDKCLKFY 146

RESULT 10
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557

; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 55; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 VCDKCLKFY 9
| | | | |
DB 69 VCDKCLKFY 77

RESULT 11
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 55; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 VCDKCLKFY 9
| | | | |
DB 69 VCDKCLKFY 77

RESULT 12
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:

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; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHLATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 55; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKEY 9
Db 69 VCDKCLKEY 77

RESULT 13
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match      100.0%; Score 55; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKEY 9
Db 175 VCDKCLKEY 183

RESULT 14
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match      100.0%; Score 55; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCDKCLKEY 9
Db 175 VCDKCLKEY 183

Search completed: June 28, 2005, 23:37:48
Job time : 18.05 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-46
Perfect score: 52
Sequence: 1 AVCDKCLXF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt.03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	81	2 Q80886	Q80886 human papill
2	52	100.0	84	2 Q80882	Q80882 human papill
3	52	100.0	90	2 Q80884	Q80884 human papill
4	52	100.0	90	2 Q80885	Q80885 human papill
5	52	100.0	91	2 Q80887	Q80887 human papill
6	52	100.0	99	2 Q919B2	Q919B2 human papill
7	52	100.0	103	2 Q919D6	Q919D6 human papill
8	52	100.0	130	2 Q919B4	Q919B4 human papill
9	52	100.0	130	2 Q919B8	Q919B8 human papill
10	52	100.0	130	2 Q919C0	Q919C0 human papill
11	52	100.0	130	2 Q919C2	Q919C2 human papill
12	52	100.0	130	2 Q919C8	Q919C8 human papill
13	52	100.0	130	2 Q919D0	Q919D0 human papill
14	52	100.0	138	2 Q919D2	Q919D2 human papill
15	52	100.0	143	2 Q919B6	Q919B6 human papill
16	52	100.0	143	2 Q919C4	Q919C4 human papill
17	52	100.0	151	2 Q12335	Q12335 human papill
18	52	100.0	151	2 Q12336	Q12336 human papill
19	52	100.0	151	2 Q76TS0	Q76TS0 human papill
20	52	100.0	151	2 Q778I6	Q778I6 human papill
21	52	100.0	151	2 Q778I6	Q778I6 human papill
22	52	100.0	151	2 Q77JG7	Q77JG7 human papill
23	52	100.0	151	2 Q77ZJ5	Q77ZJ5 human papill
24	52	100.0	151	2 Q80963	Q80963 human papill
25	52	100.0	151	2 Q80966	Q80966 human papill
26	52	100.0	151	2 Q89640	Q89640 human papill
27	52	100.0	151	2 Q89648	Q89648 human papill
28	52	100.0	151	2 Q89708	Q89708 human papill
29	52	100.0	151	2 Q89755	Q89755 human papill
30	52	100.0	151	2 Q89852	Q89852 human papill
31	52	100.0	151	2 Q89887	Q89887 human papill

32	52	100.0	151	2 Q8B564	Q8B564 human papill
33	52	100.0	151	2 Q8BB19	Q8BB19 human papill
34	52	100.0	151	2 Q8BB20	Q8BB20 human papill
35	52	100.0	151	2 Q8BB21	Q8BB21 human papill
36	52	100.0	151	2 Q8W8C3	Q8W8C3 human papill
37	52	100.0	151	2 Q9W931	Q9W931 human papill
38	52	100.0	151	2 Q9WMP2	Q9WMP2 human papill
39	52	100.0	151	2 Q9WMP4	Q9WMP4 human papill
40	52	100.0	151	2 Q9WMP5	Q9WMP5 human papill
41	52	100.0	158	1 V56 HPV16	P03126 human papill
42	52	100.0	158	2 Q8JMU8	Q8JMU8 human papill
43	52	100.0	158	2 Q8QHN0	Q8QHN0 human papill
44	52	100.0	158	2 Q8QHP5	Q8QHP5 human papill
45	52	100.0	158	2 Q8QHT0	Q8QHT0 human papill

ALIGNMENTS

RESULT 1
Q80886 PRELIMINARY; PRT; 81 AA.
AC Q80886;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSU=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBSJ databases.
DR EMBL; U14515; AAB60569.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON TER 1
FT NON TER 81
SQ SEQUENCE 81 AA; 9784 MW; DD5FEDBC9F845B97 CRC64;
Query Match Similarity 100.0%; Score 52; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.27; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
QY 1 AVCDKCLXF 9
Db 20 AVCDKCLXF 28

RESULT 2
Q80882 PRELIMINARY; PRT; 84 AA.
AC Q80882;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSU=Cervical;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBSJ databases.
DR EMBL; U14511; AAB60565.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

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DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 84
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B96469E1CAA CRC64;
Query Match 100.0%; Score 52; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.28; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVCDKCLKF 9
Db 17 AVCDKCLKF 25

RESULT 3
Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFAFACCC01 CRC64;
Query Match 100.0%; Score 52; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.28; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVCDKCLKF 9
Db 20 AVCDKCLKF 28

RESULT 4
Q80885 PRELIMINARY; PRT; 90 AA.
AC Q80885;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14514; AAB60568.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.

DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.

FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10964 MW; BC2531643ACBA76C CRC64;
Query Match 100.0%; Score 52; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.29; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVCDKCLKF 9
Db 20 AVCDKCLKF 28

RESULT 5
Q80887 PRELIMINARY; PRT; 91 AA.
AC Q80887;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14516; AAB60570.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 11136 MW; 22PDF3EA185ACBA7 CRC64;
Query Match 100.0%; Score 52; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.29; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVCDKCLKF 9
Db 20 AVCDKCLKF 28

RESULT 6
Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404704; AAL01365.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 11136 MW; 22PDF3EA185ACBA7 CRC64;
Query Match 100.0%; Score 52; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.29; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVCDKCLKF 9
Db 20 AVCDKCLKF 28

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QY      1  AVCDKCLKF 9
Db      40  AVCDKCLKF 48

RESULT 11
Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  AVCDKCLKF 9
Db      40  AVCDKCLKF 48

RESULT 12
Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404696; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  AVCDKCLKF 9
Db      40  AVCDKCLKF 48

RESULT 13
Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404695; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15735 MW; 98FB30EEDCA21AF3 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  AVCDKCLKF 9
Db      40  AVCDKCLKF 48

RESULT 14
Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404694; AAL01345.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  AVCDKCLKF 9
Db      48  AVCDKCLKF 56

RESULT 15

```


Q919B6
ID Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404702; AAL01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E56BE2AC CRC64;
Query Match 100.0%; Score 52; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AVCDKCLKF 9
Db 53 AVCDKCLKF 61

Search completed: June 28, 2005, 23:28:10
Job time : 55.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)
78.367 Million cell updates/sec

Title: US-08-170-344-46

Perfect score: 52

Sequence: 1 AVCDKCLKF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	158	1 W6WLS	protein E6 - human
2	42	80.8	740	2 E69420	hydrogenase expres
3	39	75.0	149	1 W6WL35	E6 protein - human
4	39	75.0	604	1 S00726	protein kinase A-r
5	39	75.0	606	1 TVHUAF	protein kinase A-r
6	39	75.0	761	2 E64449	hypothetical prote
7	39	75.0	766	2 A64389	hydrogenase acces
8	39	75.0	773	2 A71079	probable transcrip
9	38	73.1	149	1 W6WL31	E6 protein - human
10	38	73.1	680	2 T29204	hypothetical prote
11	38	73.1	1334	2 E86451	probable copia-typ
12	38	73.1	1613	2 G64488	reverse gyrase (in
13	38	73.1	3078	2 T28432	variant-specific s
14	37	71.2	242	2 E88250	protein T21B10.5 (
15	37	71.2	272	2 T25044	hypothetical prote
16	37	71.2	2440	2 S39162	transcription coac
17	37	71.2	2441	2 S39161	CREB-binding prote
18	37	71.2	3190	2 T13828	CREB-binding prote
19	36	69.2	101	2 E71607	metal binding prot
20	36	69.2	409	2 S48352	DNA primase (EC 2.
21	36	69.2	510	2 T24396	hypothetical prote
22	36	69.2	2231	2 S53416	SEN1 protein - yea
23	35	67.3	69	2 A70308	ribosomal protein
24	35	67.3	72	2 B82047	ribosomal protein
25	35	67.3	98	2 F96643	hypothetical prote
26	35	67.3	154	2 S36584	E6 protein - human
27	35	67.3	158	1 W6WL39	E6 protein - human
28	35	67.3	158	1 W6WLPR	E6 protein - human
29	35	67.3	187	2 T32826	hypothetical prote

ALIGNMENTS

RESULT 1

W6WLS

protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

J.Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

R. Virology 65, 2093-2097, 1991

A:Title: A negative element in the human papillomavirus type 16 genome acts at the level

A:Reference number: 217014; MUID:91162763; PMID:1848319

A:Accession: T10427

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C:Genetics:

C:Gene: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 52; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.24;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AVCDKCLKF 9

Db 68 AVCDKCLKF 76

RESULT 2

E69420

hydrogenase expression/formaton regulatory protein (hypF) homolog - Archaeoglobus fulgic

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 14-Apr-2003

C:Accession: E69420

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.A.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: E69420
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-740 <KLE>
 A;Cross-references: GB:AE001009; GB:AE000782; NID:G2689332; PIDN:AA89876.1; PID:G264920
 C;Superfamily: carbamoyl phosphate-converting enzyme ([NiFe]-hydrogenase maturation factor)

Query Match 80.8%; Score 42; DB 2; Length 740;
 Best Local Similarity 87.5%; Pred. No. 27;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVCDKCLK 8

|||||

100 AVCDKCLE 107

RESULT 3

W6WL35

E6 protein - human papillomavirus type 35

C;Species: human papillomavirus type 35

A;Note: host Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Accession: E40824; S36521

R;Marich, J.E.; Pontaler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.

Virology 186, 770-776, 1992

A;Title: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35
 A;Reference number: A40824; MUID:92124753; PMID:1310198

A;Accession: E40824

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-149 <MAR>

A;Cross-references: UNIPROT:P27228; GB:M74117; NID:G333050; PIDN:AAA46966.1; PID:G333051

R;Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A;Description: Primer-directed sequencing of human papillomavirus types.

A;Reference number: S36469

A;Accession: S36521

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-149

A;Cross-references: EMBL:X74477; NID:G396997; PIDN:CAA52561.1; PID:G396998

A;Experimental source: strain 35H

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

F;30-66/Region: zinc finger CCCC motif

F;103-139/Region: zinc finger CCCC motif

Query Match 75.0%; Score 39; DB 1; Length 149;
 Best Local Similarity 87.5%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VCDKCLKF 9

|||||

62 VCMKCLKF 69

RESULT 4

S00726

N;Alternate names: A-raf-1 (EC 2.7.1.-) - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-1989 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004

C;Accession: S00726

R;Ishikawa, F.; Takaku, F.; Nagao, M.; Sugimura, T.

Oncogene Res. 1, 243-253, 1987

A;Title: The complete primary structure of the rat A-raf cDNA coding region: conservative
 A;Reference number: S00726; MUID:88217324; PMID:3449797

A;Accession: S00726

A;Molecule type: mRNA

A;Residues: 1-604 <ISH>

A;Cross-references: UNIPROT:P14056; EMBL:X06942; NID:G55756; PIDN:CAA30023.1; PID:G55757

C;Function:

A;Description: signal transduction between cell membrane and nucleus; after phosphorylation
 A;Pathway: MAP kinase cascade
 A;Note: in mouse, expressed in urogenital tissues and, at lower levels, in other tissues
 C;Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; protein kinase C; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene;
 F;99-144/Domain: protein kinase C zinc-binding repeat homology <KZN>

F;306-572/Domain: protein kinase homology <KIN>

F;314-322/Region: protein kinase ATP-binding motif

F;99,125,128,144/Binding site: zinc (His, Cys, Cys) #status predicted

F;112,115,133,136/Binding site: zinc (Cys, Cys, His, Cys) #status predicted

F;214/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

F;223/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

F;334/Active site: Lys #status predicted

F;580/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 75.0%; Score 39; DB 1; Length 604;
 Best Local Similarity 77.8%; Pred. No. 69;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVCDKCLKF 9

|||||

110 AFCDFCLKF 118

RESULT 5

TVHUAF

N;Alternate names: A-raf-1 (EC 2.7.1.-) - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1988 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004

C;Accession: A53026; A26439; A21541

R;Lee, J.E.; Beck, T.W.; Brennscheidt, U.; DeGennaro, L.J.; Rapp, U.R.

Genomics 20, 43-55, 1994

A;Title: The complete sequence and promoter activity of the human A-raf-1 gene (ARAF1).

A;Reference number: A53026; MUID:94292185; PMID:8020955

A;Accession: A53026

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-606 <LEE>

A;Cross-references: UNIPROT:P10398; GB:L24038; NID:G508473; PIDN:AAA65219.1; PID:G780127

R;Beck, T.W.; Huleihel, M.; Gurnell, M.; Bonner, T.I.; Rapp, U.R.

Nucleic Acids Res. 15, 595-609, 1987

A;Title: The complete coding sequence of the human A-raf-1 oncogene and transforming acti

A;Reference number: A26439; MUID:87146380; PMID:3029685

A;Accession: A26439

A;Molecule type: mRNA

A;Residues: 1-297, 'X', 299-606 <BEC>

A;Cross-references: EMBL:X04790; NID:G28820; PIDN:CAA28476.1; PID:G1340152

R;Mark, G.E.; Seeley, T.W.; Shows, T.B.; Mountz, J.D.

Proc. Natl. Acad. Sci. U.S.A. 83, 6312-6316, 1986

A;Title: pks, a raf-related sequence in humans.

A;Reference number: A23541; MUID:86313571; PMID:3529082

A;Accession: A23541

A;Molecule type: mRNA

A;Residues: 292-367, 'p', 369-377, 'v', 379-468, 'p', 470-477, 't', 479-589 <MAR>

A;Cross-references: GB:M13829; NID:G189999; PIDN:AA808754.1; PID:G387023

C;Genetics:

A;Gene: GDB:ARAF1

A;Cross-references: GDB:I19004; OMIM:311010

A;Map position: Xp11.3-Xp11.23

A;Introns: 32/3; 67/2; 101/3; 153/2; 186/2; 230/3; 240/1; 288/3; 356/2; 415/2; 431/1; 470/

C;Function:

A;Description: signal transduction between cell membrane and nucleus; after phosphorylation

A;Pathway: MAP kinase cascade

A;Note: in mouse, expressed in urogenital tissues and, at lower levels, in other tissues

C;Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; protein kinase C; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene;

C;Keywords: Afp; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene;

F;99-144/Domain: protein kinase C zinc-binding repeat homology <KZN>

F;308-574/Domain: protein kinase homology <KIN>

F;316-324/Region: protein kinase ATP-binding motif

F;99,125,128,144/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F;112,115,133,136/Binding site: zinc (Cys, Cys, His, Cys) #status predicted

F;214/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

F:223/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted
 F:336/Active site: lys #status predicted
 F:582/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 75.0%; Score 39; DB 1; Length 606;
 Best Local Similarity 77.8%; Pred. No. 69;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVCDKCLK 9
 DB 110 AFCDCLKF 118
 ||| |||

RESULT 6
 E64449
 Hypothetical protein MJ1198 - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C:Accession: E64449
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MUID:96337999; PMID:8688087
 A:Accession: E64449
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-761 <BUL>
 A:Cross-references: UNIPROT:Q58598; GB:U67561; GB:L77117; NID:G2826373; PIDN:AAB99202.1;
 C:Genetics:
 A:Map position: FOR1142325-1144610
 C:Superfamily: conserved hypothetical protein MJ1198

Query Match 75.0%; Score 39; DB 2; Length 761;
 Best Local Similarity 85.7%; Pred. No. 81;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VCDKCLK 8
 DB 102 LCDKCLK 108
 :||| |||

RESULT 7
 A64389
 Hydrogenase accessory protein - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C:Accession: A64389
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MUID:96337999; PMID:8688087
 A:Accession: A64389
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-766 <BUL>
 A:Cross-references: UNIPROT:Q58123; GB:U67518; GB:L77117; NID:G2826312; PIDN:AAB98708.1;
 C:Genetics:
 A:Map position: REV648382-646082
 C:Superfamily: carbamoyl phosphate-converting enzyme ([NiFe]-hydrogenase maturation fac

Query Match 75.0%; Score 39; DB 2; Length 766;
 Best Local Similarity 75.0%; Pred. No. 82;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVCDKCLK 8
 DB 115 AICDDCLK 122
 ||| |||

RESULT 8

A71079

Probable transcription regulatory protein hypF - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 14-Apr-2003

C:Accession: A71079

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine,

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: A71079

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-773 <KAN>

A:Cross-references: GB:APO00004; NID:G236131; PIDN:BA29991.1; PID:G3257308

A:Experimental source: strain OT3

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH0897

C:Superfamily: carbamoyl phosphate-converting enzyme ([NiFe]-hydrogenase maturation fac

Query Match 75.0%; Score 39; DB 2; Length 773;

Best Local Similarity 75.0%; Pred. No. 82;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVCDKCLK 8

DB 108 AICDDCLK 115

||| |||

RESULT 9

E6 protein - human papillomavirus type 31

C:Species: human papillomavirus type 31

A:Note: host Homo sapiens (man)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C:Accession: A32444

R:Goldsbrough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.

Virology 171, 306-311, 1989

A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associ

A:Reference number: A94398; MUID:89299478; PMID:2545036

A:Accession: A32444

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-149 <GOL>

A:Cross-references: UNIPROT:P17386; GB:J04353; NID:G333048; PIDN:AAA46950.1; PID:G459916

C:Comment: This protein may be involved in the oncogenic potential of this virus.

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:30-66/Region: zinc finger CCCC motif

F:103-139/Region: zinc finger CCCC motif

Query Match 73.1%; Score 38; DB 1; Length 149;

Best Local Similarity 75.0%; Pred. No. 35;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VCDKCLK 9

DB 62 VCTKCLRF 69

||| |||

RESULT 10

T29204

Hypothetical protein F28F9.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T29204

R:Nelson, J.; Wohldmann, P.

submitted to the EMBL Data Library, September 1996

A:Description: The sequence of C. elegans cosmid F28F9.

A;Reference number: Z20587

A;Accession: T23204

A;Status: Preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-680 <NEL>

A;Cross-references: UNIPROT:Q94196; EMBL:U70850; PIDN:AAB09122.1; GSPDB:GN00022; CESP:F2

A;Experimental source: strain Bristol N2; clone F28F9

C;Genetics:

A;Gene: CESP:F28F9.1

A;Map position: 4

A;Introns: 53/3; 234/3; 268/3; 331/3; 485/2; 531/3; 589/1

Query Match

Best Local Similarity 73.1%; Score 38; DB 2; Length 680;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CDKCLK 8

Db 623 CDKCLK 628

RESULT 11

E86451

Probable copia-type polyprotein, 28768-32772 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: E86451

R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: E86451

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1334 <STO>

A;Cross-references: UNIPROT:Q9C7V1; GB:AE005172; NID:g10092575; PIDN:AAG12968.1; GSPDB:G

C;Genetics:

A;Map position: 1

C;Superfamily: retrovirus-related polyprotein

Query Match

Best Local Similarity 73.1%; Score 38; DB 2; Length 1334;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVCDKCLK 8

Db 469 AVCDICLK 476

RESULT 12

G64488

reverse gyrase (intein-containing) - Methanococcus jannaschii

N;Contains: intein

C;Species: Methanococcus jannaschii

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C;Accession: G64488

R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,

; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;

reon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C

A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

A;Reference number: A64300; MUID:96337999; PMID:8688087

A;Accession: G64488

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-1613 <BUL>

A;Cross-references: UNIPROT:Q58907; GB:U67592; GB:L77117; NID:g2826425; PIDN:AAB99531.1;

C;Genetics:

A;Map position: FOR1483759-1488600

C;Keywords: ATP; nucleotide binding; P-loop; protein splicing

F;100-107/Region: nucleotide-binding motif A (P-loop)

F;219-224/Region: nucleotide-binding motif B

F;225-228/Region: DEAD/H motif #status atypical

Query Match

Best Local Similarity 73.1%; Score 38; DB 2; Length 1613;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VCDKCLK 8

Db 26 VCEKCLK 32

RESULT 13

T28432

variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum)

N;Alternate names: erythrocyte membrane binding protein 1 (EMPI)

C;Species: Plasmodium falciparum

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T28432

R;Su, X.Z.; Heatwole, V.M.; Wertheimer, S.P.; Guinet, F.; Herrfeldt, J.A.; Peterson, D.S.

Cell 82, 89-100, 1995

A;Title: The large diverse gene family var encodes proteins involved in cytoadherence and

A;Reference number: Z20487; MUID:95330813; PMID:7606788

A;Accession: T28432

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-3078 <SUX>

A;Cross-references: UNIPROT:Q26031; EMBL:L40608; NID:g886374; PID:g886375; PIDN:AAA75396.

C;Genetics:

A;Gene: var-1

A;Introns: 2611/3

Query Match

Best Local Similarity 73.1%; Score 38; DB 2; Length 3078;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CDKCLKF 9

Db 2220 CDCLKF 2226

RESULT 14

E88250

protein T21B10.5 [imported] - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: E88250

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_elec

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A;Accession: E88250

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-242 <STO>

A;Cross-references: UNIPROT:Q22626; GB:chr_II; PIDN:CAA92695.1; PID:g3879989; GSPDB:GN001

C;Genetics:

A;Gene: T21B10.5

A;Map position: 2

Query Match

Best Local Similarity 71.2%; Score 37; DB 2; Length 242;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CDKCLKF 9

Db 62 CDKCNKF 68
|||||
RESULT 15
T25044
hypothetical protein T21B10.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25044
R;Baynes, C.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19973
A;Accession: T25044
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-272 <WIL>
A;Cross-references: UNIPROT:Q22626; EMBL:Z68318; PIDN:CAA92695.2; GSPDB:GN000020; CESP:T2
A;Experimental source: clone T21B10
C;Genetics:
A;Gene: CESP:T21B10.5
A;Map position: 2
A;Introns: 34/3; 69/1; 91/1; 212/1; 243/1
Query Match 71.2%; Score 37; DB 2; Length 272;
Best Local Similarity 85.7%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 CDKCLKF 9
Db 92 CDKCNKF 98
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Search completed: June 28, 2005, 23:32:03
Job time : 12.05 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-46

Perfect score: 52

Sequence: 1 AVCDKCLKP 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	20	16	US-10-476-570-11
2	52	100.0	22	16	US-10-612-818-4
3	52	100.0	151	14	US-10-177-390-6
4	52	100.0	151	17	US-10-484-063-20
5	52	100.0	151	17	US-10-484-063-27
6	52	100.0	158	17	US-10-858-384-2
7	52	100.0	158	17	US-10-367-057-16
8	52	100.0	171	16	US-10-472-724-2
9	52	100.0	266	9	US-09-367-309A-1
10	52	100.0	273	13	US-10-000-903-4
11	52	100.0	273	17	US-10-899-771-4
					Sequence 11, Appli
					Sequence 4, Appli
					Sequence 6, Appli
					Sequence 20, Appli
					Sequence 27, Appli
					Sequence 2, Appli
					Sequence 16, Appli
					Sequence 2, Appli
					Sequence 1, Appli
					Sequence 4, Appli

12	52	100.0	292	13	US-10-000-903-10	Sequence 10, Appli
13	52	100.0	292	17	US-10-899-771-10	Sequence 10, Appli
14	52	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
15	52	100.0	371	17	US-10-899-771-6	Sequence 6, Appli
16	52	100.0	390	13	US-10-000-903-14	Sequence 14, Appli
17	52	100.0	390	17	US-10-899-771-14	Sequence 14, Appli
18	42	80.8	241	15	US-10-425-114-53267	Sequence 53267, A
19	42	80.8	256	15	US-10-424-599-197309	Sequence 197309, A
20	41	78.8	9	17	US-10-484-063-6	Sequence 6, Appli
21	41	78.8	10	8	US-08-344-824-237	Sequence 237, App
22	39	75.0	152	15	US-10-424-599-199555	Sequence 199555, A
23	39	75.0	228	15	US-10-424-599-242913	Sequence 242913, A
24	39	75.0	604	14	US-10-205-342-1	Sequence 1, Appli
25	39	75.0	604	17	US-10-732-923-13443	Sequence 13443, A
26	39	75.0	606	14	US-10-440-341-5	Sequence 5, Appli
27	39	75.0	606	15	US-10-394-322A-53	Sequence 53, Appli
28	39	75.0	606	16	US-10-311-527-4	Sequence 4, Appli
29	39	75.0	606	16	US-10-473-127-1815	Sequence 1815, Ap
30	39	75.0	606	16	US-10-473-127-1816	Sequence 1816, Ap
31	39	75.0	606	16	US-10-473-127-1818	Sequence 1818, Ap
32	39	75.0	606	16	US-10-473-127-1819	Sequence 1819, Ap
33	39	75.0	606	16	US-10-473-127-1820	Sequence 1820, Ap
34	39	75.0	606	16	US-10-473-127-1821	Sequence 1821, Ap
35	39	75.0	606	17	US-10-732-923-13689	Sequence 13689, A
36	39	75.0	606	18	US-10-491-545A-2	Sequence 2, Appli
37	39	75.0	606	18	US-10-491-545A-4	Sequence 4, Appli
38	39	75.0	609	16	US-10-473-127-1817	Sequence 1817, Ap
39	39	75.0	609	16	US-10-473-127-1822	Sequence 1822, Ap
40	38	73.1	2710	13	US-10-153-273-12	Sequence 12, Appli
41	37.5	72.1	53	16	US-10-425-115-272852	Sequence 272852, A
42	37.5	72.1	139	16	US-10-437-963-121605	Sequence 121605, A
43	37.5	72.1	139	16	US-10-767-701-41080	Sequence 41080, A
44	37.5	72.1	139	16	US-10-425-115-199043	Sequence 199043, A
45	37.5	72.1	144	15	US-10-425-114-61603	Sequence 61603, A

ALIGNMENTS

RESULT 1

US-10-476-570-11
; Sequence 11, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: Papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 61-80

Query Match 100.0%; Score 52; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVCDKCLKF 9
 |||||
 Db 8 AVCDKCLKF 16

RESULT 2

US-10-612-818-4
 ; Sequence 4, Application US/10612818
 ; Publication No. US20040110925A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Impact Diagnostics
 ; APPLICANT: Impact Diagnostics
 ; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus
 ; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papi
 ; TITLE OF INVENTION: Associated Cancers
 ; FILE REFERENCE: 3352-2-2
 ; CURRENT APPLICATION NUMBER: US/10/612,818
 ; CURRENT FILING DATE: 2003-07-01
 ; PRIOR APPLICATION NUMBER: US 60/394,172
 ; PRIOR FILING DATE: 2002-07-02
 ; PRIOR APPLICATION NUMBER: US 09/828,645
 ; PRIOR FILING DATE: 2001-04-05
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 22
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Derived from the E6 early coding region of HPV 16
 US-10-612-818-4

Query Match 100.0%; Score 52; DB 16; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.22;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVCDKCLKF 9
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 Db 7 AVCDKCLKF 15

RESULT 3

US-10-177-390-6
 ; Sequence 6, Application US/10177390
 ; Publication No. US20030143743A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schuler, Gerold
 ; APPLICANT: N.V. Antwerp Innovatiecentrum
 ; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
 ; TITLE OF INVENTION: Polynucleotides by Electroporation
 ; FILE REFERENCE: 021505wo/TH/ml
 ; CURRENT APPLICATION NUMBER: US/10/177,390
 ; CURRENT FILING DATE: 2002-06-20
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus type 16
 US-10-177-390-6

Query Match 100.0%; Score 52; DB 14; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVCDKCLKF 9
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 Db 61 AVCDKCLKF 69

RESULT 4

US-10-484-063-20
 ; Sequence 20, Application US/10484063

; Publication No. US20050048467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SASTRY, K. JAGANNADHA
 ; APPLICANT: TORTOLERO-LUNA, GUILLERMO
 ; APPLICANT: FOLLEN, MICHELE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
 ; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
 ; FILE REFERENCE: UTSC:560US
 ; CURRENT APPLICATION NUMBER: US/10/484,063
 ; CURRENT FILING DATE: 2004-01-16
 ; PRIOR APPLICATION NUMBER: PCT/US02/23198
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 60/306,809
 ; PRIOR FILING DATE: 2001-07-20
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus
 US-10-484-063-20

Query Match 100.0%; Score 52; DB 17; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVCDKCLKF 9
 |||||
 Db 61 AVCDKCLKF 69

RESULT 5

US-10-484-063-27
 ; Sequence 27, Application US/10484063
 ; Publication No. US20050048467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SASTRY, K. JAGANNADHA
 ; APPLICANT: TORTOLERO-LUNA, GUILLERMO
 ; APPLICANT: FOLLEN, MICHELE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
 ; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
 ; FILE REFERENCE: UTSC:560US
 ; CURRENT APPLICATION NUMBER: US/10/484,063
 ; CURRENT FILING DATE: 2004-01-16
 ; PRIOR APPLICATION NUMBER: PCT/US02/23198
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 60/306,809
 ; PRIOR FILING DATE: 2001-07-20
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 27
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus type 16
 US-10-484-063-27

Query Match 100.0%; Score 52; DB 17; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVCDKCLKF 9
 |||||
 Db 61 AVCDKCLKF 69

RESULT 6

US-10-858-384-2
 ; Sequence 2, Application US/10858384
 ; Publication No. US2005003025A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHOPPIN, JEANNINE
 ; APPLICANT: BOURGAULT VILLADA, ISABELLE
 ; APPLICANT: GUILLET, JEAN-GERARD

```

; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULALLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match      100.0%; Score 52; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVCDKCLKF 9
DB 68 AVCDKCLKF 76

RESULT 7
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chuan Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match      100.0%; Score 52; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVCDKCLKF 9
DB 68 AVCDKCLKF 76

RESULT 8
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7

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; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match      100.0%; Score 52; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVCDKCLKF 9
DB 73 AVCDKCLKF 81

RESULT 9
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 52; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVCDKCLKF 9
DB 68 AVCDKCLKF 76

RESULT 10
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4

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; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match          100.0%; Score 52; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVCDKCLKF 9
Db 174 AVCDKCLKF 182

RESULT 11
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

Query Match          100.0%; Score 52; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVCDKCLKF 9
Db 174 AVCDKCLKF 182

RESULT 12
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match          100.0%; Score 52; DB 13; Length 292;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVCDKCLKF 9
Db 193 AVCDKCLKF 201

RESULT 13
US-10-899-771-10
; Sequence 10, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus
; OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-10

Query Match          100.0%; Score 52; DB 17; Length 292;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVCDKCLKF 9
Db 193 AVCDKCLKF 201

RESULT 14
US-10-000-903-6
; Sequence 6, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
```

```

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-6

Query Match      100.0%; Score 52; DB 13; Length 371;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVCDKCLKF 9
Db 174 AVCDKCLKF 182

RESULT 15
US-10-899-771-6
; Sequence 6, Application US/10899771
; Publication NO. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 927262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 16)
US-10-899-771-6

Query Match      100.0%; Score 52; DB 17; Length 371;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVCDKCLKF 9
Db 174 AVCDKCLKF 182

Search completed: June 29, 2005, 05:18:11
Job time : 116.15 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-45
Perfect score: 53
Sequence: 1 YAVCDKCLK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	81	2 Q80886	Q80886 human papil
2	53	100.0	84	2 Q80882	Q80882 human papil
3	53	100.0	90	2 Q80883	Q80883 human papil
4	53	100.0	90	2 Q80884	Q80884 human papil
5	53	100.0	90	2 Q80885	Q80885 human papil
6	53	100.0	91	2 Q80887	Q80887 human papil
7	53	100.0	99	2 Q19B2	Q19B2 human papil
8	53	100.0	103	2 Q19D6	Q19D6 human papil
9	53	100.0	130	2 Q19B4	Q19B4 human papil
10	53	100.0	130	2 Q19B8	Q19B8 human papil
11	53	100.0	130	2 Q19C0	Q19C0 human papil
12	53	100.0	130	2 Q19C2	Q19C2 human papil
13	53	100.0	130	2 Q19C8	Q19C8 human papil
14	53	100.0	130	2 Q19D0	Q19D0 human papil
15	53	100.0	138	2 Q19D2	Q19D2 human papil
16	53	100.0	143	2 Q19B6	Q19B6 human papil
17	53	100.0	143	2 Q19C4	Q19C4 human papil
18	53	100.0	151	2 Q12335	Q12335 human papil
19	53	100.0	151	2 Q12336	Q12336 human papil
20	53	100.0	151	2 Q76TS0	Q76TS0 human papil
21	53	100.0	151	2 Q778I6	Q778I6 human papil
22	53	100.0	151	2 Q778I6	Q778I6 human papil
23	53	100.0	151	2 Q77JC7	Q77JC7 human papil
24	53	100.0	151	2 Q77ZJ5	Q77ZJ5 human papil
25	53	100.0	151	2 Q80963	Q80963 human papil
26	53	100.0	151	2 Q80966	Q80966 human papil
27	53	100.0	151	2 Q89640	Q89640 human papil
28	53	100.0	151	2 Q89648	Q89648 human papil
29	53	100.0	151	2 Q89708	Q89708 human papil
30	53	100.0	151	2 Q89755	Q89755 human papil
31	53	100.0	151	2 Q89852	Q89852 human papil

32	53	100.0	151	2 Q89887	Q89887 human papil
33	53	100.0	151	2 Q8B564	Q8B564 human papil
34	53	100.0	151	2 Q8BB19	Q8BB19 human papil
35	53	100.0	151	2 Q8BB20	Q8BB20 human papil
36	53	100.0	151	2 Q8BB21	Q8BB21 human papil
37	53	100.0	151	2 Q8B8C3	Q8B8C3 human papil
38	53	100.0	151	2 Q9W931	Q9W931 human papil
39	53	100.0	151	2 Q9WMP2	Q9WMP2 human papil
40	53	100.0	151	2 Q9WMP4	Q9WMP4 human papil
41	53	100.0	151	2 Q9WMP5	Q9WMP5 human papil
42	53	100.0	158	1 V56 HPV16	P03126 human papil
43	53	100.0	158	2 Q8JMU8	Q8Jmu8 human papil
44	53	100.0	158	2 Q8QHN0	Q8qhn0 human papil
45	53	100.0	158	2 Q8QHP5	Q8qhp5 human papil

ALIGNMENTS

RESULT 1
Q80886 PRELIMINARY; PRT; 81 AA.
AC Q80886;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G. Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14515; AAB60569.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9784 MW; DD5FEDBC9F845B97 CRC64;
Query Match 100.0%; Score 53; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.18; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0

QY 1 YAVCDKCLK 9
Db 19 YAVCDKCLK 27
RESULT 2
Q80882 PRELIMINARY; PRT; 84 AA.
AC Q80882;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=HPV16; TISSUE=Cervical;
RA Haegert D.G. Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14511; AAB60565.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

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DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 84
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;
  Query Match 100.0%; Score 53; DB 2; Length 84;
  Best Local Similarity 100.0%; Pred. No. 0.19;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 9
Db 16 YAVCDKCLK 24

RESULT 3
Q80883
ID Q80883 PRELIMINARY; PRT; 90 AA.
AC Q80883
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14512; AAB60566.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10904 MW; 5D3ADF843AD6060B CRC64;
  Query Match 100.0%; Score 53; DB 2; Length 90;
  Best Local Similarity 100.0%; Pred. No. 0.19;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 9
Db 19 YAVCDKCLK 27

RESULT 4
Q80884
ID Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.

FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFACCC01 CRC64;
  Query Match 100.0%; Score 53; DB 2; Length 90;
  Best Local Similarity 100.0%; Pred. No. 0.19;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 9
Db 19 YAVCDKCLK 27

RESULT 5
Q80885
ID Q80885 PRELIMINARY; PRT; 90 AA.
AC Q80885
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14514; AAB60568.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10964 MW; BC2531643ACBA76C CRC64;
  Query Match 100.0%; Score 53; DB 2; Length 90;
  Best Local Similarity 100.0%; Pred. No. 0.19;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 9
Db 19 YAVCDKCLK 27

RESULT 6
Q80887
ID Q80887 PRELIMINARY; PRT; 91 AA.
AC Q80887
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14516; AAB60570.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 11136 MW; 22FDF3EA185ACBA7 CRC64;

```



```
Query Match      100.0%; Score 53; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
DB 19 YAVCDKCLK 27

RESULT 7
Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404704; AAL01365.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;

Query Match      100.0%; Score 53; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
DB 36 YAVCDKCLK 44

RESULT 8
Q919D6 PRELIMINARY; PRT; 103 AA.
AC Q919D6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404692; AAL01342.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 103
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;

Query Match      100.0%; Score 53; DB 2; Length 103;

Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
DB 12 YAVCDKCLK 20

RESULT 9
Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227BEDDC CRC64;

Query Match      100.0%; Score 53; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
DB 39 YAVCDKCLK 47

RESULT 10
Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01359.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match      100.0%; Score 53; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 YAVCDKCLK 9
|||||
DB 39 YAVCDKCLK 47

RESULT 11

Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0; (Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
SQ

Query Match 100.0%; Score 53; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
|||||
DB 39 YAVCDKCLK 47

RESULT 12

Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2; (Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01355.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
SQ

Query Match 100.0%; Score 53; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
|||||
DB 39 YAVCDKCLK 47

RESULT 13

Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8; (Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404696; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;
SQ

Query Match 100.0%; Score 53; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
|||||
DB 39 YAVCDKCLK 47

RESULT 14

Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0; (Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404695; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 130 AA; 15735 MW; 98FB30EEDCA21AF3 CRC64;
SQ

Query Match 100.0%; Score 53; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
|||||
DB 39 YAVCDKCLK 47

RESULT 15

Q919D2 PRELIMINARY; PRT; 138 AA.
 AC Q919D2;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404694; AAL01345.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 SQ SEQUENCE 138 AA; 16696 MW; 481ESA90895FC2 CRC64;
 Query Match 100.0%; Score 53; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAVCDKCLK 9
 Db 47 YAVCDKCLK 55

Search completed: June 28, 2005, 23:28:10
 Job time : 56.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-46
Perfect score: 52
Sequence: 1 AVCDKCLKF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	52	100.0	10	3	US-08-159-339A-561
2	52	100.0	11	3	US-08-159-339A-1170
3	52	100.0	158	4	US-09-980-523A-2
4	52	100.0	162	1	US-08-316-239B-3
5	52	100.0	162	1	US-08-316-239B-4
6	52	100.0	172	3	US-08-860-165-12
7	52	100.0	172	3	US-08-860-165-14
8	52	100.0	172	3	US-09-359-382-12
9	52	100.0	172	3	US-09-359-382-14
10	52	100.0	266	3	US-08-860-165-10
11	52	100.0	266	3	US-09-359-382-10
12	52	100.0	266	4	US-09-367-309A-1
13	52	100.0	273	3	US-09-485-885-4
14	52	100.0	292	3	US-09-485-885-10
15	52	100.0	371	3	US-09-485-885-6
16	52	100.0	390	3	US-09-485-885-14
17	48	92.3	9	3	US-08-159-339A-74
18	47	90.4	20	2	US-08-934-915-162
19	46	88.5	8	3	US-08-159-339A-1169
20	39	75.0	606	4	US-08-207-954-5
21	38	73.1	2710	2	US-08-568-459A-12
22	38	73.1	2710	2	US-08-487-826B-12
23	38	73.1	2710	3	US-09-210-288-12
24	38	73.1	3060	2	US-08-487-826B-14
25	37	71.2	2441	1	US-08-194-468-2
26	37	71.2	2441	3	US-08-961-739-2
27	37	71.2	2441	3	US-09-514-247A-8

28	37	71.2	2441	4	US-09-686-316-2	Sequence 2, Appli
29	37	71.2	2442	3	US-09-514-247A-10	Sequence 10, Appl
30	37	71.2	2442	4	US-09-538-092-1370	Sequence 1370, Ap
31	36	69.2	74	4	US-09-134-000C-4206	Sequence 4206, Ap
32	35	67.3	69	4	US-09-732-210-151	Sequence 151, App
33	35	67.3	74	4	US-09-543-681A-8341	Sequence 8341, Ap
34	35	67.3	165	4	US-09-706-722A-3	Sequence 3, Appli
35	35	67.3	184	1	US-08-464-339A-2	Sequence 2, Appli
36	35	67.3	184	1	US-08-468-847B-18	Sequence 18, Appl
37	35	67.3	184	4	US-09-706-722A-2	Sequence 2, Appli
38	35	67.3	184	4	US-09-949-016-6782	Sequence 6782, Ap
39	35	67.3	184	5	PCT-US94-14388-2	Sequence 2, Appli
40	35	67.3	202	4	US-09-949-016-10546	Sequence 10546, A
41	35	67.3	308	2	US-09-047-026A-23	Sequence 23, Appl
42	35	67.3	352	4	US-09-248-796A-18530	Sequence 18530, A
43	35	67.3	377	4	US-09-252-991A-19705	Sequence 19705, A
44	35	67.3	642	3	US-08-872-855-10	Sequence 10, Appl
45	35	67.3	921	4	US-09-252-991A-20327	Sequence 20327, A

ALIGNMENTS

RESULT 1
US-08-159-339A-561
; Sequence 561, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cellis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 561:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-561

Query Match 100.0%; Score 52; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVCDKCLKF 9
| | | | | | | | | |
Db 1 AVCDKCLKF 9

RESULT 2

US-08-159-339A-1170
; Sequence 1170, Application US/08159339A

; Patent No. 6037135

; GENERAL INFORMATION:

; APPLICANT: Kubo, Ralph T.

; APPLICANT: Grey, Howard M.

; APPLICANT: Sette, Alessandro

; APPLICANT: Celis, Betteban

; TITLE OF INVENTION: HLA Binding peptides and Their

; TITLE OF INVENTION: Uses

; NUMBER OF SEQUENCES: 1254

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/159,339A

; FILING DATE: 29-NOV-1993

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/926,666

; FILING DATE: 07-AUG-1992

; APPLICATION NUMBER: US 08/027,746

; FILING DATE: 05-MAR-1993

; APPLICATION NUMBER: US 08/103,396

; FILING DATE: 06-AUG-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Ellen Lauver

; REGISTRATION NUMBER: 32,762

; REFERENCE/DOCKET NUMBER: 018623-005030US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; TELEX:

; INFORMATION FOR SEQ ID NO: 1170:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-159-339A-1170

Query Match 100.0%; Score 52; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVCDKCLKF 9
| | | | | | | | | |
Db 3 AVCDKCLKF 11

RESULT 3

US-09-980-523A-2

; Sequence 2, Application US/09980523A

; Patent No. 6783763

; GENERAL INFORMATION:

; APPLICANT: CHOPPIN, JEANNINE

; APPLICANT: BOURGAULT VILLADA, ISABELLE

; APPLICANT: GUILLET, JEAN-GERARD

; APPLICANT: CONNAN, FRANCINE

; APPLICANT: FERRIES, ESTELLE

; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 AND E7

; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE

; TITLE OF INVENTION: PARTICULARLY IN VACCINATION

; FILE REFERENCE: WO/1 AO INS

; CURRENT APPLICATION NUMBER: US/09/980,523A

; PRIOR FILING DATE: 2002-04-29

; PRIOR FILING DATE: 2000-05-31

; PRIOR APPLICATION NUMBER: FR 99/07012

; PRIOR FILING DATE: 1999-06-03

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 158

; TYPE: PRT

; ORGANISM: Human Papillomavirus

US-09-980-523A-2

Query Match 100.0%; Score 52; DB 4; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.32;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVCDKCLKF 9

| | | | | | | | | |

Db 68 AVCDKCLKF 76

RESULT 4

US-08-316-239B-3

; Sequence 3, Application US/08316239B

; Patent No. 5679509

; GENERAL INFORMATION:

; APPLICANT: Wheeler, Cosette M.

; APPLICANT: Parmenter, Cheryl A.

; TITLE OF INVENTION: Methods and a Diagnostic Aid for

; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an

; TITLE OF INVENTION: Increased Risk of Developing Cervical Cancer

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jagtiani & Associates

; STREET: 6126 Rocky Way Court

; CITY: Centreville

; STATE: VA

; COUNTRY: USA

; ZIP: 20120-3400

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/316,239B

; FILING DATE: 30-SEP-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Jagtiani, Ajay A.

; REGISTRATION NUMBER: 35,205

; REFERENCE/DOCKET NUMBER: UNME-0001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 817-9453

; TELEFAX: (703) 803-9387

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

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; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 52; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVCDKCLKF 9
Db 68 AVCDKCLKF 76

RESULT 5
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 52; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVCDKCLKF 9
Db 68 AVCDKCLKF 76

RESULT 6
US-08-860-165-12
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; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match 100.0%; Score 52; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVCDKCLKF 9
Db 6 AVCDKCLKF 14

RESULT 7
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match 100.0%; Score 52; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVCDKCLKF 9
Db 137 AVCDKCLKF 145

RESULT 8
US-09-359-382-12
; Sequence 12, Application US/09359382
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; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; OTHER INFORMATION: Description of Artificial Sequence: type 16
US-09-359-382-12

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Query Match      100.0%; Score 52; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 AVCDKCLKP 9
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Db 6 AVCDKCLKP 14

```

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RESULT 9
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; OTHER INFORMATION: Description of Artificial Sequence: type 16
US-09-359-382-14

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Query Match      100.0%; Score 52; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 AVCDKCLKP 9
   |||||
Db 137 AVCDKCLKP 145

```

```

RESULT 10
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557

```

```

; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

```

```

Query Match      100.0%; Score 52; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 AVCDKCLKP 9
   |||||
Db 68 AVCDKCLKP 76

```

```

RESULT 11
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; OTHER INFORMATION: Description of Artificial Sequence: type 16
US-09-359-382-10

```

```

Query Match      100.0%; Score 52; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 AVCDKCLKP 9
   |||||
Db 68 AVCDKCLKP 76

```

```

RESULT 12
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:

```



```

; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 52; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVCDKCLKF 9
Db 68 AVCDKCLKF 76

RESULT 13
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match      100.0%; Score 52; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVCDKCLKF 9
Db 174 AVCDKCLKF 182

RESULT 14
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match      100.0%; Score 52; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVCDKCLKF 9
Db 174 AVCDKCLKF 182

Search completed: June 28, 2005, 23:37:47
Job time : 17.05 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)
78.367 Million cell updates/sec

Title: US-08-170-344-45
Perfect score: 53
Sequence: 1 YAVCDKCLK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	158	1 W6WLHS	protein E6 - human
2	42	79.2	740	2 E69420	hydrogenase expres
3	40	75.5	149	1 W6WL35	E6 protein - human
4	39	73.6	761	2 E64449	hypothetical prote
5	39	73.6	766	2 E64389	hydrogenase acces
6	39	73.6	773	2 A71079	probable transcrip
7	38	71.7	107	2 T16784	hypothetical prote
8	38	71.7	123	2 D72856	AcOrf-52 protein -
9	38	71.7	187	2 T32826	hypothetical prote
10	38	71.7	194	2 T41796	AcMNPV orf52 - Bom
11	38	71.7	552	2 S45886	hypothetical prote
12	38	71.7	680	2 T29204	hypothetical prote
13	38	71.7	688	2 E88197	protein him-14 (im
14	38	71.7	1334	2 E86451	probable copia-tyr
15	38	71.7	1613	2 G64488	reverse gyrase (in
16	37	69.8	151	1 W6WL51	E6 protein - human
17	37	69.8	456	2 T24796	hypothetical prote
18	37	69.8	2440	2 S39162	transcription coac
19	37	69.8	2441	2 S39161	CREB-binding prote
20	37	69.8	3190	2 T13828	CREB-binding prote
21	36	67.9	101	2 E71607	metal binding prot
22	36	67.9	117	2 E64628	hydrogenase expres
23	36	67.9	153	1 S15621	E6 protein - human
24	36	67.9	296	1 JQ1325	DNA excision repai
25	36	67.9	510	2 T24396	hypothetical prote
26	36	67.9	657	2 S64073	hypothetical prote
27	36	67.9	1404	1 A48196	protein-tyrosine k
28	36	67.9	2231	2 S53416	SEN1 protein - yea
29	35	66.0	69	2 A70308	ribosomal protein

ALIGNMENTS

RESULT 1

W6WLHS

protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virolgy 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SEB>

A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

J.Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

R. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10427

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C:Genetics:

A:Gene: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 100.0% Score 53; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 9

Db 67 YAVCDKCLK 75

RESULT 2

E69420

hydrogenase expression/formation regulatory protein (hypF) homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 14-Apr-2003

C:Accession: E69420

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,

.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeos

A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: E69420
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-740 <KLE>
A;Cross-references: GB:AE001009; GB:AE000782; NID:g2689332; PIDN:AAB98976.1; PID:g264920
C;Superfamily: carbamoyl phosphate-converting enzyme ([NiFe]-hydrogenase maturation factor)

Query Match 79.2%; Score 42; DB 2; Length 740;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVCDKCLK 9
|:|:|:|:|:
Db 100 AVCDKCLK 107

RESULT 3
W6WL35
E6 protein - human papillomavirus type 35
C;Species: human papillomavirus type 35
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: E40824; S36521
R;Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A;Title: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35
A;Reference number: A40824; MUID:92124753; PMID:1310198
A;Accession: E40824
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-149 <MAR>
A;Cross-references: UNIPROT:P27228; GB:M74117; NID:G333050; PIDN:AAA46966.1; PID:G333051
R;Delius, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36521
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149
A;Cross-references: EMBL:X74477; NID:G396997; PIDN:CAA52561.1; PID:G396998
A;Experimental source: strain 35H
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 75.5%; Score 40; DB 1; Length 149;
Best Local Similarity 77.8%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
|:|:|:|:|:
Db 60 YGVCMKCLK 68

RESULT 4
E64449
hypoetical protein MJ1198 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: E64449
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: E64449
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;Residues: 1-761 <BUL>
A;Cross-references: UNIPROT:Q58598; GB:U67561; GB:L77117; NID:g2826373; PIDN:AAB99202.1;
C;Genetics:
A;Map position: FOR1142325-1144610
C;Superfamily: conserved hypothetical protein MJ1198

Query Match 73.6%; Score 39; DB 2; Length 761;
Best Local Similarity 85.7%; Pred. No. 87;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VCDKCLK 9
|:|:|:|:|:
Db 102 LCDKCLK 108

RESULT 5
A64389
hydrogenase accessory protein - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: A64389
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: A64389
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-766 <BUL>
A;Cross-references: UNIPROT:Q58123; GB:U67518; GB:L77117; NID:g2826312; PIDN:AAB98708.1;
C;Genetics:
A;Map position: REV648382-646082
C;Superfamily: carbamoyl phosphate-converting enzyme ([NiFe]-hydrogenase maturation factor)

Query Match 73.6%; Score 39; DB 2; Length 766;
Best Local Similarity 75.0%; Pred. No. 87;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AVCDKCLK 9
|:|:|:|:|:
Db 115 AICDDCLK 122

RESULT 6
A71079
probable transcription regulatory protein hypF - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 14-Apr-2003
C;Accession: A71079
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon, Pyrococcus horikoshii
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: A71079
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-773 <KAW>
A;Cross-references: GB:AP000004; NID:g3236131; PIDN:BAA29991.1; PID:g3257308
A;Experimental source: strain OF3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH0897
C;Superfamily: carbamoyl phosphate-converting enzyme ([NiFe]-hydrogenase maturation factor)

Query Match 73.6%; Score 39; DB 2; Length 773;
Best Local Similarity 75.0%; Pred. No. 88;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AVCDKCLK 9

Db 108 AICDDCLK 115
|:|:| |

RESULT 7
T16784
hypothetical protein T02G5.6 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16784
R:Pauley, A.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of *C. elegans* cosmid T02G5.
A:Reference number: Z18577
A:Accession: T16784
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-107 <PAU>
A:Cross-references: UNIPROT:Q22103; EMBL:U41105; NID:g1086772; PID:g1086777; PIDN:AAA824
C:Genetics:
A:Gene: CESP:T02G5.6
A:Introns: 63/3; 87/2

Query Match 71.7%; Score 38; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 9
|:|:| |

Db 53 YAICEKVLK 61
|:|:| |

RESULT 8
D72856
AcOrf-52 protein - *Autographa californica* nuclear polyhedrosis virus
C:Species: *Autographa californica* nuclear polyhedrosis virus, AcMNPV
A:Note: dsDNA virus
C>Date: 12-Nov-1999
C:Accession: D72856
R:Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A:Title: The complete DNA sequence of *Autographa californica* nuclear polyhedrosis virus.
A:Reference number: A72850; MUID:94303173; PMID:8030224
A:Accession: D72856
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-123 <AYR>
A:Cross-references: UNIPROT:P41456; GB:L22858; NID:g510708; PIDN:AAA66682.1; PID:g559121
C:Genetics:
A:Gene: AcOrf-52

Query Match 71.7%; Score 38; DB 2; Length 123;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 8
|:|:| |

Db 73 YLCCDCKL 80
|:|:| |

RESULT 9
T32826
hypothetical protein H19M22.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
C:Accession: T32826
R:Wilson, R.; Wamsley, P.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of *C. elegans* cosmid H19M22.
A:Reference number: Z21229
A:Accession: T32826
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-187 <WIL>
A:Cross-references: EMBL:AF040648; PIDN:AA895000.1; GSPDB:GN00021; CESP:H19M22.4
A:Experimental source: strain Bristol N2; clone H19M22
C:Genetics:
A:Gene: CESP:H19M22.4
A:Map position: 3
A:Introns: 33/3; 100/3
C:Superfamily: *Caenorhabditis elegans* hypothetical protein H19M22.4

Query Match 71.7%; Score 38; DB 2; Length 187;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 8
|:|:| |

Db 159 FAVCQKCL 166
|:|:| |

RESULT 10
T41796
AcMNPV orf52 - *Bombyx mori* nuclear polyhedrosis virus (isolate T3)
C:Species: *Bombyx mori* nuclear polyhedrosis virus, BmSNPV
A:Variety: isolate T3
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41796
R:Gomi, S.; Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A:Title: Sequence analysis of the genome of *Bombyx mori* nucleopolyhedrovirus.
A:Reference number: Z22020; MUID:9281911; PMID:10355780
A:Accession: T41796
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-194 <KAM>
A:Cross-references: UNIPROT:O92417; EMBL:L33180; PIDN:AAC63725.1
A:Experimental source: isolate T3
C:Genetics:
A:Note: Orf_41

Query Match 71.7%; Score 38; DB 2; Length 194;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 8
|:|:| |

Db 73 YLCCDCKL 80
|:|:| |

RESULT 11
S45886
hypothetical protein YBR030w - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: hypothetical protein YBR0314
C:Species: *Saccharomyces cerevisiae*
C>Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: S45886; S46560
R:Grivell, L.A.; de Haan, M.; Maat, M.J.; Smits, P.H.M.
submitted to the Protein Sequence Database, August 1994
A:Reference number: S45875
A:Accession: S45886
A:Molecule type: DNA
A:Residues: 1-552 <GRI>
A:Cross-references: UNIPROT:P38222; EMBL:Z35899; NID:g536241; PIDN:CAA84972.1; PID:g53624
A:Experimental source: strain S288C
R:Smits, P.H.M.; de Haan, M.; Maat, C.; Grivell, L.A.
Yeast 10(Suppl.A), S75-S80, 1994
A:Title: The complete sequence of a 33 kb fragment on the right arm of chromosome II from
ly identified genes and a homologue of the SCO1 gene.
A:Reference number: S46551; MUID:94378725; PMID:8091864
A:Accession: S46560
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-552 <SMI>
A:Cross-references: EMBL:X76078; NID:g498748; PIDN:CAA53686.1; PID:g498758
A:Experimental source: strain S288C

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993

C:Genetics:

C:Cross-references: SGD:S0000234

A:Map position: 2R

C:Superfamily: Saccharomyces cerevisiae hypothetical protein YBR030W

Query Match 71.7%; Score 38; DB 2; Length 552;
Best Local Similarity 85.7%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAVCDK 7
| | | | |
DB 238 YVCDK 244

RESULT 12

T29204

hypothetical protein F28F9.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T29204

R:Nelson, J.; Wohldmann, P.

submitted to the EMBL Data Library, September 1996

A:Description: The sequence of C. elegans cosmid F28F9.

A:Reference number: Z20587

C:Genetics:

A:Accession: T29204

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-680 <NEL>

C:Cross-references: UNIPROT:Q94196; EMBL:U70850; PIDN:AA09122.1; GSPDB:GN00022; CESP:F2

A:Experimental source: strain Bristol N2; clone F28F9

C:Genetics:

A:Gene: CESP:F28F9.1

A:Map position: 4

A:Introns: 53/3; 234/3; 268/3; 331/3; 485/2; 531/3; 589/1

Query Match 71.7%; Score 38; DB 2; Length 680;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CDKCLK 9
| | | | |
DB 623 CDKCLK 628

RESULT 13

E88197

protein him-14 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

C:Accession: E88197

R:anonymous; The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A>Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A:Reference number: A75000; MUID:99069613; PMID:9851916

A>Note: see websites genome.wustl.edu/gac/C_elegans/ and www.sanger.ac.uk/Projects/C_ele

A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

C:Accession: E88197

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-688 <STO>

A:Cross-references: GB:chr_II; PIDN:AB93433.1; PID:gl330382; GSPDB:GN00020

C:Genetics:

A:Gene: him-14

A:Map position: 2

Query Match 71.7%; Score 38; DB 2; Length 688;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
| | | | |
DB 529 YAICEKVLK 537

RESULT 14

E86451

probable copia-type polyprotein, 28768-32772 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: E86451

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chiu, C.W.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: E86451

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1334 <STO>

C:Cross-references: UNIPROT:Q9C7Y1; GB:AB005172; NID:gi0092575; PIDN:AAG12968.1; GSPDB:G

C:Genetics:

A:Map position: 1

C:Superfamily: retrovirus-related polyprotein

Query Match 71.7%; Score 38; DB 2; Length 1334;
Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AVCDKCLK 9
| | | | |
DB 469 AVCDKCLK 476

RESULT 15

G64488

reverse gyrase (intein-containing) - Methanococcus jannaschii

N:Contains: intein

C:Species: Methanococcus jannaschii

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C:Accession: G64488

R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.

Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;

son, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.

A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.

A:Reference number: A64300; MUID:96337999; PMID:8688087

A:Accession: G64488

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1613 <BUL>

A:Cross-references: UNIPROT:Q58907; GB:U67592; GB:L77117; NID:g2826425; PIDN:AAB99531.1;

C:Genetics:

A:Map position: FOR1483759-1488600

C:Keywords: ATP; nucleotide binding; P-loop; protein splicing

F:100-107/Region: nucleotide-binding motif A (P-loop)

F:219-224/Region: nucleotide-binding motif B

F:225-228/Region: DEAD/H motif #status atypical

Query Match 71.7%; Score 38; DB 2; Length 1613;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VCDKCLK 9
| | | | |
DB 26 VCEKCLK 32

Search completed: June 28, 2005, 23:32:02

Job time : 12.05 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-45

Perfect score: 53

Sequence: 1 YAVCDKCLK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PTC_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PTCUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	53	100.0	20	16	US-10-476-570-11
2	53	100.0	22	16	US-10-612-818-4
3	53	100.0	151	14	US-10-177-390-6
4	53	100.0	151	17	US-10-484-063-20
5	53	100.0	151	17	US-10-484-063-27
6	53	100.0	158	17	US-10-858-384-2
7	53	100.0	158	17	US-10-367-057-16
8	53	100.0	171	16	US-10-472-724-2
9	53	100.0	266	9	US-09-367-309A-1
10	53	100.0	273	13	US-10-000-903-4
11	53	100.0	273	17	US-10-899-771-4

12	53	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
13	53	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
14	53	100.0	371	13	US-10-000-903-6	Sequence 6, Appl
15	53	100.0	371	17	US-10-899-771-6	Sequence 6, Appl
16	53	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
17	53	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
18	48	90.6	9	17	US-10-484-063-6	Sequence 6, Appl
19	48	90.6	10	8	US-08-344-824-237	Sequence 237, Appl
20	44	81.0	9	8	US-08-344-824-346	Sequence 346, App
21	43	81.1	292	15	US-10-424-599-205655	Sequence 205655,
22	42	79.2	241	15	US-10-425-114-53267	Sequence 53267, A
23	42	79.2	256	15	US-10-424-599-197309	Sequence 197309,
24	39	73.6	152	15	US-10-424-599-199555	Sequence 199555,
25	38	71.7	43	17	US-10-721-793-222	Sequence 222, App
26	38	71.7	43	17	US-10-721-793-224	Sequence 224, App
27	38	71.7	688	15	US-10-369-493-5438	Sequence 5438, Ap
28	38	71.7	781	15	US-10-424-599-265840	Sequence 265840,
29	37	69.8	330	16	US-10-437-963-157042	Sequence 157042,
30	37	69.8	1696	16	US-10-437-963-128565	Sequence 128565,
31	37	69.8	2429	17	US-10-732-923-18427	Sequence 18427, A
32	37	69.8	2440	17	US-10-732-923-18452	Sequence 18452, A
33	37	69.8	2441	13	US-10-109-886-8	Sequence 8, Appli
34	37	69.8	2441	16	US-10-628-957-2	Sequence 2, Appli
35	37	69.8	2441	16	US-10-473-127-643	Sequence 643, App
36	37	69.8	2441	17	US-10-732-923-18428	Sequence 18428, A
37	37	69.8	2441	17	US-10-732-923-18429	Sequence 18429, A
38	37	69.8	2442	13	US-10-109-886-10	Sequence 10, Appl
39	37	69.8	2442	16	US-10-473-127-631	Sequence 631, App
40	37	69.8	2442	16	US-10-473-127-633	Sequence 633, App
41	37	69.8	2442	16	US-10-473-127-645	Sequence 645, App
42	37	69.8	2442	16	US-10-473-127-647	Sequence 647, App
43	37	69.8	2442	17	US-10-732-923-18450	Sequence 18450, A
44	37	69.8	2442	17	US-10-732-923-18451	Sequence 18451, A
45	37	69.8	3190	17	US-10-732-923-18448	Sequence 18448, A

ALIGNMENTS

RESULT 1

US-10-476-570-11
; Sequence 11, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: Papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476, 570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 61-80

Query Match 100.0%; Score 53; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
 Db 7 YAVCDKCLK 15

RESULT 2

US-10-612-818-4
 ; Sequence 4, Application US/10612818
 ; Publication No. US20040110925A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Impact Diagnostics
 ; TITLE OF INVENTION: Impact Diagnostics
 ; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus
 ; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papi
 ; TITLE OF INVENTION: Associated Cancers
 ; FILE REFERENCE: 3352-2-2
 ; CURRENT APPLICATION NUMBER: US/10/612,818
 ; CURRENT FILING DATE: 2003-07-01
 ; PRIOR APPLICATION NUMBER: US 60/394,172
 ; PRIOR FILING DATE: 2002-07-02
 ; PRIOR APPLICATION NUMBER: US 09/828,645
 ; PRIOR FILING DATE: 2001-04-05
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 22
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Derived from the E6 early coding region of HPV 16
 US-10-612-818-4

Query Match 100.0%; Score 53; DB 16; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
 Db 6 YAVCDKCLK 14

RESULT 3

US-10-177-390-6
 ; Sequence 6, Application US/10177390
 ; Publication No. US20030143743A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schuler, Gerold
 ; APPLICANT: N.V. Antwerps Innovatiecentrum
 ; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
 ; TITLE OF INVENTION: Polynucleotides by Electroporation
 ; FILE REFERENCE: 021505wo/JH/ml
 ; CURRENT APPLICATION NUMBER: US/10/177,390
 ; CURRENT FILING DATE: 2002-06-20
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus type 16
 US-10-177-390-6

Query Match 100.0%; Score 53; DB 14; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
 Db 6 YAVCDKCLK 68

RESULT 4

US-10-484-063-20
 ; Sequence 20, Application US/10484063

; Publication No. US20050048467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SASTRY, K. JAGANNADHA
 ; APPLICANT: TORTOLERO-LUNA, GUILLERMO
 ; APPLICANT: FOLLEN, MICHELE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
 ; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
 ; FILE REFERENCE: UTSC:560US
 ; CURRENT APPLICATION NUMBER: US/10/484,063
 ; CURRENT FILING DATE: 2004-01-16
 ; PRIOR APPLICATION NUMBER: PCT/US02/23198
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 60/306,809
 ; PRIOR FILING DATE: 2001-07-20
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus
 US-10-484-063-20

Query Match 100.0%; Score 53; DB 17; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
 Db 60 YAVCDKCLK 68

RESULT 5

US-10-484-063-27
 ; Sequence 27, Application US/10484063
 ; Publication No. US20050048467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SASTRY, K. JAGANNADHA
 ; APPLICANT: TORTOLERO-LUNA, GUILLERMO
 ; APPLICANT: FOLLEN, MICHELE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
 ; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
 ; FILE REFERENCE: UTSC:560US
 ; CURRENT APPLICATION NUMBER: US/10/484,063
 ; CURRENT FILING DATE: 2004-01-16
 ; PRIOR APPLICATION NUMBER: PCT/US02/23198
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 60/306,809
 ; PRIOR FILING DATE: 2001-07-20
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 27
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus type 16
 US-10-484-063-27

Query Match 100.0%; Score 53; DB 17; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
 Db 60 YAVCDKCLK 68

RESULT 6

US-10-858-384-2
 ; Sequence 2, Application US/10858384
 ; Publication No. US2005003302SAI
 ; GENERAL INFORMATION:
 ; APPLICANT: CHOPPIN, JEANNINE
 ; APPLICANT: BOURGAULT VILLADA, ISABELLE
 ; APPLICANT: GUILLET, JEAN-GERARD

```
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match      100.0%; Score 53; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 9
Db 67 YAVCDKCLK 75

RESULT 7
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Cui, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match      100.0%; Score 53; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 9
Db 67 YAVCDKCLK 75

RESULT 8
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
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; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match      100.0%; Score 53; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 9
Db 72 YAVCDKCLK 80

RESULT 9
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 53; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 9
Db 67 YAVCDKCLK 75

RESULT 10
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05385
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
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; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match          100.0%; Score 53; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.7; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 YAVCDKCLK 9
Db 173 YAVCDKCLK 181

RESULT 11
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

Query Match          100.0%; Score 53; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.7; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 YAVCDKCLK 9
Db 173 YAVCDKCLK 181

RESULT 12
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match          100.0%; Score 53; DB 13; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.8; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 YAVCDKCLK 9
Db 192 YAVCDKCLK 200

RESULT 13
US-10-899-771-10
; Sequence 10, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus
; pneumoniae and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-10

Query Match          100.0%; Score 53; DB 17; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.8; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 YAVCDKCLK 9
Db 192 YAVCDKCLK 200

RESULT 14
US-10-000-903-6
; Sequence 6, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-6

Query Match      100.0%; Score 53; DB 13; Length 371;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAVCDKCLK 9
Db      173 YAVCDKCLK 181

RESULT 15
US-10-899-771-6
; Sequence 6, Application US/10899771
; Publication NO. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and B6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 16)
US-10-899-771-6

Query Match      100.0%; Score 53; DB 17; Length 371;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAVCDKCLK 9
Db      173 YAVCDKCLK 181

Search completed: June 29, 2005, 05:18:11
Job time : 117.15 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-45
Perfect score: 53
Sequence: 1 YAVCDKCLK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	11	3	US-08-159-339A-1170
2	53	100.0	158	4	US-09-980-523A-2
3	53	100.0	162	1	US-08-316-239B-3
4	53	100.0	162	1	US-08-316-239B-4
5	53	100.0	172	3	US-08-860-165-12
6	53	100.0	172	3	US-08-860-165-14
7	53	100.0	172	3	US-09-359-382-12
8	53	100.0	172	3	US-09-359-382-14
9	53	100.0	266	3	US-08-860-165-10
10	53	100.0	266	3	US-09-359-382-10
11	53	100.0	266	4	US-09-367-309A-1
12	53	100.0	273	3	US-09-485-885-4
13	53	100.0	292	3	US-09-485-885-10
14	53	100.0	371	3	US-09-485-885-6
15	53	100.0	390	3	US-09-485-885-14
16	48	90.6	20	2	US-08-934-915-162
17	46	86.8	8	3	US-08-159-339A-1169
18	46	86.8	10	3	US-08-159-339A-561
19	42	79.2	9	3	US-08-159-339A-74
20	39	73.6	170	4	US-09-270-767-32119
21	39	73.6	170	4	US-09-270-767-47336
22	37	69.8	2441	1	US-08-194-468-2
23	37	69.8	2441	3	US-08-961-739-2
24	37	69.8	2441	3	US-09-514-247A-8
25	37	69.8	2441	4	US-09-686-316-2
26	37	69.8	2442	3	US-09-514-247A-10
27	37	69.8	2442	4	US-09-538-092-1370

28	36	67.9	74	4	US-09-134-000C-4206	Sequence 4206, Ap
29	36	67.9	1404	4	US-09-345-473E-24	Sequence 24, Appl
30	35	66.0	9	3	US-08-159-339A-239	Sequence 239, App
31	35	66.0	69	4	US-09-732-210-151	Sequence 151, App
32	35	66.0	132	4	US-09-513-999C-6410	Sequence 6410, Ap
33	35	66.0	342	2	US-08-871-288A-17	Sequence 17, Appl
34	35	66.0	342	3	US-08-871-267B-25	Sequence 25, Appl
35	35	66.0	342	3	US-09-618-419-25	Sequence 25, Appl
36	35	66.0	342	3	US-09-163-674-17	Sequence 17, Appl
37	35	66.0	395	3	US-09-032-372-1	Sequence 1, Appl
38	35	66.0	2414	1	US-08-227-536-2	Sequence 2, Appl
39	35	66.0	2414	4	US-09-538-092-1289	Sequence 1289, Ap
40	35	66.0	2414	5	PCT-US95-04862-2	Sequence 2, Appl
41	34	64.2	74	4	US-09-513-999C-7370	Sequence 7370, Ap
42	34	64.2	94	1	US-08-456-265A-108	Sequence 108, App
43	34	64.2	94	2	US-08-971-217-108	Sequence 108, App
44	34	64.2	94	3	US-09-350-600-108	Sequence 108, App
45	34	64.2	94	4	US-09-906-234-108	Sequence 108, App

ALIGNMENTS

RESULT 1
US-08-159-339A-1170
; Sequence 1170, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cellis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-1170

Query Match 100.0%; Score 53; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 9
Db 2 YAVCDKCLK 10

RESULT 2

US-09-980-523A-2

; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/1 AO INS

; CURRENT APPLICATION NUMBER: US/09/980,523A

; CURRENT FILING DATE: 2002-04-29

; PRIOR APPLICATION NUMBER: PCT/FR00/01513

; PRIOR FILING DATE: 2000-05-31

; PRIOR APPLICATION NUMBER: FR 99/07012

; PRIOR FILING DATE: 1999-06-03

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 158

; TYPE: PRT

; ORGANISM: Human Papillomavirus

US-09-980-523A-2

Query Match 100.0%; Score 53; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 9
Db 67 YAVCDKCLK 75

RESULT 3

US-08-316-239B-3

; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Jagtiani & Associates

STREET: 6126 Rocky Way Court

CITY: Centreville

STATE: VA

COUNTRY: USA

ZIP: 20120-3400

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

NAME: Jagtiani, Ajay A.

REGISTRATION NUMBER: 35,205

REFERENCE/DOCKET NUMBER: UNME-0001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 817-9453

TELEFAX: (703) 803-9387

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 162 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: protein

HYPOTHETICAL: NO

US-08-316-239B-3

Query Match 100.0%; Score 53; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 9

Db 67 YAVCDKCLK 75

RESULT 4

US-08-316-239B-4

; Sequence 4, Application US/08316239B

; Patent No. 5679509

; GENERAL INFORMATION:

; APPLICANT: Wheeler, Cosette M.

; APPLICANT: Parmenter, Cheryl A.

; TITLE OF INVENTION: Methods and a Diagnostic Aid for

; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an

; TITLE OF INVENTION: Increased Risk of Developing Cervical Cancer

; TITLE OF INVENTION: Cervical Cancer

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Jagtiani & Associates

STREET: 6126 Rocky Way Court

CITY: Centreville

STATE: VA

COUNTRY: USA

ZIP: 20120-3400

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/316,239B

FILING DATE: 30-SEP-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jagtiani, Ajay A.

REGISTRATION NUMBER: 35,205

REFERENCE/DOCKET NUMBER: UNME-0001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 817-9453

TELEFAX: (703) 803-9387

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 162 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: protein

HYPOTHETICAL: NO

US-08-316-239B-4

Query Match 100.0%; Score 53; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
DB 67 YAVCDKCLK 75

RESULT 5
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match 100.0%; Score 53; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
DB 5 YAVCDKCLK 13

RESULT 6
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match 100.0%; Score 53; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
DB 136 YAVCDKCLK 144

RESULT 7
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match 100.0%; Score 53; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAVCDKCLK 9
DB 5 YAVCDKCLK 13

RESULT 8
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match 100.0%; Score 53; DB 3; Length 172;

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Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 9
Db 136 YAVCDKCLK 144

RESULT 9
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 53; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 9
Db 67 YAVCDKCLK 75

RESULT 10
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 53; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 9
Db 136 YAVCDKCLK 144

RESULT 11
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 53; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 9
Db 67 YAVCDKCLK 75

RESULT 12
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 53; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAVCDKCLK 9
Db 173 YAVCDKCLK 181
```

```
RESULT 13
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match      100.0%; Score 53; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAVCDKCLK 9
DB      192 YAVCDKCLK 200
```

```
RESULT 14
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match      100.0%; Score 53; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAVCDKCLK 9
DB      173 YAVCDKCLK 181
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```
RESULT 15
US-09-485-885-14
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```
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match      100.0%; Score 53; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAVCDKCLK 9
DB      192 YAVCDKCLK 200
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Search completed: June 28, 2005, 23:37:47
Job time : 18.05 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-44
Perfect score: 52
Sequence: 1 IVYRDGNPY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	81	2 Q80886	Q80886 human papil
2	52	100.0	84	2 Q80882	Q80882 human papil
3	52	100.0	90	2 Q80883	Q80883 human papil
4	52	100.0	90	2 Q80884	Q80884 human papil
5	52	100.0	90	2 Q80885	Q80885 human papil
6	52	100.0	91	2 Q80887	Q80887 human papil
7	52	100.0	99	2 Q1982	Q1982 human papil
8	52	100.0	103	2 Q19D6	Q19D6 human papil
9	52	100.0	130	2 Q19B4	Q19B4 human papil
10	52	100.0	130	2 Q19B8	Q19B8 human papil
11	52	100.0	130	2 Q19C0	Q19C0 human papil
12	52	100.0	130	2 Q19C2	Q19C2 human papil
13	52	100.0	130	2 Q19C8	Q19C8 human papil
14	52	100.0	130	2 Q19D0	Q19D0 human papil
15	52	100.0	138	2 Q19D2	Q19D2 human papil
16	52	100.0	143	2 Q19B6	Q19B6 human papil
17	52	100.0	151	2 Q12335	Q12335 human papil
18	52	100.0	151	2 Q12336	Q12336 human papil
19	52	100.0	151	2 Q76TS0	Q76TS0 human papil
20	52	100.0	151	2 Q77E16	Q77E16 human papil
21	52	100.0	151	2 Q77E16	Q77E16 human papil
22	52	100.0	151	2 Q77JC7	Q77JC7 human papil
23	52	100.0	151	2 Q77ZJ5	Q77ZJ5 human papil
24	52	100.0	151	2 Q80966	Q80966 human papil
25	52	100.0	151	2 Q89640	Q89640 human papil
26	52	100.0	151	2 Q89648	Q89648 human papil
27	52	100.0	151	2 Q89708	Q89708 human papil
28	52	100.0	151	2 Q89755	Q89755 human papil
29	52	100.0	151	2 Q89852	Q89852 human papil
30	52	100.0	151	2 Q89887	Q89887 human papil
31	52	100.0	151	2 Q8B564	Q8B564 human papil

32 52 100.0 151 2 Q8BB19 human papil
33 52 100.0 151 2 Q8BB20 human papil
34 52 100.0 151 2 Q8BB21 human papil
35 52 100.0 151 2 Q8W8C3 human papil
36 52 100.0 151 2 Q8W8C3 human papil
37 52 100.0 151 2 Q8W8C3 human papil
38 52 100.0 151 2 Q8W8C3 human papil
39 52 100.0 151 2 Q8W8C3 human papil
40 52 100.0 151 2 Q8W8C3 human papil
41 52 100.0 158 1 V56 HPV16 human papil
42 52 100.0 158 2 Q8JMU8 human papil
43 52 100.0 158 2 Q8JMU8 human papil
44 52 100.0 158 2 Q8JMU8 human papil
45 52 100.0 158 2 Q8JMU8 human papil

ALIGNMENTS

RESULT 1
Q80886 PRELIMINARY; PRT; 81 AA.
AC Q80886;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
RN NCBI_TaxID=10566;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haggert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14515; AAB60569.2; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9784 MW; DD5FEDBC9F845B97 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.19; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 IVYRDGNPY 9
Db 11 IVYRDGNPY 19

RESULT 2
Q80882 PRELIMINARY; PRT; 84 AA.
AC Q80882;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
RN NCBI_TaxID=10566;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical;
RA Haggert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14511; AAB60565.2; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.

```

DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 84
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;
  Query Match 100.0%; Score 52; DB 2; Length 84;
  Best Local Similarity 100.0%; Pred. No. 0.19; 0; Indels 0; Gaps 0;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IVYRDGNPY 9
Db 8 IVYRDGNPY 16

RESULT 3
Q80883 PRELIMINARY; PRT; 90 AA.
AC Q80883
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14512; AAB60566.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10904 MW; 5D3ADF843AD6060B CRC64;
  Query Match 100.0%; Score 52; DB 2; Length 90;
  Best Local Similarity 100.0%; Pred. No. 0.21; 0; Indels 0; Gaps 0;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IVYRDGNPY 9
Db 11 IVYRDGNPY 19

RESULT 4
Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.

DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.

FT NON_TER 1
FT NON_TER 84
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;
  Query Match 100.0%; Score 52; DB 2; Length 84;
  Best Local Similarity 100.0%; Pred. No. 0.19; 0; Indels 0; Gaps 0;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IVYRDGNPY 9
Db 8 IVYRDGNPY 16

RESULT 5
Q80885 PRELIMINARY; PRT; 90 AA.
AC Q80885
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14514; AAB60568.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10964 MW; BC2531643ACBA76C CRC64;
  Query Match 100.0%; Score 52; DB 2; Length 90;
  Best Local Similarity 100.0%; Pred. No. 0.21; 0; Indels 0; Gaps 0;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IVYRDGNPY 9
Db 11 IVYRDGNPY 19

RESULT 6
Q80887 PRELIMINARY; PRT; 91 AA.
AC Q80887
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14516; AAB60570.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 11136 MW; 22FDF3EA185ACBA7 CRC64;
  Query Match 100.0%; Score 52; DB 2; Length 90;
  Best Local Similarity 100.0%; Pred. No. 0.21; 0; Indels 0; Gaps 0;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IVYRDGNPY 9
Db 11 IVYRDGNPY 19

```

```

Query Match      100.0%; Score 52; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
   |||||
DB 11 IVYRDGNPY 19

RESULT 7
Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404704; AAL01365.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT NON_TER 99
FT SEQUENCE 99 AA; 12005 MW; C2B96025EC370B38- CRC64;

Query Match      100.0%; Score 52; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
   |||||
DB 28 IVYRDGNPY 36

RESULT 8
Q919D6 PRELIMINARY; PRT; 103 AA.
AC Q919D6;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404692; AAL01342.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT NON_TER 103
FT SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B- CRC64;

Query Match      100.0%; Score 52; DB 2; Length 103;

Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
   |||||
DB 11 IVYRDGNPY 19

RESULT 9
Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT NON_TER 130
FT SEQUENCE 130 AA; 15792 MW; B6C2147D227EEDDC- CRC64;

Query Match      100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
   |||||
DB 31 IVYRDGNPY 39

RESULT 10
Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01359.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT NON_TER 130
FT SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F- CRC64;

Query Match      100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
QY 1 IVYRDGNPY 9
Db 31 IVYRDGNPY 39

RESULT 11
Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404696; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
Db 31 IVYRDGNPY 39

RESULT 12
Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01355.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
Db 31 IVYRDGNPY 39

RESULT 13
Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404696; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 130 AA; 15778 MW; 2830147D37880DC9 CRC64;
SQ SEQUENCE 130 AA; 15778 MW; 2830147D37880DC9 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
Db 31 IVYRDGNPY 39

RESULT 14
Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 130 AA; 15735 MW; 9EFB30BEDCA21AF3 CRC64;
SQ SEQUENCE 130 AA; 15735 MW; 9EFB30BEDCA21AF3 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
Db 31 IVYRDGNPY 39

RESULT 15
```


Q919D2
ID Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404694; AAL01345.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;
Query Match 100.0%; Score 52; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IVYRDGNPY 9
Db 39 IVYRDGNPY 47

Search completed: June 28, 2005, 23:28:09
Job time : 55.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)

78.367 Million cell updates/sec

Title: US-08-170-344-44

Perfect score: 52

Sequence: 1 IVYRDGNPY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	158	1 W6WLS8	protein E6 - human
2	48	92.3	149	1 W6WLS8	E6 protein - human
3	46	88.5	148	2 A61237	E6 protein - human
4	46	88.5	148	2 S35573	E6 protein - human
5	46	88.5	151	1 W6WLS1	E6 protein - human
6	43	82.7	149	1 W6WLS1	E6 protein - human
7	43	82.7	154	2 S36527	E6 protein - human
8	42	80.8	149	1 W6WLS3	E6 protein - human
9	40	76.9	2499	1 A30788	mannose 6-phosphat
10	39	75.0	196	2 S74510	signal peptidase I
11	39	75.0	409	2 D90268	conserved hypothet
12	38	73.1	150	2 S36544	E6 protein - human
13	38	73.1	158	1 W6WLS3	E6 protein - human
14	38	73.1	439	2 C75009	glutamine syntheta
15	38	73.1	443	2 D71143	probable glutamine
16	38	73.1	460	2 B82549	hypothetical prote
17	38	73.1	521	2 S76556	hypothetical prote
18	37	71.2	113	1 K2HUPR	Ig kappa chain V-I
19	37	71.2	237	2 A98357	hypothetical prote
20	37	71.2	237	2 AD2925	hypothetical prote
21	37	71.2	284	2 C70367	hypothetical prote
22	37	71.2	301	2 C71034	probable typeII DN
23	37	71.2	322	2 B69690	ribose ABC transpo
24	37	71.2	382	2 F75179	DNA topoisomerase
25	37	71.2	435	2 S52268	malate dehydrogena
26	37	71.2	441	2 S33066	malate dehydrogena
27	37	71.2	441	2 S38346	malate dehydrogena
28	37	71.2	719	2 S51739	transcription repr
29	37	71.2	845	2 JCS256	adipocyte transcri

30 37 71.2 857 2 JC4169 phosphoenolpyruvat
31 37 71.2 1227 2 T23004 hypothetical prote
32 36.5 70.2 351 2 H90139 x-pro aminopeptida
33 36 69.2 83 2 S34095 Ig kappa chain V r
34 36 69.2 114 2 S49572 Ig kappa chain pre
35 36 69.2 120 2 S42268 Ig kappa chain V r
36 36 69.2 120 2 S42267 Ig kappa chain V r
37 36 69.2 122 2 S40338 Ig kappa chain - h
38 36 69.2 133 1 K2HUPR Ig kappa chain pre
39 36 69.2 261 2 G47116 trifoliotoxin resis
40 36 69.2 344 2 F72524 probable acidic ri
41 36 69.2 353 2 T01978 hypothetical prote
42 36 69.2 413 2 D70137 cell division prot
43 36 69.2 583 2 G87261 gamma-glutamyltran
44 36 69.2 697 2 T26707 hypothetical prote
45 36 69.2 1082 2 T31112 ATPase 2 (EC 3.6.1

ALIGNMENTS

RESULT 1

W6WLS8

protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C>Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Krammer, G.; Duret, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

J.Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

R. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: 217014; MUID:91162763; PMID:1848319

A:Accession: T10427

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

A:Gene: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 52; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.05; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVYRDGNPY 9

Db 59 IVYRDGNPY 67

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A;Molecule type: DNA
A;Residues: 1-149 <KIR>
A;Cross-references: UNIPROT:P26555; GB:D90400; NID:G222386; PIDN:BA31845.1; PID:G333709
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 92.3%; Score 48; DB 1; Length 149;
Best Local Similarity 88.9%; Pred. No. 0.24;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
| | | | |
Db 52 IVYRDGNPF 60

RESULT 3
A61237
E6 protein - human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996
C;Accession: A61237
R;Takami, Y.; Kondoh, G.; Saito, J.; Noda, K.; Sudiro, T.M.; Sjahrurachman, A.; Warsa, U.
Int. J. Cancer 48, 516-522, 1991
A;Title: Cloning and characterization of human papillomavirus type 52 from cervical carcinoma
A;Reference number: A61237; MUID:91258022; PMID:1646174
A;Accession: A61237
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-148 <TAK>
C;Superfamily: papillomavirus E6 protein

Query Match 88.5%; Score 46; DB 2; Length 148;
Best Local Similarity 88.9%; Pred. No. 0.54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
| | | | |
Db 52 IVYRDNNPY 60

RESULT 4
S36573
E6 protein - human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36573
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36573
A;Molecule type: DNA
A;Residues: 1-148
A;Cross-references: UNIPROT:P36814; EMBL:X74481; NID:G397038; PIDN:CAA52585.1; PID:G397038
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 88.5%; Score 46; DB 2; Length 148;
Best Local Similarity 88.9%; Pred. No. 0.54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
| | | | |
Db 52 IVYRDNNPY 60

RESULT 5
WGWL51
E6 protein - human papillomavirus type 51
C;Species: human papillomavirus type 51
A;Note: host Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: E40415
R;Jungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991
A;Title: Biologic properties and nucleotide sequence analysis of human papillomavirus type 33
A;Reference number: A40415; MUID:91303675; PMID:1649326
C;Accession: E40415
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-151 <LUN>
A;Cross-references: UNIPROT:P26554; GB:M62877
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 88.5%; Score 46; DB 1; Length 151;
Best Local Similarity 88.9%; Pred. No. 0.55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
| | | | |
Db 52 IVYRDNNPY 60

RESULT 6
M6WL33
E6 protein - human papillomavirus type 33
C;Species: human papillomavirus type 33
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A03683
R;Cole, S.T.; Streeck, R.E.
J. Virol. 58, 991-995, 1986
A;Title: Genome organization and nucleotide sequence of human papillomavirus type 33, which
A;Reference number: A93020; MUID:86200464; PMID:3009902
A;Accession: A03683
A;Molecule type: DNA
A;Residues: 1-149 <COL>
A;Cross-references: UNIPROT:P06427; GB:M12732; NID:G333049; PIDN:AAA46958.1; PID:G463177
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 82.7%; Score 43; DB 1; Length 149;
Best Local Similarity 66.7%; Pred. No. 1.9;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
| | | | |
Db 52 VVYREGNPF 60

RESULT 7
S36527
E6 protein - human papillomavirus type 53
C;Species: human papillomavirus type 53
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36527
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36527
A;Molecule type: DNA
A;Residues: 1-154
A;Cross-references: UNIPROT:P36815; EMBL:X74482; NID:G397046; PIDN:CAA52591.1; PID:G397046
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 82.7%; Score 43; DB 2; Length 154;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
 :|||||
 Db 56 VVYRDGYPY 64

 RESULT 8
 W6WL35
 E6 protein - human papillomavirus type 35
 C:Species: human papillomavirus type 35
 A:Note: host Homo sapiens (man)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: E40824; S36521
 R:Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
 Virol. 186, 770-776, 1992
 A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35
 A:Reference number: A40824; MUID:92124753; PMID:1310198
 A:Accession: E40824
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-149 <MAR>
 A:Cross-references: UNIPROT:P27228; GB:M74117; NID:G333050; PIDN:AAA46966.1; PID:G333051
 R:Deilus, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A:Description: Primer-directed sequencing of human papillomavirus types.
 A:Reference number: S36469
 A:Accession: S36521
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-149
 A:Cross-references: EMBL:X74477; NID:G396997; PIDN:CAA52561.1; PID:G396998
 A:Experimental source: strain 35H
 C:Superfamily: papillomavirus E6 protein
 C:Keywords: DNA binding; early protein; zinc finger
 F:30-66/Region: zinc finger CCCC motif
 F:103-139/Region: zinc finger CCCC motif

 Query Match 80.8%; Score 42; DB 1; Length 149;
 Best Local Similarity 77.8%; Pred. No. 2.8;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 1 IVYRDGNPY 9
 :|||||
 Db 52 IVYREGQPY 60

 RESULT 9
 A30788
 mannose 6-phosphate receptor protein, cation-independent - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A25908; A30788; S09404
 R:Lebel, P.; Dahms, N.M.; Kornfeld, S.
 J. Biol. Chem. 263, 2563-2570, 1988
 A:Title: Cloning and sequence analysis of the cation-independent mannose 6-phosphate receptor
 A:Reference number: A32706; MUID:88115411; PMID:2963004
 A:Accession: A25908
 A:Molecule type: mRNA
 A:Residues: 1-2499 <LOB>
 A:Cross-references: UNIPROT:P08169; GB:J03527; NID:G162873; PIDN:AAA30455.1; PID:G162874
 R:Glickman, J.N.; Conibear, E.; Pearse, B.M.F.
 EMBO J. 8, 1041-1047, 1989
 A:Title: Specificity of binding of clathrin adaptors to signals on the mannose-6-phosphate
 A:Reference number: S09404; MUID:89305502; PMID:2545438
 A:Contents: annotation; HA-II adaptor binding
 C:Comment: This protein binds phosphorylated lysosomal enzymes and insulin-like growth factor
 C:Superfamily: mannose 6-phosphate receptor, cation-independent; fibronectin type II repeat
 C:Keywords: Golgi apparatus; membrane protein
 F:1912-1951/Domain: fibronectin type II repeat homology <2F1>
 F:2360-2363/Region: HA-II adaptor binding

 Query Match 76.9%; Score 40; DB 1; Length 2499;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 QY 1 IVYRDGNPY 9
 :|||||
 Db 715 LTYRDGTPY 723

 RESULT 10
 S74510
 signal peptidase I (EC 3.4.21.89) sl10716 - Synecocystis sp. (strain PCC 6803)
 N:Alternate names: leader peptidase I; protein sl10716
 C:Species: Synecocystis sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C:Accession: S74510
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis sp.
 A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S74510
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-196 <KAN>
 A:Cross-references: UNIPROT:P72660; EMBL:D90899; GB:AB001339; NID:G1651650; PIDN:BAA1666;
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Genetics:
 A:Gene: lep8
 C:Superfamily: signal peptidase I sips
 C:Keywords: hydrolase; serine proteinase

 Query Match 75.0%; Score 39; DB 2; Length 196;
 Best Local Similarity 87.5%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 IVYRDGNP 8
 :|||||
 Db 110 IVYRDGQP 117

 RESULT 11
 D90268
 conserved hypothetical protein [imported] - Sulfolobus solfataricus
 C:Species: Sulfolobus solfataricus
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C:Accession: D90268
 R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awaye, M.J.; Chan-arrrett, R.A.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. submitted to GenBank, April 2001
 A:Description: Sulfolobus solfataricus complete genome.
 A:Reference number: A99139
 A:Accession: D90268
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-409 <KUR>
 A:Cross-references: UNIPROT:Q97Y27; GB:AE006641; NID:G13814341; PIDN:AAK41403.1; GSPDB:G
 C:Genetics:
 A:Gene: SSO1152

 Query Match 75.0%; Score 39; DB 2; Length 409;
 Best Local Similarity 75.0%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 QY 1 IVYRDGNP 8
 :|||||
 Db 348 VVYRGNP 355

 RESULT 12
 S36544
 E6 protein - human papillomavirus type 26

C;Species: human papillomavirus type 26
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36544
R;Delius, H.; Hofmann, B.
A;Description: The EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36544
A;Molecule type: DNA
A;Residues: 1-150
A;Cross-references: UNIPROT:P36807; EMBL:X74472; NID:G396956; PIDN:CAA52530.1; PID:G396956
C;Superfamily: papillomavirus E6 protein
C;Keywords: early protein; zinc finger

Query Match 73.1%; Score 38; DB 2; Length 150;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVYRDGNPY 9
Db 52 VYRDRSPY 60
:|||||:|||

RESULT 13
W6WL39
E6 protein - human papillomavirus type 39
C;Species: human papillomavirus type 39
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A38502
R;Volpers, C.; Streeck, R.E.
Virolgy 181, 419-423, 1991
A;Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
A;Reference number: A38502; MUID:91135017; PMID:1847266
A;Accession: A38502
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-158 <VOL>
A;Cross-references: UNIPROT:P24835; GB:M62849; EMBL:M38185; NID:G333245; PIDN:AAA47050.1
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;32-68/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif

Query Match 73.1%; Score 38; DB 1; Length 158;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVYRDGNP 8
Db 54 VYRDGEP 61
:|||||

RESULT 14
C75009
Glutamine synthetase (glna) PAB1292 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: C75009
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A;Reference number: A75001
A;Accession: C75009
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-439 <KAW>
A;Cross-references: UNIPROT:Q9UY99; GB:AJ248288; GB:AL096836; NID:G5458960; PIDN:CAB5051
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1292
C;Superfamily: glutamate-ammonia ligase

Query Match 73.1%; Score 38; DB 2; Length 439;
Best Local Similarity 62.5%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VYRDGNPY 9
Db 88 IYKDGKPY 95
:|||||

RESULT 15
D71143
probable glutamine synthetase - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: D71143
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: D71143
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-443 <KAW>
A;Cross-references: UNIPROT:O58097; GB:AP000002; NID:G3236129; PIDN:BAA29433.1; PID:G3256
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH0359

Query Match 73.1%; Score 38; DB 2; Length 443;
Best Local Similarity 62.5%; Pred. No. 45;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VYRDGNPY 9
Db 92 IYKDGKPY 99
:|||||

Search completed: June 28, 2005, 23:32:01
Job time : 12.05 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-44
Perfect score: 52
Sequence: 1 IVYRDGNPY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	9	17 US-10-751-845-83	Sequence 83, Appl
2	52	100.0	15	16 US-10-476-570-30	Sequence 30, Appl
3	52	100.0	21	16 US-10-476-570-54	Sequence 54, Appl
4	52	100.0	22	16 US-10-476-570-26	Sequence 26, Appl
5	52	100.0	22	17 US-10-858-384-6	Sequence 6, Appl
6	52	100.0	23	16 US-10-476-570-27	Sequence 27, Appl
7	52	100.0	24	17 US-10-751-845-65	Sequence 65, Appl
8	52	100.0	117	17 US-10-751-845-126	Sequence 126, App
9	52	100.0	151	14 US-10-177-390-6	Sequence 6, Appl
10	52	100.0	151	17 US-10-484-063-20	Sequence 20, Appl
11	52	100.0	151	17 US-10-484-063-27	Sequence 27, Appl

12	52	100.0	158	17	US-10-858-384-2	Sequence 2, Appl
13	52	100.0	158	17	US-10-367-057-16	Sequence 16, Appl
14	52	100.0	171	16	US-10-472-724-2	Sequence 2, Appl
15	52	100.0	236	17	US-10-751-845-157	Sequence 157, App
16	52	100.0	237	17	US-10-751-845-158	Sequence 158, App
17	52	100.0	261	17	US-10-751-845-160	Sequence 160, App
18	52	100.0	266	9	US-09-367-309A-1	Sequence 1, Appl
19	52	100.0	273	13	US-10-000-903-4	Sequence 4, Appl
20	52	100.0	273	13	US-10-899-771-4	Sequence 4, Appl
21	52	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
22	52	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
23	52	100.0	371	13	US-10-000-903-6	Sequence 6, Appl
24	52	100.0	371	17	US-10-899-771-6	Sequence 6, Appl
25	52	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
26	52	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
27	48	92.3	9	11	US-09-739-466C-11	Sequence 11, Appl
28	45	86.5	536	15	US-10-367-095-10	Sequence 10, Appl
29	45	86.5	536	15	US-10-368-046-10	Sequence 10, Appl
30	45	86.5	536	16	US-10-367-367-10	Sequence 10, Appl
31	45	86.5	536	17	US-10-918-337-10	Sequence 10, Appl
32	44	84.6	20	16	US-10-476-570-11	Sequence 11, Appl
33	42	80.8	436	15	US-10-424-599-270568	Sequence 270568, A
34	42	80.8	443	15	US-10-425-114-45886	Sequence 45886, A
35	42	80.8	443	15	US-10-425-114-46250	Sequence 46250, A
36	42	80.8	443	15	US-10-425-114-51704	Sequence 51704, A
37	39	75.0	374	16	US-10-437-963-195496	Sequence 195496, A
38	39	75.0	415	16	US-10-437-963-195493	Sequence 195493, A
39	39	75.0	453	16	US-10-437-963-170490	Sequence 170490, A
40	39	75.0	582	16	US-10-437-963-180853	Sequence 180853, A
41	38	73.1	595	15	US-10-424-599-200824	Sequence 200824, A
42	37	71.2	9	14	US-10-161-097-42	Sequence 42, Appl
43	37	71.2	22	16	US-10-612-818-4	Sequence 4, Appl
44	37	71.2	103	15	US-10-424-599-270563	Sequence 270563, A
45	37	71.2	112	17	US-10-877-773-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-10-751-845-83
; Sequence 83, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiccz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751.845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-83

Query Match 100.0%; Score 52; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IVYRDGNPY 9
| | | | | | | | | |
Db 1 IVYRDGNPY 9

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RESULT 2
US-10-476-570-30
; Sequence 30, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 55-69
US-10-476-570-30

Query Match      100.0%; Score 52; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVYRDGNPY 9
Db 5 IVYRDGNPY 13

RESULT 3
US-10-476-570-54
; Sequence 54, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 21
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 46-67
US-10-476-570-54

Query Match      100.0%; Score 52; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 IVYRDGNPY 9
Db 13 IVYRDGNPY 21

RESULT 4
US-10-476-570-26
; Sequence 26, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 22
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 45-67
US-10-476-570-26

Query Match      100.0%; Score 52; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVYRDGNPY 9
Db 14 IVYRDGNPY 22

RESULT 5
US-10-858-384-6
; Sequence 6, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E6 of HPV
US-10-858-384-6

```



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Query Match      100.0%; Score 52; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
Db 14 IVYRDGNPY 22

RESULT 6
US-10-476-570-27
; Sequence 27, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 23
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 44-67
US-10-476-570-27

Query Match      100.0%; Score 52; DB 16; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
Db 15 IVYRDGNPY 23

RESULT 7
US-10-751-845-65
; Sequence 65, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Human Papilloma virus

Query Match      100.0%; Score 52; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
Db 16 IVYRDGNPY 24

RESULT 8
US-10-751-845-126
; Sequence 126, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-126

Query Match      100.0%; Score 52; DB 17; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
Db 36 IVYRDGNPY 44

RESULT 9
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiscentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match      100.0%; Score 52; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
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Db          52 IVYRDGNPY 60
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RESULT 10
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match          100.0%; Score 52; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
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Db 52 IVYRDGNPY 60

RESULT 11
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match          100.0%; Score 52; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
|||||
Db 52 IVYRDGNPY 60

RESULT 12

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US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANGINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match          100.0%; Score 52; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
|||||
Db 59 IVYRDGNPY 67

RESULT 13
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match          100.0%; Score 52; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
|||||
Db 59 IVYRDGNPY 67

RESULT 14
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald

```

; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154

; CURRENT APPLICATION NUMBER: US/10/472,724

; CURRENT FILING DATE: 2003-09-17

; PRIOR APPLICATION NUMBER: PCT/EP02/03271

; PRIOR FILING DATE: 2002-03-22

; PRIOR APPLICATION NUMBER: EP 01107271.7

; PRIOR FILING DATE: 2001-03-23

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2

; LENGTH: 171

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Construct

US-10-472-724-2

Query Match

Best Local Similarity 100.0%; Score 52; DB 16; Length 171;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9

Db 64 IVYRDGNPY 72

RESULT 15

US-10-751-845-157

; Sequence 157, Application US/10751845

; Publication No. US20050100928A1

; GENERAL INFORMATION:

; APPLICANT: Hedley, Mary Lynne

; APPLICANT: Urban, Robert G.

; APPLICANT: Chicz, Roman M.

; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES

; FILE REFERENCE: 08191-013001

; CURRENT APPLICATION NUMBER: US/10/751,845

; CURRENT FILING DATE: 2004-01-05

; PRIOR APPLICATION NUMBER: US/09/664,225

; PRIOR FILING DATE: 2000-08-18

; PRIOR APPLICATION NUMBER: US 60/169,846

; PRIOR FILING DATE: 1999-12-09

; PRIOR APPLICATION NUMBER: US 60/154,665

; PRIOR FILING DATE: 1999-09-16

; NUMBER OF SEQ ID NOS: 163

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 157

; LENGTH: 236

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Artificial fusion sequence

US-10-751-845-157

Query Match

Best Local Similarity 100.0%; Score 52; DB 17; Length 236;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9

Db 36 IVYRDGNPY 44

Search completed: June 29, 2005, 05:18:10

Job time : 116.15 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-44

Perfect score: 52

Sequence: 1 IVYRDGNY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	9	US-08-159-339A-133	Sequence 133, Appl
2	52	100.0	22	US-09-980-523A-6	Sequence 6, Appl
3	52	100.0	23	US-09-601-729-276	Sequence 276, Appl
4	52	100.0	158	US-09-980-523A-2	Sequence 2, Appl
5	52	100.0	162	US-08-316-239B-3	Sequence 3, Appl
6	52	100.0	162	US-08-316-239B-4	Sequence 4, Appl
7	52	100.0	172	US-08-860-165-14	Sequence 14, Appl
8	52	100.0	172	US-09-359-382-14	Sequence 14, Appl
9	52	100.0	266	US-08-860-165-10	Sequence 10, Appl
10	52	100.0	266	US-09-359-382-10	Sequence 10, Appl
11	52	100.0	266	US-09-367-309A-1	Sequence 1, Appl
12	52	100.0	273	US-09-485-885-4	Sequence 4, Appl
13	52	100.0	292	US-09-485-885-10	Sequence 10, Appl
14	52	100.0	371	US-09-485-885-6	Sequence 6, Appl
15	52	100.0	390	US-09-485-885-14	Sequence 14, Appl
16	44	84.6	9	US-08-159-339A-219	Sequence 219, Appl
17	40	76.9	20	US-08-934-915-161	Sequence 161, Appl
18	40	76.9	197	US-09-902-540-12611	Sequence 12611, A
19	38	73.1	390	US-09-328-352-4913	Sequence 4913, Ap
20	37	71.2	9	US-09-574-749B-42	Sequence 42, Appl
21	37	71.2	484	US-08-111-939-12	Sequence 12, Appl
22	37	71.2	719	US-09-641-741-28	Sequence 28, Appl
23	37	71.2	845	US-09-641-741-29	Sequence 29, Appl
24	37	71.2	1128	US-08-111-939-2	Sequence 2, Appl
25	37	71.2	1128	US-09-641-741-30	Sequence 30, Appl
26	37	71.2	1128	US-09-060-482-8	Sequence 8, Appl
27	37	71.2	1158	US-09-060-482-2	Sequence 2, Appl

28	37	71.2	1172	4	US-09-949-016-8593	Sequence 8593, Ap
29	36	69.2	100	4	US-09-472-087-113	Sequence 113, Appl
30	36	69.2	112	1	US-07-942-245-28	Sequence 28, Appl
31	36	69.2	112	4	US-09-840-459-56	Sequence 56, Appl
32	36	69.2	112	4	US-09-840-459-66	Sequence 66, Appl
33	36	69.2	112	4	US-09-840-459-70	Sequence 70, Appl
34	36	69.2	112	4	US-09-497-625A-56	Sequence 56, Appl
35	36	69.2	112	4	US-09-497-625A-66	Sequence 66, Appl
36	36	69.2	112	4	US-09-497-625A-70	Sequence 70, Appl
37	36	69.2	112	4	US-09-254-180C-8	Sequence 8, Appl
38	36	69.2	139	4	US-09-472-087-25	Sequence 25, Appl
39	36	69.2	139	4	US-09-472-087-114	Sequence 114, Appl
40	36	69.2	253	4	US-09-710-279-2428	Sequence 2428, Ap
41	41	69.2	281	3	US-09-134-001C-3445	Sequence 3445, Ap
42	36	69.2	389	4	US-09-949-016-10069	Sequence 10069, A
43	36	69.2	476	4	US-09-949-016-6905	Sequence 6905, Ap
44	36	69.2	581	3	US-09-534-407-3	Sequence 3, Appl
45	36	69.2	581	4	US-09-999-201B-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-159-339A-133
; Sequence 133, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauwer
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-133

Query Match 100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVYRDGNPY 9
| | | | | | | | |
Db 1 IVYRDGNPY 9

RESULT 2

US-09-980-523A-6
; Sequence 6, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/1 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-6

Query Match 100.0%; Score 52; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVYRDGNPY 9
| | | | | | | | |
Db 14 IVYRDGNPY 22

RESULT 3

US-09-601-729-276
; Sequence 276, Application US/09601729
; Patent No. 6683052
; GENERAL INFORMATION:
; APPLICANT: THIAM, KADER
; APPLICANT: AURIAULT, CLAUDE
; APPLICANT: GRAS-MASSE, HELENE
; APPLICANT: LOING, ESTELLE
; APPLICANT: VERWAERDE, CLAUDIE
; APPLICANT: GUILLET, JEAN GERARD
; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
; TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: USB-97-AU-IN
; CURRENT APPLICATION NUMBER: US/09/601,729
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: PCT/FR99/00259
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 98 01439
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 276
; LENGTH: 23
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-601-729-276

Query Match 100.0%; Score 52; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVYRDGNPY 9
| | | | | | | | |
Db 15 IVYRDGNPY 23

RESULT 4

US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/1 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 52; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVYRDGNPY 9
| | | | | | | | |
Db 59 IVYRDGNPY 67

RESULT 5

US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; TITLE OF INVENTION: 4
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNNE-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 52; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVYRDGNPY 9
Db 59 IVYRDGNPY 67

RESULT 6

US-08-316-239B-4
; Sequence 4, Application US/0816239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNNE-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 52; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVYRDGNPY 9
Db 59 IVYRDGNPY 67

RESULT 7

US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match 100.0%; Score 52; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVYRDGNPY 9
Db 128 IVYRDGNPY 136

RESULT 8

US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172

```
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match      100.0%; Score 52; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
Db 128 IVYRDGNPY 136

RESULT 9
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; FILE REFERENCE: 17227/130
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match      100.0%; Score 52; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
Db 59 IVYRDGNPY 67

RESULT 10
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; FILE REFERENCE: 017227/0148
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match      100.0%; Score 52; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
Db 59 IVYRDGNPY 67

RESULT 11
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 52; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVYRDGNPY 9
Db 59 IVYRDGNPY 67

RESULT 12
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match      100.0%; Score 52; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 IVYRDGNPY 9
Db      165 IVYRDGNPY 173

RESULT 13
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match      100.0%; Score 52; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 IVYRDGNPY 9
Db      184 IVYRDGNPY 192

RESULT 14
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match      100.0%; Score 52; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 IVYRDGNPY 9
Db      184 IVYRDGNPY 192

RESULT 15
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match      100.0%; Score 52; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 IVYRDGNPY 9
Db      184 IVYRDGNPY 192

Search completed: June 28, 2005, 23:37:46
Job time : 17.05 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)
78.367 Million cell updates/sec

Title: US-08-170-344-43
Perfect score: 44
Sequence: 1 QQLLRREYV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	44	100.0	158	1	W6WLHS	protein E6 - human
2	33	75.0	229	2	F87705	YghA protein [impo
3	33	75.0	451	2	A86304	hypothetical prote
4	33	75.0	580	2	D63645	myo-inositol catab
5	33	75.0	778	2	I38487	tastin - human
6	32	72.7	304	2	S59414	hypothetical prote
7	32	72.7	312	2	AB0306	probable membrane
8	32	72.7	384	2	E75295	conserved hypothet
9	32	72.7	525	2	AD2022	hypothetical prote
10	32	72.7	610	2	F83384	probable asparagin
11	32	72.7	660	2	A84232	spore cortex synth
12	32	72.7	861	2	H64102	leucine-tRNA ligas
13	32	72.7	3190	2	T13828	CREB-binding prote
14	32	72.7	4859	2	S74173	ryanodine receptor
15	32	72.7	4868	2	B54161	ryanodine-binding
16	32	72.7	4869	2	S6572	ryanodine receptor
17	32	72.7	4872	2	S27272	ryanodine receptor
18	31	70.5	148	2	A61237	E6 protein - human
19	31	70.5	148	2	S36573	E6 protein - human
20	31	70.5	205	2	T37103	hypothetical prote
21	31	70.5	237	2	AD3474	transporter BHE117
22	31	70.5	273	2	A86476	protein F1504.49 [
23	31	70.5	383	2	G96989	probable permease
24	31	70.5	390	2	A47312	NS34 homolog - mur
25	31	70.5	396	2	H87356	hypothetical prote
26	31	70.5	473	1	RGBYM3	regulatory protein
27	31	70.5	622	2	A32742	murine ecotropic r
28	31	70.5	624	2	A53035	ecotropic retrovir
29	31	70.5	629	2	S29685	retroviral recepto

30 70.5 680 2 C82353 oligopeptidase A V
31 70.5 884 2 S77031 hypothetical prote
32 70.5 913 2 AB2587 translation initia
33 70.5 913 2 B97369 translation initia
34 70.5 974 2 T29545 hypothetical prote
35 70.5 1417 2 H83132 probable sensor/re
36 70.5 1582 2 T15308 hypothetical prote
37 68.2 150 2 AE2595 hypothetical prote
38 68.2 160 2 D98138 probable transcrip
39 68.2 172 2 AF3149 transcription regu
40 68.2 226 2 T24125 hypothetical prote
41 68.2 249 2 S76822 hypothetical prote
42 68.2 268 2 T24118 hypothetical prote
43 68.2 270 2 T24126 hypothetical prote
44 68.2 279 2 A37945 thymidylate syntha
45 68.2 279 2 E95077 thymidylate syntha

RESULT 1
W6WLHS
protein E6 - human papillomavirus type 16
C:Species: human papillomavirus type 16
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A03682; T10427
R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A:Title: Human papillomavirus type 16 DNA sequence.
A:Reference number: A22355; MUID:85246220; PMID:2990099
A:Accession: A03682
A:Molecule type: DNA
A:Residues: 1-158 <SEE>
A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
J.Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A:Reference number: Z17014; MUID:91162763; PMID:1848319
A:Accession: T10427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-158 <KEN>
A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
A:Gene: E6
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:37-73/Region: zinc finger CCCC motif
F:110-146/Region: zinc finger CCCC motif

Query Match 100.0% Score 44; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.081; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0

Qy 1 QQLLRREYV 9
Db 42 QQLLRREYV 50
|||||||

RESULT 2
F87705
YghA protein [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: F87705
R:Nierman, W.C.; DeBooy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
B.; Laub, M.T.; Paulsen, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: AB7249; MUID:21173698; PMID:11259647
A:Accession: F87705

ALIGNMENTS

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-229 <STO>
A;Cross-references: UNIPROT:Q9A286; GB:AE005673; NID:gi13425440; PIDN:AAK25642.1; GSPDB:C
C;Genetics:
A;Gene: CC3680
C;Superfamily: hypothetical protein b1832

Query Match 75.0%; Score 33; DB 2; Length 229;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLREVVY 9
:|||||:
Db 163 LLREIY 169

RESULT 3
A86304
hypothetical protein F611.13 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86304
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 818-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86304
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-451 <STO>
A;Cross-references: UNIPROT:Q9F746; GB:AE005172; NID:g9802777; PIDN:AAF99846.1; GSPDB:GN
C;Genetics:
A;Map position: 1

Query Match 75.0%; Score 33; DB 2; Length 451;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLLRREVV 9
:|||||:
Db 416 QRLVRREVF 424

RESULT 4
D69645
myo-inositol catabolism fold - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
C;Accession: D69645
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Broutillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrazi, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, K.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: D69645
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-580 <KUN>
A;Cross-references: UNIPROT:P42415; GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB16009.1
A;Experimental source: strain 168
C;Genetics:
A;Gene: ioid
C;Superfamily: Acetolactate synthase, large subunit/pyruvate oxidase; thiamin pyrophospho

Query Match 75.0%; Score 33; DB 2; Length 580;
Best Local Similarity 55.6%; Pred. No. 64;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLLRREVV 9
:|||||:
Db 21 QQLRRKIY 29

RESULT 5
I38487
tastin - human
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
C;Accession: I38487
R;Fukuda, M.N.; Sato, T.; Nakayama, J.; Klier, G.; Mikami, M.; Aoki, D.; Nozawa, S.
Genes Dev. 9, 1193-1210, 1995
A;Title: Trophinin and tastin, a novel cell adhesion molecule complex with potential inv
A;Reference number: I38487; MUID:95278733; PMID:7758945
A;Accession: I38487
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-778 <RES>
A;Cross-references: UNIPROT:Q12815; EMBL:U04810; NID:g905355; PIDN:AAA79333.1; PID:g9053

Query Match 75.0%; Score 33; DB 2; Length 778;
Best Local Similarity 87.5%; Pred. No. 87;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLLRREV 8
:|||||:
Db 439 QQLLRQEV 446

RESULT 6
S59414
hypothetical protein YLR455w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L9122.4
C;Species: Saccharomyces cerevisiae
C;Date: 30-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: S59414
R;Kirsten, J.
Submitted to the EMBL Data Library, March 1995
A;Description: The sequence of S. cerevisiae cosmid 9122.
A;Reference number: S59414
A;Accession: S59414
A;Molecule type: DNA
A;Residues: 1-304 <KIR>
A;Cross-references: UNIPROT:Q06188; EMBL:U22383; NID:g2264349; PIDN:AAB64719.1; PID:g717
A;Experimental source: strain S288C (AB972)
C;Genetics:
A;Gene: MIPS:YLR455w
A;Cross-references: SGD:S0004447
A;Map position: 12R

Query Match 72.7%; Score 32; DB 2; Length 304;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLLRREVV 9
:|||||:
Db 28 QQLLRNDVY 36

```

RESULT 7
AB0306
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AB0306
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AB0306
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-312 <KUR>
A:Cross-references: UNIPROT:Q8ZDQ1; GB:AL590842; PIDN:CAC91310.1; PID:G15980499; GSPDB:G
C:Genetics:
A:Gene: YPO2505

Query Match 72.7%; Score 32; DB 2; Length 312;
Best Local Similarity 55.6%; Pred. No. 54;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLRREVY 9
Db 19 QQLRRSIF 27

RESULT 8
E75295
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: E75295
R:White, O.; Eilen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: E75295
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-384 <WHI>
A:Cross-references: UNIPROT:Q9RS74; GB:AE002058; GB:AE000513; NID:G6460059; PIDN:AAF1180
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR2253
A:Map position: 1

Query Match 72.7%; Score 32; DB 2; Length 384;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLRREVY 9
Db 372 BELRRAVY 380

RESULT 9
AD2022
hypothetical protein all1730 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AD2022
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840

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A:Accession: AD2022
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-525 <KUR>
A:Cross-references: UNIPROT:O8YWG6; GB:BA000019; PIDN:BA873429.1; PID:G17130820; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all1730

Query Match 72.7%; Score 32; DB 2; Length 525;
Best Local Similarity 87.5%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLRREV 8
Db 493 QQLRREV 500

RESULT 10
F83384
C:Species: Pseudomonas aeruginosa (strain PA01)
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: F83384
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: F83384
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-610 <STO>
A:Cross-references: UNIPROT:Q91231; GB:AE004636; GB:AE004091; NID:G9948093; PIDN:AAG0547;
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2084

Query Match 72.7%; Score 32; DB 2; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QQLRREV 8
Db 411 QQLRREV 417

RESULT 11
A84232
spore cortex synthesis protein [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: A84232
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: A84232
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-660 <STO>
A:Cross-references: UNIPROT:Q9HRD7; GB:AE004437; NID:G10580323; PIDN:AAG19221.1; GSPDB:G
C:Genetics:
A:Gene: spoVR

Query Match 72.7%; Score 32; DB 2; Length 660;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 2 QLLRRREVY 9
.:|||||
Db 266 ELLRRREAY 273

RESULT 12
H64102
leucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)
N/Alternate names: leucyl-tRNA synthetase
C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
R/Accession: H64102
C/Flerschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A/Reference number: A64000; MUID:95350630; PMID:7542800
A/Accession: H64102
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-861 <TIGR>
A/Cross-references: UNIPROT:P43827; GB:U32774; GB:L42023; NID:g1573942; PIDN:AAC22581.1;
C/Genetics:
A/Gene: leuS
C/Superfamily: leucine-tRNA ligase
C/Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 72.7%; Score 32; DB 2; Length 861;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLLRREVY 9
|:|||||
Db 698 QKVLRRREVH 706

RESULT 13
T13828
CREB-binding protein homolog - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T13828
R/Akamaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; G.
Nature 386, 735-738, 1997
A/Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling.
A/Reference number: Z17785; MUID:97263578; PMID:9109493
A/Accession: T13828
A/Status: preliminary; translated from GB/EMBL/DBDJ
A/Molecule type: mRNA
A/Residues: 1-3190 <AKI>
A/Cross-references: UNIPROT:O01368; EMBL:U88570; NID:g1916930; PIDN:AAB530
C/Genetics:
A/Cross-references: FlyBase:FBgn0015624
A/Map position: X
F:1723-1780/Domain: bromodomain homology <BRO>

Query Match 72.7%; Score 32; DB 2; Length 3190;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLLRREV 8
|:|||||
Db 2489 QQLLRREV 2496

RESULT 14
S74173
ryanodine receptor 3 - Mustela sp.
C/Species: Mustela sp.
C/Date: 23-Apr-1998 #sequence_revision 01-May-1998 #text_change 09-Jul-2004
C/Accession: S74173

R/Marziali, G.; Rossi, D.; Giannini, G.; Charlesworth, A.; Sorrentino, V.
FEBS Lett. 394, 76-82, 1996
A/Title: cDNA cloning reveals a tissue specific expression of alternatively spliced trans
A/Reference number: S74173; MUID:97074208; PMID:8925932
A/Accession: S74173
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-4859 <MAR>
A/Cross-references: UNIPROT:Q7M2T9
A/Experimental source: mink lung epithelial cell line CCL64
C/Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homolog
C/Keywords: alternative splicing; calcium channel; glycoprotein; phosphoprotein; transmem
F:697-702/Region: adenine nucleotide binding #status predicted
F:849-934/Domain: repeat #status predicted <RPT1>
F:963-1048/Domain: repeat #status predicted <RPT2>
F:1134-1139/Region: adenine nucleotide binding #status predicted
F:2234-2239/Region: adenine nucleotide binding #status predicted
F:2521-2526/Region: adenine nucleotide binding #status predicted
F:2596-2681/Domain: repeat #status predicted <RPT3>
F:2714-2792/Domain: repeat #status predicted <RPT4>
F:3834-3854/Domain: transmembrane #status predicted <TM1>
F:3862-3880/Domain: transmembrane #status predicted <TM2>
F:3914-3932/Domain: calcium binding #status predicted <CAL>
F:4119-4142/Domain: transmembrane #status predicted <TM3>
F:4184-4204/Domain: transmembrane #status predicted <TM4>
F:4399-4420/Domain: transmembrane #status predicted <TM5>
F:4471-4494/Domain: transmembrane #status predicted <TM6>
F:4611-4642/Domain: transmembrane #status predicted <TM7>
F:4659-4678/Domain: transmembrane #status predicted <TM8>
F:4701-4720/Domain: transmembrane #status predicted <TM9>
F:4736-4759/Domain: transmembrane #status predicted <TM10>
F:130, 290, 1243/Binding site: phosphate (Thr) (covalent) (by cAMP- and calmodulin-dependen
F:2706/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status
F:4686/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 72.7%; Score 32; DB 2; Length 4859;
Best Local Similarity 77.8%; Pred. No. 9.7e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLLRREVY 9
|:|||||
Db 2481 QQLLRRLVF 2489

RESULT 15
B54161
ryanodine-binding protein beta form - bullfrog
C/Species: Rana catesbeiana (bullfrog)
C/Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C/Accession: B54161
R/Oyamada, H.; Murayama, T.; Takagi, T.; Iino, M.; Iwabe, N.; Miyata, T.; Ogawa, Y.; Endo
J. Biol. Chem. 269, 17206-17214, 1994
A/Title: Primary structure and distribution of ryanodine-binding protein isoforms of the
A/Reference number: A54161; MUID:94274714; PMID:8006029
A/Accession: B54161
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-4868 <OYA>
A/Cross-references: UNIPROT:Q91319; GB:D21071; NID:g1856973; PIDN:BAA04647.1; PID:g53824;
C/Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homolog

Query Match 72.7%; Score 32; DB 2; Length 4868;
Best Local Similarity 77.8%; Pred. No. 9.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLLRREVY 9
|:|||||
Db 2486 QQLLRRLVF 2494

Search completed: June 28, 2005, 23:32:00
Job time : 12.05 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-43
Perfect score: 44
Sequence: 1 QQLLRREYV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	26	2 Q81956	Q81956 human papill
2	44	100.0	99	2 Q919B2	Q919B2 human papill
3	44	100.0	130	2 Q919B4	Q919B4 human papill
4	44	100.0	130	2 Q919B8	Q919B8 human papill
5	44	100.0	130	2 Q919C0	Q919C0 human papill
6	44	100.0	130	2 Q919C2	Q919C2 human papill
7	44	100.0	130	2 Q919C8	Q919C8 human papill
8	44	100.0	130	2 Q919D0	Q919D0 human papill
9	44	100.0	138	2 Q919D2	Q919D2 human papill
10	44	100.0	143	2 Q919B6	Q919B6 human papill
11	44	100.0	143	2 Q919C4	Q919C4 human papill
12	44	100.0	151	2 Q12335	Q12335 human papill
13	44	100.0	151	2 Q12336	Q12336 human papill
14	44	100.0	151	2 Q76TS0	Q76TS0 human papill
15	44	100.0	151	2 Q778I6	Q778I6 human papill
16	44	100.0	151	2 Q778I6	Q778I6 human papill
17	44	100.0	151	2 Q77JC7	Q77JC7 human papill
18	44	100.0	151	2 Q77ZJ5	Q77ZJ5 human papill
19	44	100.0	151	2 Q80963	Q80963 human papill
20	44	100.0	151	2 Q80966	Q80966 human papill
21	44	100.0	151	2 Q89640	Q89640 human papill
22	44	100.0	151	2 Q89648	Q89648 human papill
23	44	100.0	151	2 Q89708	Q89708 human papill
24	44	100.0	151	2 Q89755	Q89755 human papill
25	44	100.0	151	2 Q89852	Q89852 human papill
26	44	100.0	151	2 Q89887	Q89887 human papill
27	44	100.0	151	2 Q8B564	Q8B564 human papill
28	44	100.0	151	2 Q8BB19	Q8BB19 human papill
29	44	100.0	151	2 Q8BB20	Q8BB20 human papill
30	44	100.0	151	2 Q8BB21	Q8BB21 human papill
31	44	100.0	151	2 Q9W8C3	Q9W8C3 human papill

32	44	100.0	151	2 Q9W931	Q9W931 human papill
33	44	100.0	151	2 Q9WMP2	Q9WMP2 human papill
34	44	100.0	151	2 Q9WMP3	Q9WMP3 human papill
35	44	100.0	151	2 Q9WMP4	Q9WMP4 human papill
36	44	100.0	151	2 Q9WMP5	Q9WMP5 human papill
37	44	100.0	158	1 VE6_HPV16	P03126 human papill
38	44	100.0	158	2 Q8JMU8	Q8JMU8 human papill
39	44	100.0	158	2 Q8QHN0	Q8QHN0 human papill
40	44	100.0	158	2 Q8QHP5	Q8QHP5 human papill
41	44	100.0	158	2 Q8QHT0	Q8QHT0 human papill
42	44	100.0	158	2 Q8QRD5	Q8QRD5 human papill
43	44	100.0	158	2 Q8QRD6	Q8QRD6 human papill
44	44	100.0	158	2 Q8QRD7	Q8QRD7 human papill
45	44	100.0	158	2 Q8QRD8	Q8QRD8 human papill

ALIGNMENTS

RESULT 1
Q81956 PRELIMINARY; PRT; 26 AA.
AC Q81956;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE E6E7 (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SIHA:
RA Shippy R., Siwkowski A., Hampel A.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59900; AAB03505.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 26 AA; 3208 MW; F06EBBE995EB67D5 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLLRREYV 9
DB 18 QQLLRREYV 26

RESULT 2
Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404704; AAL01365.1; -.

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DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;
Query Match 100.0%; Score 44; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQLLRREYV 9
DB 11 QQLLRREYV 19
RESULT 3
Q919B4
ID Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01359.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EBDDC CRC64;
Query Match 100.0%; Score 44; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQLLRREYV 9
DB 14 QQLLRREYV 22
RESULT 4
Q919B8
ID Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01359.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
Query Match 100.0%; Score 44; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQLLRREYV 9
DB 14 QQLLRREYV 22
RESULT 5
Q919C0
ID Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
Query Match 100.0%; Score 44; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQLLRREYV 9
DB 14 QQLLRREYV 22
RESULT 6
Q919C2
ID Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01355.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
```



```

Query Match      100.0%; Score 44; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLLRREYV 9
   |||||
Db 14 QQLLRREYV 22

RESULT 7
Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404696; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match      100.0%; Score 44; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLLRREYV 9
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Db 14 QQLLRREYV 22

RESULT 8
Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404695; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;

Query Match      100.0%; Score 44; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.34;

QY 1 QQLLRREYV 9
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Db 14 QQLLRREYV 22

RESULT 9
Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404694; AAL01345.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481ESA90895FC2 CRC64;

Query Match      100.0%; Score 44; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLLRREYV 9
   |||||
Db 22 QQLLRREYV 30

RESULT 10
Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404702; AAL01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match      100.0%; Score 44; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLLRREYV 9

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Db 27 QQLLRREVY 35

RESULT 11
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AC Q919C4
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874 (2002).
DR EMBL; AF404698; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;
SQ

Query Match 100.0%; Score 44; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.38; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0

Qy 1 QQLLRREVY 9
Db 27 QQLLRREVY 35

RESULT 12
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AC O12335
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Girardo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208 (1997).
DR EMBL; AF003015; AAB70732.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;
SQ

Query Match 100.0%; Score 44; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.4; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0

Qy 1 QQLLRREVY 9
Db 35 QQLLRREVY 43

RESULT 13
O12336 PRELIMINARY; PRT; 151 AA.
AC O12336
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Girardo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208 (1997).
DR EMBL; AF003016; AAB70733.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;
SQ

Query Match 100.0%; Score 44; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.4; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0

Qy 1 QQLLRREVY 9
Db 35 QQLLRREVY 43

RESULT 14
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AC Q76TSO
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34114; AAA91661.1; -.
DR EMBL; U34125; AAA91672.1; -.
DR EMBL; U34130; AAA91677.1; -.
DR EMBL; U34131; AAA91678.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;
SQ

Query Match 100.0%; Score 44; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLRREYV 9
 DB 35 QQLRREYV 43

RESULT 15

Q77816 PRELIMINARY; PRT; 151 AA.
 AC Q77816;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
 RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325(2000).
 DR EMBL; AJ388056; CAB45104.1; -;
 DR EMBL; AJ388061; CAB45114.1; -;
 DR EMBL; AJ388066; CAB45124.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18334 MW; F8F2A2FCBA6C02 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLRREYV 9
 DB 35 QQLRREYV 43

Search completed: June 28, 2005, 23:28:09
 Job time : 55.1 secs

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OM protein : protein search, using sw model

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29.797 Million cell updates/sec

Title: US-08-170-344-43

Perfect score: 44

Sequence: 1 QQLLRREYV 9

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Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/1/pubpaa/US09D_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	44	100.0	9	14	US-10-239-313A-525
2	44	100.0	15	16	US-10-476-570-25
3	44	100.0	15	16	US-10-476-570-28
4	44	100.0	21	16	US-10-476-570-10
5	44	100.0	151	14	US-10-177-390-6
6	44	100.0	151	17	US-10-484-063-20
7	44	100.0	151	17	US-10-484-063-27
8	44	100.0	151	17	US-10-858-384-2
9	44	100.0	158	17	US-10-367-057-16
10	44	100.0	171	16	US-10-472-724-2
11	44	100.0	266	9	US-09-367-309A-1

12	44	100.0	273	13	US-10-000-903-4	Sequence 4, Appli
13	44	100.0	273	17	US-10-899-771-4	Sequence 4, Appli
14	44	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
15	44	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
16	44	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
17	44	100.0	371	17	US-10-899-771-6	Sequence 6, Appli
18	44	100.0	390	13	US-10-000-903-14	Sequence 10, Appl
19	44	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
20	44	100.0	536	15	US-10-367-095-10	Sequence 10, Appl
21	44	100.0	536	15	US-10-368-046-10	Sequence 10, Appl
22	44	100.0	536	16	US-10-367-367-10	Sequence 10, Appl
23	44	100.0	536	17	US-10-918-337-10	Sequence 10, Appl
24	39	88.6	15	17	US-10-484-063-4	Sequence 4, Appli
25	34	77.3	9	17	US-10-476-570-27	Sequence 27, Appl
26	34	77.3	23	16	US-10-751-845-82	Sequence 82, Appl
27	34	77.3	24	17	US-10-751-845-65	Sequence 65, Appl
28	34	77.3	117	17	US-10-751-845-126	Sequence 126, App
29	34	77.3	236	17	US-10-751-845-157	Sequence 157, App
30	34	77.3	237	17	US-10-751-845-158	Sequence 158, App
31	34	77.3	261	17	US-10-751-845-160	Sequence 160, App
32	34	77.3	337	15	US-10-425-114-50845	Sequence 50845, A
33	34	77.3	363	15	US-10-425-114-59344	Sequence 59344, A
34	33	75.0	77	15	US-10-424-599-242846	Sequence 242846,
35	33	75.0	87	15	US-10-424-599-155399	Sequence 155399,
36	33	75.0	122	15	US-10-424-599-228526	Sequence 228526,
37	33	75.0	231	15	US-10-424-599-262641	Sequence 262641,
38	33	75.0	1506	16	US-10-754-115-49	Sequence 49, Appl
39	32	72.7	34	15	US-10-424-599-269879	Sequence 269879,
40	32	72.7	48	16	US-10-425-115-252206	Sequence 252206,
41	32	72.7	59	16	US-10-425-115-331363	Sequence 331363,
42	32	72.7	100	16	US-10-425-115-251808	Sequence 251808,
43	32	72.7	105	16	US-10-437-963-170284	Sequence 170284,
44	32	72.7	164	15	US-10-425-114-68311	Sequence 68311, A
45	32	72.7	171	15	US-10-425-114-71647	Sequence 71647, A

ALIGNMENTS

RESULT 1

US-10-239-313A-525
; Sequence 525, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 525
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-239-313A-525

Query Match 100.0%; Score 44; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLLRREYV 9

Db 1 QQLLRREYV 9

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US-10-476-570-25
; Sequence 25, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POURVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 36-50
US-10-476-570-25

Query Match 100.0%; Score 44; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLLRREVY 9
Db 7 QQLLRREVY 15

RESULT 3
US-10-476-570-28
; Sequence 28, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POURVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 42-56
US-10-476-570-28

Query Match 100.0%; Score 44; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLLRREVY 9
Db 7 QQLLRREVY 15

RESULT 4
US-10-476-570-10
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; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POURVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 21
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 30-50
US-10-476-570-10

Query Match 100.0%; Score 44; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLLRREVY 9
Db 13 QQLLRREVY 21

RESULT 5
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerps Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match 100.0%; Score 44; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLLRREVY 9
Db 35 QQLLRREVY 43
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RESULT 6
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR FILING DATE: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match      100.0%; Score 44; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLRRREVY 9
Db 35 QQLRRREVY 43

RESULT 7
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR FILING DATE: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match      100.0%; Score 44; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLRRREVY 9
Db 35 QQLRRREVY 43

RESULT 8
US-10-858-384-2
; Sequence 2, Application US/10858384
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; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match      100.0%; Score 44; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLRRREVY 9
Db 42 QQLRRREVY 50

RESULT 9
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match      100.0%; Score 44; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLRRREVY 9
Db 42 QQLRRREVY 50

RESULT 10
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
```

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; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match          100.0%; Score 44; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOLLREVVY 9
Db 47 QOLLREVVY 55

RESULT 11
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAKOS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match          100.0%; Score 44; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOLLREVVY 9
Db 42 QOLLREVVY 50

RESULT 12
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezón Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17

; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match          100.0%; Score 44; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOLLREVVY 9
Db 47 QOLLREVVY 55

RESULT 11
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAKOS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match          100.0%; Score 44; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOLLREVVY 9
Db 42 QOLLREVVY 50

RESULT 12
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezón Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17

; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match          100.0%; Score 44; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOLLREVVY 9
Db 148 QOLLREVVY 156

RESULT 13
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemaus, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

Query Match          100.0%; Score 44; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOLLREVVY 9
Db 148 QOLLREVVY 156

RESULT 14
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezón Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
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; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match      100.0%; Score 44; DB 13; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLRRREV 9
Db 167 QQLRRREV 175

RESULT 15
US-10-899-771-10
; Sequence 10, Application US/10899771
; Publication No. US20050031838A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (Clyta from Streptococcus
; OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-10

Query Match      100.0%; Score 44; DB 17; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLRRREV 9
Db 167 QQLRRREV 175

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Search completed: June 29, 2005, 05:18:10
Job time : 117.15 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-43

Perfect score: 44

Sequence: 1 QQLLRREVV 9

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Searched: 513545 seqs, 74649064 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	9	US-08-159-339A-135	Sequence 135, App
2	44	100.0	20	US-08-934-915-160	Sequence 160, App
3	44	100.0	158	US-09-980-523A-2	Sequence 2, Appli
4	44	100.0	162	US-08-316-239B-3	Sequence 3, Appli
5	44	100.0	162	US-08-316-239B-4	Sequence 4, Appli
6	44	100.0	172	US-08-860-165-14	Sequence 14, Appl
7	44	100.0	172	US-09-359-382-14	Sequence 14, Appl
8	44	100.0	182	US-08-117-083-10	Sequence 10, Appl
9	44	100.0	266	US-08-860-165-10	Sequence 10, Appl
10	44	100.0	266	US-09-359-382-10	Sequence 10, Appl
11	44	100.0	266	US-09-367-309A-1	Sequence 1, Appli
12	44	100.0	273	US-09-485-885-4	Sequence 4, Appli
13	44	100.0	292	US-09-485-885-10	Sequence 10, Appl
14	44	100.0	371	US-09-485-885-6	Sequence 6, Appli
15	44	100.0	390	US-09-485-885-14	Sequence 14, Appl
16	35	79.5	415	US-09-248-796A-17467	Sequence 17467, A
17	34	77.3	9	US-08-159-339A-252	Sequence 252, App
18	33	75.0	732	US-08-317-522A-5	Sequence 5, Appli
19	33	75.0	778	US-08-439-818A-5	Sequence 5, Appli
20	33	75.0	778	US-08-751-965-5	Sequence 5, Appli
21	33	75.0	778	US-08-738-975-5	Sequence 5, Appli
22	33	75.0	778	US-08-728-626-5	Sequence 5, Appli
23	33	75.0	778	US-08-808-599A-5	Sequence 5, Appli
24	32	72.7	639	US-09-252-931A-25089	Sequence 25089, A
25	32	72.7	4866	US-09-424-783-2	Sequence 2, Appli
26	32	72.7	4872	US-09-424-783-3	Sequence 3, Appli
27	31	70.5	212	US-08-861-774E-42	Sequence 42, Appl

28	31	70.5	622	2	US-08-132-990A-4	Sequence 4, Appli
29	31	70.5	622	5	PCT-US92-09382-4	Sequence 4, Appli
30	31	70.5	629	2	US-08-132-990A-8	Sequence 8, Appli
31	31	70.5	629	5	PCT-US92-09382-8	Sequence 8, Appli
32	31	70.5	644	4	US-09-949-016-9507	Sequence 9507, Ap
33	31	70.5	1441	4	US-09-252-931A-28143	Sequence 28143, A
34	30	68.2	14	1	US-07-909-122-4	Sequence 4, Appli
35	30	68.2	23	4	US-09-601-729-276	Sequence 276, App
36	30	68.2	147	4	US-09-265-585C-98	Sequence 98, Appl
37	30	68.2	196	4	US-09-489-039A-7430	Sequence 7430, Ap
38	30	68.2	295	4	US-09-265-585C-101	Sequence 101, App
39	30	68.2	322	4	US-09-710-279-586	Sequence 586, App
40	30	68.2	322	4	US-09-710-279-984	Sequence 984, App
41	30	68.2	327	3	US-09-134-001C-3477	Sequence 3477, Ap
42	30	68.2	435	4	US-09-489-039A-13740	Sequence 13740, A
43	30	68.2	437	4	US-09-328-352-7401	Sequence 7401, Ap
44	30	68.2	481	4	US-09-902-540-13111	Sequence 13111, A
45	30	68.2	486	4	US-09-252-931A-17543	Sequence 17543, A

ALIGNMENTS

RESULT 1
US-08-159-339A-135
; Sequence 135, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-135

Query Match 100.0%; Score 44; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLLRREYV 9
| | | | | | | |
Db 1 QQLLRREYV 9

RESULT 2

US-08-934-915-160
; Sequence 160, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Fouch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-934-915-160

Query Match 100.0%; Score 44; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLLRREYV 9
| | | | | | | |
Db 11 QQLLRREYV 19

RESULT 3

US-08-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:

; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 44; DB 4; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLLRREYV 9
| | | | | | | |
Db 42 QQLLRREYV 50

RESULT 4

US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:

; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant

```
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match      100.0%; Score 44; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.33; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLRREVV 9
Db 42 QQLRREVV 50

RESULT 5
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNNE-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match      100.0%; Score 44; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.33; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLRREVV 9
Db 42 QQLRREVV 50

RESULT 6
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John

; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match      100.0%; Score 44; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.35; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLRREVV 9
Db 111 QQLRREVV 119

RESULT 7
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match      100.0%; Score 44; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.35; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLRREVV 9
Db 111 QQLRREVV 119

RESULT 8
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Bournell, Michael E.
; APPLICANT: Inglis, Stephen C.
```

APPLICANT: Munro, Alan J.
TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
TITLE OF INVENTION: Papilloma Virus Proteins
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58783
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..182
OTHER INFORMATION: /note="Xaa refers to stop codon in
the open reading frame."
US-08-117-083-10

Query Match 100.0%; Score 44; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.37; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 QQLRRREVY 9
Db 43 QQLRRREVY 51

RESULT 9
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 44; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.53; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 QQLRRREVY 9
Db 42 QQLRRREVY 50

RESULT 10
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 44; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.53; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 QQLRRREVY 9
Db 42 QQLRRREVY 50

RESULT 11
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 44; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLRREVY 9
Db 42 QQLRREVY 50

RESULT 12
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 44; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLRREVY 9
Db 148 QQLRREVY 156

RESULT 13
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match 100.0%; Score 44; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 44; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLRREVY 9
Db 167 QQLRREVY 175

RESULT 14
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match 100.0%; Score 44; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLRREVY 9
Db 148 QQLRREVY 156

RESULT 15
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match 100.0%; Score 44; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLRREVY 9
Db 148 QQLRREVY 156

Db 167 QOLLREVV 175

Search completed: June 28, 2005, 23:37:46
Job time : 18.05 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-42
Perfect score: 48
Sequence: 1 VYCKQQLLR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	26	Q81956	Q81956 human papil
2	48	100.0	99	Q919B2	Q919B2 human papil
3	48	100.0	130	Q919B4	Q919B4 human papil
4	48	100.0	130	Q919B8	Q919B8 human papil
5	48	100.0	130	Q919C0	Q919C0 human papil
6	48	100.0	130	Q919C2	Q919C2 human papil
7	48	100.0	130	Q919C8	Q919C8 human papil
8	48	100.0	130	Q919D0	Q919D0 human papil
9	48	100.0	138	Q919D2	Q919D2 human papil
10	48	100.0	143	Q919B6	Q919B6 human papil
11	48	100.0	143	Q919C4	Q919C4 human papil
12	48	100.0	151	Q12335	Q12335 human papil
13	48	100.0	151	Q12336	Q12336 human papil
14	48	100.0	151	Q76TS0	Q76TS0 human papil
15	48	100.0	151	Q77816	Q77816 human papil
16	48	100.0	151	Q77E16	Q77E16 human papil
17	48	100.0	151	Q77JC7	Q77JC7 human papil
18	48	100.0	151	Q77ZJ5	Q77ZJ5 human papil
19	48	100.0	151	Q80963	Q80963 human papil
20	48	100.0	151	Q80966	Q80966 human papil
21	48	100.0	151	Q89640	Q89640 human papil
22	48	100.0	151	Q89648	Q89648 human papil
23	48	100.0	151	Q89708	Q89708 human papil
24	48	100.0	151	Q89755	Q89755 human papil
25	48	100.0	151	Q89852	Q89852 human papil
26	48	100.0	151	Q89887	Q89887 human papil
27	48	100.0	151	Q8B564	Q8B564 human papil
28	48	100.0	151	Q8BB19	Q8BB19 human papil
29	48	100.0	151	Q8BB20	Q8BB20 human papil
30	48	100.0	151	Q8BB21	Q8BB21 human papil
31	48	100.0	151	Q9W8C3	Q9W8C3 human papil

32	48	100.0	151	2	Q9W931	Q9W931 human papil
33	48	100.0	151	2	Q9WMP2	Q9WMP2 human papil
34	48	100.0	151	2	Q9WMP3	Q9WMP3 human papil
35	48	100.0	151	2	Q9WMP4	Q9WMP4 human papil
36	48	100.0	151	2	Q9WMP5	Q9WMP5 human papil
37	48	100.0	158	1	V56 HPV16	P01126 human papil
38	48	100.0	158	2	Q8JMU8	Q8JMU8 human papil
39	48	100.0	158	2	Q8QHN0	Q8QHN0 human papil
40	48	100.0	158	2	Q8QHP5	Q8QHP5 human papil
41	48	100.0	158	2	Q8QHT0	Q8QHT0 human papil
42	48	100.0	158	2	Q8QRD5	Q8QRD5 human papil
43	48	100.0	158	2	Q8QRD6	Q8QRD6 human papil
44	48	100.0	158	2	Q8QRD7	Q8QRD7 human papil
45	48	100.0	158	2	Q8QRD8	Q8QRD8 human papil

ALIGNMENTS

RESULT 1
Q81956 PRELIMINARY; PRT; 26 AA.
AC Q81956;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6E7 (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_taxid=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SIHA;
RA Shippy R., Sliwowski A., Hampel A.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59900; AAB03505.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 26 AA; 3208 MW; F06EBBE95EB67D5 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
Db 14 VYCKQQLLR 22

RESULT 2
Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_taxid=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404704; AAL01365.1; -.

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DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370B38 CRC64;
Query Match 100.0%; Score 48; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYCKQQLLR 9
Db 7 VYCKQQLLR 15

RESULT 3
Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01353.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EBDDC CRC64;
Query Match 100.0%; Score 48; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYCKQQLLR 9
Db 10 VYCKQQLLR 18

RESULT 4
Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01353.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
Query Match 100.0%; Score 48; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYCKQQLLR 9
Db 10 VYCKQQLLR 18

RESULT 5
Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
Query Match 100.0%; Score 48; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYCKQQLLR 9
Db 10 VYCKQQLLR 18

RESULT 6
Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01355.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
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Query Match      100.0%; Score 48; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
Db 10 VYCKQQLLR 18

RESULT 7
Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040469; AAL01345.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match      100.0%; Score 48; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
Db 10 VYCKQQLLR 18

RESULT 8
Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040469; AAL01345.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
SQ SEQUENCE 130 AA; 15735 MW; 9EPB30EEDCA21AF3 CRC64;

Query Match      100.0%; Score 48; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.14;

Qy 1 VYCKQQLLR 9
Db 10 VYCKQQLLR 18

RESULT 9
Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040469; AAL01345.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481ESA90895FC2 CRC64;

Query Match      100.0%; Score 48; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
Db 18 VYCKQQLLR 26

RESULT 10
Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404702; AAL01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match      100.0%; Score 48; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
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Db          23 VYCKQQLR 31
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RESULT 11
Q919C4
ID Q919C4 PRELIMINARY; PRT; 143 AA.
AC Q919C4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404698; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;
SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLR 9
|||||
Db 23 VYCKQQLR 31

RESULT 12
ID Q12335 PRELIMINARY; PRT; 151 AA.
AC Q12335;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003015; AAB70732.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;
SQ SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLR 9
|||||
Db 31 VYCKQQLR 39

RESULT 13
ID Q12336 PRELIMINARY; PRT; 151 AA.
AC Q12336;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003016; AAB70733.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match 100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLR 9
|||||
Db 31 VYCKQQLR 39

RESULT 14
ID Q76TS0 PRELIMINARY; PRT; 151 AA.
AC Q76TS0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
DR EMBL; U34131; AAA91678.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;
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Db          23 VYCKQQLR 31
|||||
RESULT 11
Q919C4
ID Q919C4 PRELIMINARY; PRT; 143 AA.
AC Q919C4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404698; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;
SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLR 9
|||||
Db 23 VYCKQQLR 31

RESULT 12
ID Q12335 PRELIMINARY; PRT; 151 AA.
AC Q12335;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003015; AAB70732.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;
SQ SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLR 9
|||||
Db 31 VYCKQQLR 39

RESULT 13
ID Q12336 PRELIMINARY; PRT; 151 AA.
AC Q12336;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003016; AAB70733.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match 100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLR 9
|||||
Db 31 VYCKQQLR 39

RESULT 14
ID Q76TS0 PRELIMINARY; PRT; 151 AA.
AC Q76TS0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
DR EMBL; U34131; AAA91678.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NON TER 1
FT SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;
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Query Match 100.0%; Score 48; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYCKQQLLR 9
 Db 31 VYCKQQLLR 39

RESULT 15

Q778I6 PRELIMINARY; PRT; 151 AA.
 AC Q778I6;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20112892; PubMed-10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
 RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325(2000).
 DR EMBL; AJ388056; CAB45104.1; -.
 DR EMBL; AJ388061; CAB45114.1; -.
 DR EMBL; AJ388066; CAB45124.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCBEA6C02 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYCKQQLLR 9
 Db 31 VYCKQQLLR 39

Search completed: June 28, 2005, 23:28:09
 Job time : 55.1 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)
78.367 Million cell updates/sec

Title: US-08-170-344-42
Perfect score: 48
Sequence: 1 VYCKQQLLR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	158	1 W6WLS	protein E6 - human
2	39	81.2	149	1 W6WL35	E6 protein - human
3	38	79.2	496	2 T46356	hypothetical prote
4	37	77.1	483	2 F8850	UDP-MurNac-tripept
5	36	75.0	151	1 W6WL51	E6 protein - human
6	36	75.0	155	1 W6WL56	E6 protein - human
7	36	75.0	1058	2 T30178	mitotic checkpoint
8	36	75.0	1102	2 T31004	probable mitotic c
9	35	72.9	148	2 S36515	E6 protein - human
10	35	72.9	158	1 W6WLPR	E6 protein - human
11	34.5	71.9	356	2 F82277	citrate (pro-3S)-l
12	34	70.8	100	2 S13796	retinoic acid-bind
13	34	70.8	592	2 D84431	probable endosomal
14	33	68.8	86	2 I50030	cellular retinoic
15	33	68.8	181	2 C63768	conserved hypothet
16	33	68.8	282	2 G84081	hypothetical prote
17	33	68.8	306	2 T26126	hypothetical prote
18	33	68.8	362	2 AF0159	probable membrane
19	33	68.8	366	2 D83350	hypothetical prote
20	33	68.8	407	2 T37242	transforming growt
21	33	68.8	563	2 T20192	hypothetical prote
22	32	66.7	101	2 E82380	conserved hypothet
23	32	66.7	125	2 S04503	pancreatic ribonuc
24	32	66.7	149	1 W6WL31	E6 protein - human
25	32	66.7	153	2 S36503	E6 protein - human
26	32	66.7	155	2 A44890	E6 protein - human
27	32	66.7	329	2 T28412	ORF MSV251 hypothe
28	32	66.7	340	2 T28110	hypothetical prote
29	32	66.7	373	2 E84647	hypothetical prote

30	32	66.7	1500	2 S36149	copper-transportin
31	32	66.7	1866	1 GNWE2C	genome polypeptid
32	32	66.7	1906	2 AD2443	hypothetical prote
33	31	64.6	83	2 AE0713	conserved hypothet
34	31	64.6	128	2 S55211	hypothetical prote
35	31	64.6	184	2 H83409	hypothetical prote
36	31	64.6	253	2 AC1338	transcription regu
37	31	64.6	253	2 A11708	transcription regu
38	31	64.6	268	2 B30819	interferon-regulat
39	31	64.6	290	2 S69841	TYA protein - yess
40	31	64.6	290	2 S41555	TYA protein - yess
41	31	64.6	419	2 H95919	probable reverse t
42	31	64.6	419	2 H96025	probable reverse t
43	31	64.6	419	2 A95386	Reverse transcript
44	31	64.6	478	2 S77358	ATP-dependent DNA
45	31	64.6	501	2 S16711	ABC1 protein precu

ALIGNMENTS

RESULT 1

W6WLS

protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virol. 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SBE>

A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

R.Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10427

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C:Genetics:

A:Gene: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 48; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.068; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0;

Oy 1 VYCKQQLLR 9

Db 38 VYCKQQLLR 46

RESULT 2

W6WL35

E6 protein - human papillomavirus type 35

C:Species: human papillomavirus type 35

A:Note: host Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: E40824; S36521

R:Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.

Virol. 186, 770-776, 1992

A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillon

A:Reference number: A40824; MUID:92124753; PMID:1310198

A:Accession: E40824

A>Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-149 <MAR>
A:Cross-references: UNIPROT:P27228; GB:M74117; NID:g333050; PIDN:AAA46966.1; PID:g333051
R:Delius, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36521
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149
A:Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52561.1; PID:g396998
A:Experimental source: strain 35H
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 81.2%; Score 39; DB 1; Length 149;
Best Local Similarity 77.8%; Pred. No. 3.3;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYCKQQLR 9
|||:|
Db 31 VYCKQLQR 39

RESULT 3
T46356
Hypothetical protein DKFZp434G2016.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
A:Accession: T46356
R:Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23037
A:Accession: T46356
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-496 <AAA>
A:Cross-references: UNIPROT:Q9NTG0; EMBL:AL137289
A:Experimental source: adult testis; clone DKFZp434G2016
C:Genetics:
A:Note: DKFZp434G2016.1

Query Match 79.2%; Score 38; DB 2; Length 496;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYCKQQLR 9
|||:|
Db 335 VYCKQLLR 343

RESULT 4
F86850
UDP-MurNac-tripeptide synthetase [imported] - Lactococcus lactis subsp. lactis (strain I
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
A:Accession: F86850
R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: F86850
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-483 <STO>
A:Cross-references: UNIPROT:Q9CEN1; GB:AE005176; PID:g12724832; PIDN:AAK05904.1; GSPDB:G
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: murE
C:Superfamily: UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase

Query Match 77.1%; Score 37; DB 2; Length 483;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VYCKQQLR 9
|||:|
Db 227 VYCKQLLR 234

RESULT 5
W6WL51
E6 protein - human papillomavirus type 51
C:Species: human papillomavirus type 51
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
A:Accession: E40415
R:Lungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991
A:Title: Biologic properties and nucleotide sequence analysis of human papillomavirus ty
A:Reference number: A40415; MUID:91303675; PMID:1649326
A:Accession: E40415
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-151 <LUN>
A:Cross-references: UNIPROT:P26554; GB:M62877
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 75.0%; Score 36; DB 1; Length 151;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYCKQQLR 9
|||:|
Db 31 VYCKQLCR 39

RESULT 6
W6WL56
E6 protein - human papillomavirus type 56
C:Species: human papillomavirus type 56
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
A:Accession: A33377; S36579
R:Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; McAllister, P.; Temple, G.F.
J. Gen. Virol. 70, 3099-3104, 1989
A:Title: Human papillomavirus type 56: a new virus detected in cervical cancers.
A:Reference number: A33377; MUID:90063558; PMID:2555440
A:Accession: A33377
A:Molecule type: DNA
A:Residues: 1-155 <LOE>
A:Cross-references: UNIPROT:P24836
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36579
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-155
A:Cross-references: EMBL:X74483; NID:g397053; PIDN:CAA52596.1; PID:g397054
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:33-69/Region: zinc finger CCCC motif
F:106-142/Region: zinc finger CCCC motif

Query Match 75.0%; Score 36; DB 1; Length 155;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYCKQQLR 9

Db 34 VYCKELTR 42
||||:|

RESULT 7

T310178
mitotic checkpoint protein kinase Bub1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T310178
R:Taylor, S.S.; McKeon, F.
Cell 89, 727-735, 1997
A:Title: Kinetochores localization of murine Bub1 is required for normal mitotic timing a
A:Reference number: Z08902; MUID:97325748; PMID:9182760
A:Accession: T310178
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1058 <TAY>
A:Cross-references: UNIPROT:O08901; EMBL:AF002823; NID:G2150135; PID:G2150136; PIDN:AAC5
C:Genetics:
A:Gene: Bub1

Query Match 75.0%; Score 36; DB 2; Length 1058;
Best Local Similarity 55.6%; Pred. No. 65;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLR 9
:||||:|

Db 235 MYCKEKLIR 243

RESULT 8

T31004
probable mitotic checkpoint control protein kinase BUB1 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: T31004
R:Pangilinan, F.; Li, Q.; Weaver, T.; Lewis, B.C.; Dang, C.V.; Spencer, F.
Genomics 46, 379-388, 1997
A:Title: Mammalian BUB1 protein kinases: map positions and in vivo expression.
A:Reference number: Z20958; MUID:98110573; PMID:9441741
A:Accession: T31004
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1102 <PAN>
A:Cross-references: EMBL:U89795; NID:G2335137; PID:G2335138; PIDN:AAC53533.1
C:Genetics:
A:Map position: 2
C:Keywords: protein kinase

Query Match 75.0%; Score 36; DB 2; Length 1102;
Best Local Similarity 55.6%; Pred. No. 68;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLR 9
:||||:|

Db 279 MYCKEKLIR 287

RESULT 9

S36515
E6 protein - human papillomavirus type 34
C:Species: human papillomavirus type 34
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36515
R:Deilius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36515
A:Molecule type: DNA
A:Residues: 1-148
A:Cross-references: UNIPROT:P36811; EMBL:X74476; NID:G396989; PIDN:CAA52555.1; PID:G3969

C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 72.9%; Score 35; DB 2; Length 148;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYCKQQLR 9
:||||:|

Db 32 VYCEQLYR 40

RESULT 10

W6WLPR
E6 protein - human papillomavirus type ME180 (provirus)
C:Species: human papillomavirus type ME180
A:Note: host Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: C40509
R:Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5568, 1991
A:Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma
A:Reference number: A40509; MUID:91374616; PMID:1716694
A:Accession: C40509
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-158 <REU>
A:Cross-references: UNIPROT:P27962; GB:M73258
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:105-141/Region: zinc finger CCCC motif

Query Match 72.9%; Score 35; DB 1; Length 158;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYCKQQLR 9
:||||:|

Db 33 VYCRQLQR 41

RESULT 11

F82277
citrate (pro-3S)-lyase ligase VC0796 [imported] - Vibrio cholerae (strain N16961 serogro
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 12-Jul-2004
C:Accession: F82277
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: F82277
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-356 <HEI>
A:Cross-references: UNIPROT:Q9KTU2; GB:AE004166; GB:AE003852; NID:G9655259; PIDN:AAF9396
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0796
A:Map position: 1
C:Superfamily: citrate lyase ligase

Query Match 71.9%; Score 34.5; DB 2; Length 356;
Best Local Similarity 80.0%; Pred. No. 50;
Matches 8; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 VYCKQ-QLLR 9
:||||:|

Db 137 VYCKQLQLLK 146

RESULT 12

S13796
retinoic acid-binding protein, cellular - chicken
C:Species: Gallus gallus (chicken)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C:Accession: S13796
R:Vaessen, M.J.; Meijers, J.H.C.; Bootsma, D.; van Kessel, A.G.
Development 110, 371-378, 1990
A:Title: The cellular retinoic-acid-binding protein is expressed in tissues associated with retinoic acid
A:Reference number: S13796; PMID:1966833
A:Accession: S13796
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-100 <VAE>
A:Cross-references: EMBL:X53701
C:Superfamily: myelin P2 protein

Query Match 70.8%; Score 34; DB 2; Length 100;
Best Local Similarity 62.5%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYCKQQLL 8
:|||||:
Db 83 IYCKQTLI 90

RESULT 13

D84431
probable endosomal protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: D84431
R:Liu, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: D84431; PMID:10617197
A:Accession: D84431
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-592 <STO>
A:Cross-references: UNIPROT:Q9ZPS7; GB:AE002093; NID:g4406780; PIDN:AAD20090.1; GSPDB:GN
C:Genetics:
A:Gene: At2g01970
A:Map position: 2
C:Superfamily: Schizosaccharomyces pombe probable transmembrane protein SPBC1105.08

Query Match 70.8%; Score 34; DB 2; Length 592;
Best Local Similarity 66.7%; Pred. No. 96;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYCKQQLLR 9
:|||||:
Db 100 VYCKKLSR 108

RESULT 14

I50030
cellular retinoic acid binding protein I - axolotl (fragment)
C:Species: Ambystoma mexicanum [axolotl]
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50030
R:Ludolph, D.L.; Cameron, J.A.; Neff, A.W.; Stocum, D.L.
Dev. Growth Differ. 35, 341-347, 1993
A:Title: Cloning and tissue specific expression of cellular retinoic acid binding protein I
A:Reference number: I50030
A:Accession: I50030
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-86 <LUD>
A:Cross-references: UNIPROT:Q90234; EMBL:X70945; NID:g509164; PIDN:CAA50284.1; PID:g5091

C:Superfamily: myelin P2 protein

Query Match 68.8%; Score 33; DB 2; Length 86;
Best Local Similarity 62.5%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYCKQQLL 8
:|||||:
Db 52 IYCKQTLV 59

RESULT 15

C69768
conserved hypothetical protein ydaC - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 12-Jul-2004
C:Accession: C69768
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier
A.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koecher, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptrata, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; PMID:98044033; PMID:9384377
A:Accession: C69768
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-181 <KUN>
A:Cross-references: UNIPROT:P96576; GB:Z99106; GB:AL009126; NID:g2632653; PIDN:CAB12225.1
A:Experimental source: strain 168
C:Genetics:
A:Gene: ydaC
C:Superfamily: 24-sterol C-methyltransferase
F:27-128/Domain: bioC homology <BIOC>

Query Match 68.8%; Score 33; DB 2; Length 181;
Best Local Similarity 62.5%; Pred. No. 54;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YCKQQLLR 9
:|||||:
Db 39 YCMQQLMK 46

Search completed: June 28, 2005, 23:31:59
Job time : 13.05 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-42

Perfect score: 48

Sequence: 1 VYCKQQLLR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	10	17	US-10-484-063-3
2	48	100.0	15	16	US-10-476-570-25
3	48	100.0	21	16	US-10-476-570-10
4	48	100.0	33	16	US-10-476-570-19
5	48	100.0	151	14	US-10-177-390-6
6	48	100.0	151	17	US-10-484-063-20
7	48	100.0	151	17	US-10-484-063-27
8	48	100.0	158	17	US-10-858-384-2
9	48	100.0	158	17	US-10-367-057-16
10	48	100.0	171	16	US-10-472-724-2
11	48	100.0	266	9	US-09-367-309A-1

12	48	100.0	273	13	US-10-000-903-4	Sequence 4, Appli
13	48	100.0	273	17	US-10-899-771-4	Sequence 4, Appli
14	48	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
15	48	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
16	48	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
17	48	100.0	371	17	US-10-899-771-6	Sequence 6, Appli
18	48	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
19	48	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
20	48	100.0	536	15	US-10-367-095-10	Sequence 10, Appl
21	48	100.0	536	15	US-10-368-046-10	Sequence 10, Appl
22	48	100.0	536	16	US-10-367-367-10	Sequence 10, Appl
23	48	100.0	536	17	US-10-318-337-10	Sequence 10, Appl
24	43	89.6	15	16	US-10-476-570-24	Sequence 24, Appl
25	43	89.6	32	16	US-10-476-570-9	Sequence 9, Appli
26	39	81.2	30	16	US-10-476-570-53	Sequence 53, Appl
27	39	81.2	30	17	US-10-858-384-4	Sequence 4, Appli
28	38	79.2	145	16	US-10-425-115-199640	Sequence 199640,
29	37	77.1	68	16	US-10-425-115-306231	Sequence 306231,
30	36	75.0	1085	9	US-09-095-881-2	Sequence 2, Appli
31	36	75.0	1085	13	US-10-084-700-4	Sequence 4, Appli
32	36	75.0	1085	15	US-10-363-929-137	Sequence 137, App
33	36	75.0	1085	16	US-10-733-878-373	Sequence 373, App
34	36	75.0	1102	15	US-10-263-929-138	Sequence 138, App
35	36	75.0	1547	16	US-10-425-115-215541	Sequence 215541,
36	35	72.9	69	16	US-10-425-115-290415	Sequence 290415,
37	35	72.9	354	17	US-10-732-923-1366	Sequence 1366, Ap
38	35	72.9	414	10	US-09-759-1308-214	Sequence 214, App
39	35	72.9	414	16	US-10-741-790-214	Sequence 214, App
40	35	72.9	525	16	US-10-425-115-314031	Sequence 314031,
41	35	72.9	753	10	US-09-759-1308-205	Sequence 205, App
42	35	72.9	753	16	US-10-741-790-205	Sequence 205, App
43	35	72.9	778	10	US-09-759-1308-203	Sequence 203, App
44	35	72.9	778	16	US-10-741-790-203	Sequence 203, App
45	35	72.9	816	10	US-09-759-1308-216	Sequence 216, App

ALIGNMENTS

RESULT 1
US-10-484-063-3
; Sequence 3, Application US/10484063
; Publication No. US200500048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484.063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-3

Query Match 100.0%; Score 48; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VYCKQQLLR 9
Db 2 VYCKQQLLR 10

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RESULT 2
US-10-476-570-25
; Sequence 25, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 36-50
US-10-476-570-25
Query Match 100.0%; Score 48; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
Db 3 VYCKQQLLR 11

RESULT 3
US-10-476-570-10
; Sequence 10, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 21
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 30-50
US-10-476-570-10
Query Match 100.0%; Score 48; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
Db 3 VYCKQQLLR 11

RESULT 4
US-10-476-570-19
; Sequence 19, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-46
US-10-476-570-19
Query Match 100.0%; Score 48; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
Db 25 VYCKQQLLR 33

RESULT 5
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerps Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6
Query Match 100.0%; Score 48; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
Db 31 VYCKQQLLR 39
```

RESULT 6

US-10-484-063-20
 ; Sequence 20, Application US/10484063
 ; Publication No. US20050048467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SASTRY, K. JAGANNADHA
 ; APPLICANT: TORTOLERO-LUNA, GUILLERMO
 ; APPLICANT: FOLLEN, MICHELE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
 ; FILE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
 ; FILE REFERENCE: UTSC:560US
 ; CURRENT APPLICATION NUMBER: US/10/484,063
 ; CURRENT FILING DATE: 2004-01-16
 ; PRIOR APPLICATION NUMBER: PCT/US02/23198
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 60/306,809
 ; PRIOR FILING DATE: 2001-07-20
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus
 US-10-484-063-20

Query Match 100.0%; Score 48; DB 17; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.77;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYCKQQLLR 9
 DB 31 VYCKQQLLR 39

RESULT 7

US-10-484-063-27
 ; Sequence 27, Application US/10484063
 ; Publication No. US20050048467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SASTRY, K. JAGANNADHA
 ; APPLICANT: TORTOLERO-LUNA, GUILLERMO
 ; APPLICANT: FOLLEN, MICHELE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
 ; FILE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
 ; FILE REFERENCE: UTSC:560US
 ; CURRENT APPLICATION NUMBER: US/10/484,063
 ; CURRENT FILING DATE: 2004-01-16
 ; PRIOR APPLICATION NUMBER: PCT/US02/23198
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 60/306,809
 ; PRIOR FILING DATE: 2001-07-20
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 27
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus type 16
 US-10-484-063-27

Query Match 100.0%; Score 48; DB 17; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.77;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYCKQQLLR 9
 DB 31 VYCKQQLLR 39

RESULT 8

US-10-858-384-2
 ; Sequence 2, Application US/10858384
 ; Publication No. US20050033025A1
 ; GENERAL INFORMATION:

; APPLICANT: CHOPPIN, JEANNINE
 ; APPLICANT: BOURGAULT VILLADA, ISABELLE
 ; APPLICANT: GUILLET, JEAN-GERARD
 ; APPLICANT: CONNAN, FRANCINE
 ; APPLICANT: FERRIES, ESTELLE
 ; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
 ; FILE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
 ; FILE REFERENCE: 0508-1037-1
 ; CURRENT APPLICATION NUMBER: US/10/858,384
 ; CURRENT FILING DATE: 2004-06-02
 ; PRIOR APPLICATION NUMBER: FR 9907012
 ; PRIOR FILING DATE: 1999-06-03
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 2
 ; LENGTH: 158
 ; TYPE: PRT
 ; ORGANISM: Human Papillomavirus
 US-10-858-384-2

Query Match 100.0%; Score 48; DB 17; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYCKQQLLR 9
 DB 38 VYCKQQLLR 46

RESULT 9

US-10-367-057-16
 ; Sequence 16, Application US/10367057
 ; Publication No. US20050100554A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cuthill, Scott;
 ; APPLICANT: Jackson, Amanda;
 ; APPLICANT: Lewin, David A.;
 ; APPLICANT: Ooi, Chean Eng
 ; TITLE OF INVENTION: Complexes and Methods of Using Same
 ; FILE REFERENCE: 21402-559
 ; CURRENT APPLICATION NUMBER: US/10/367,057
 ; CURRENT FILING DATE: 2003-02-14
 ; PRIOR APPLICATION NUMBER: 60/256,911
 ; PRIOR FILING DATE: 2002-02-14
 ; NUMBER OF SEQ ID NOS: 198
 ; SOFTWARE: CuraseqList version 0.1
 ; SEQ ID NO 16
 ; LENGTH: 158
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-367-057-16

Query Match 100.0%; Score 48; DB 17; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYCKQQLLR 9
 DB 38 VYCKQQLLR 46

RESULT 10

US-10-472-724-2
 ; Sequence 2, Application US/10472724.
 ; Publication No. US20040171806A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cid-Arregui, Angel
 ; APPLICANT: Zur Hausen, Harald
 ; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
 ; FILE REFERENCE: 4121-154
 ; CURRENT APPLICATION NUMBER: US/10/472,724
 ; CURRENT FILING DATE: 2003-09-17

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; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match      100.0%; Score 48; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
Db 43 VYCKQQLLR 51

RESULT 11
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 48; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
Db 38 VYCKQQLLR 46

RESULT 12
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22

; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match      100.0%; Score 48; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
Db 144 VYCKQQLLR 152

RESULT 13
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

Query Match      100.0%; Score 48; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
Db 144 VYCKQQLLR 152

RESULT 14
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match      100.0%; Score 48; DB 13; Length 292;
Best Local Similarity 100.0%; Pred. NO. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYCKQQLLR 9
Db 163 VYCKQQLLR 171

RESULT 15
US-10-899-771-10
; Sequence 10, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus
; OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-10

Query Match      100.0%; Score 48; DB 17; Length 292;
Best Local Similarity 100.0%; Pred. NO. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYCKQQLLR 9
Db 163 VYCKQQLLR 171

Search completed: June 29, 2005, 05:18:09
Job time : 116:15 secs
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This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-42
Perfect score: 48
Sequence: 1 VYCKQQLLR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	10	3	US-08-159-339A-575
2	48	100.0	20	2	US-08-934-915-160
3	48	100.0	158	4	US-09-980-523A-2
4	48	100.0	162	1	US-08-316-239B-3
5	48	100.0	162	1	US-08-316-239B-4
6	48	100.0	172	3	US-08-860-165-14
7	48	100.0	172	3	US-09-353-382-14
8	48	100.0	182	1	US-08-117-083-10
9	48	100.0	266	3	US-08-860-165-10
10	48	100.0	266	3	US-09-353-382-10
11	48	100.0	266	4	US-09-367-309A-1
12	48	100.0	273	3	US-09-485-885-4
13	48	100.0	292	3	US-09-485-885-10
14	48	100.0	371	3	US-09-485-885-6
15	48	100.0	390	3	US-09-485-885-14
16	39	81.2	9	3	US-08-159-339A-238
17	39	81.2	9	3	US-08-159-339A-253
18	39	81.2	30	4	US-09-980-523A-4
19	36	75.0	78	3	US-09-448-806C-6
20	36	75.0	1085	4	US-09-095-881-2
21	36	75.0	1095	4	US-09-555-554-4
22	34	70.8	9	3	US-08-159-339A-226
23	34	70.8	80	4	US-09-252-991A-31270
24	34	70.8	156	3	US-09-134-001C-4260
25	34	70.8	334	4	US-09-270-767-37306
26	34	70.8	334	4	US-09-270-767-52523
27	33	68.8	91	4	US-09-270-767-61003

28	33	68.8	274	4	US-09-270-767-45494	Sequence 45494, A
29	33	68.8	383	4	US-09-134-000C-4139	Sequence 4139, Ap
30	33	68.8	490	4	US-09-902-540-12632	Sequence 12632, A
31	33	68.8	512	4	US-09-107-532A-7248	Sequence 7248, Ap
32	33	68.8	1711	3	US-08-369-822C-10	Sequence 10, Appl
33	33	68.8	1711	3	US-08-582-776C-10	Sequence 10, Appl
34	33	68.8	1711	3	US-08-434-831B-10	Sequence 10, Appl
35	32	66.7	65	4	US-09-248-796A-24263	Sequence 24263, A
36	32	66.7	67	4	US-09-270-767-45456	Sequence 45456, A
37	32	66.7	102	4	US-09-270-767-59962	Sequence 59962, A
38	32	66.7	149	4	US-09-270-767-40624	Sequence 40624, A
39	32	66.7	149	4	US-09-270-767-55840	Sequence 55840, A
40	32	66.7	239	4	US-09-270-767-44514	Sequence 44514, A
41	32	66.7	276	4	US-09-489-039A-9670	Sequence 9670, Ap
42	32	66.7	347	4	US-09-248-796A-24285	Sequence 24285, A
43	32	66.7	789	4	US-09-949-016-7164	Sequence 7164, Ap
44	32	66.7	1500	4	US-09-949-016-5878	Sequence 5878, Ap
45	31	64.6	60	4	US-09-248-796A-27748	Sequence 27748, A

ALIGNMENTS

RESULT 1
US-08-159-339A-575
; Sequence 575, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 575:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-575

Query Match 100.0%; Score 48; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
| | | | |
Db 2 VYCKQQLLR 10

RESULT 2

US-08-934-915-160
; Sequence 160, Application US/08934915
; Patent No. 5932412

; GENERAL INFORMATION:

; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: LOUISE A. Fouch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:

; INFORMATION FOR SEQ ID NO: 160:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-934-915-160

Query Match 100.0%; Score 48; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
| | | | |
Db 7 VYCKQQLLR 15

RESULT 3

US-09-980-523A-2

; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:

; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
; US-09-980-523A-2

Query Match 100.0%; Score 48; DB 4; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
| | | | |
Db 38 VYCKQQLLR 46

RESULT 4

US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:

; APPLICANT: Wheeler, Cosette M.

; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jagtiani & Associates

; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/316,239B
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNWE-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant

```
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match      100.0%; Score 48; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.14; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
Db 38 VYCKQQLLR 46

RESULT 5
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match      100.0%; Score 48; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.14; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
Db 38 VYCKQQLLR 46

RESULT 6
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
```

```
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match      100.0%; Score 48; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.15; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
Db 107 VYCKQQLLR 115

RESULT 7
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match      100.0%; Score 48; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.15; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
Db 107 VYCKQQLLR 115

RESULT 8
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
```

APPLICANT: Munro, Alan J.
TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
TITLE OF INVENTION: Papilloma Virus Proteins
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58783
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..182
OTHER INFORMATION: /notes "Xaa refers to stop codon in
the open reading frame."
US-08-117-083-10

Query Match 100.0%; Score 48; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
|||
Db 39 VYCKQQLLR 47

RESULT 9
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 48; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
|||
Db 38 VYCKQQLLR 46

RESULT 10
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 48; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYCKQQLLR 9
|||
Db 38 VYCKQQLLR 46

RESULT 11
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 48; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYCKQQLLR 9
|||||
DB 38 VYCKQQLLR 46

RESULT 12
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 48; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYCKQQLLR 9
|||||
DB 144 VYCKQQLLR 152

RESULT 13
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match 100.0%; Score 48; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYCKQQLLR 9
|||||
DB 163 VYCKQQLLR 171

RESULT 14
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match 100.0%; Score 48; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYCKQQLLR 9
|||||
DB 144 VYCKQQLLR 152

RESULT 15
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match 100.0%; Score 48; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYCKQQLLR 9
|||||

Db 163 VYCKQQLR 171

Search completed: June 28, 2005, 23:37:45
Job time : 18.05 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-41
Perfect score: 51
Sequence: 1 IILECVYCK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	26	2 Q81956	Q81956 human papil
2	51	100.0	99	2 Q919B2	Q919B2 human papil
3	51	100.0	130	2 Q919B4	Q919B4 human papil
4	51	100.0	130	2 Q919B8	Q919B8 human papil
5	51	100.0	130	2 Q919C0	Q919C0 human papil
6	51	100.0	130	2 Q919C2	Q919C2 human papil
7	51	100.0	130	2 Q919C8	Q919C8 human papil
8	51	100.0	130	2 Q919D0	Q919D0 human papil
9	51	100.0	138	2 Q919D2	Q919D2 human papil
10	51	100.0	143	2 Q919B6	Q919B6 human papil
11	51	100.0	143	2 Q919C4	Q919C4 human papil
12	51	100.0	151	2 O12335	O12335 human papil
13	51	100.0	151	2 O12336	O12336 human papil
14	51	100.0	151	2 Q76TS0	Q76TS0 human papil
15	51	100.0	151	2 Q778I6	Q778I6 human papil
16	51	100.0	151	2 Q77E16	Q77E16 human papil
17	51	100.0	151	2 Q77JC7	Q77JC7 human papil
18	51	100.0	151	2 Q77ZJ5	Q77ZJ5 human papil
19	51	100.0	151	2 Q80963	Q80963 human papil
20	51	100.0	151	2 Q80966	Q80966 human papil
21	51	100.0	151	2 Q89640	Q89640 human papil
22	51	100.0	151	2 Q89648	Q89648 human papil
23	51	100.0	151	2 Q89708	Q89708 human papil
24	51	100.0	151	2 Q89755	Q89755 human papil
25	51	100.0	151	2 Q89852	Q89852 human papil
26	51	100.0	151	2 Q89887	Q89887 human papil
27	51	100.0	151	2 Q8BB19	Q8BB19 human papil
28	51	100.0	151	2 Q9W8C3	Q9W8C3 human papil
29	51	100.0	151	2 Q9W931	Q9W931 human papil
30	51	100.0	151	2 Q9WMP2	Q9WMP2 human papil
31	51	100.0	151	2 Q9WMP4	Q9WMP4 human papil

32 51 100.0 158 1 VEG_HPV16 P03126 human papil
33 51 100.0 158 2 Q8JMU8 Q8JMU8 human papil
34 51 100.0 158 2 Q8QHN0 Q8QHN0 human papil
35 51 100.0 158 2 Q8QHP5 Q8QHP5 human papil
36 51 100.0 158 2 Q8QHT0 Q8QHT0 human papil
37 51 100.0 158 2 Q8QRD5 Q8QRD5 human papil
38 51 100.0 158 2 Q8QRD6 Q8QRD6 human papil
39 51 100.0 158 2 Q8QRD7 Q8QRD7 human papil
40 51 100.0 158 2 Q8QRD8 Q8QRD8 human papil
41 51 100.0 158 2 Q8QRD9 Q8QRD9 human papil
42 51 100.0 158 2 Q8QRE0 Q8QRE0 human papil
43 51 100.0 158 2 Q8QRE1 Q8QRE1 human papil
44 51 100.0 158 2 Q71B17 Q71B17 human papil
45 51 100.0 158 2 Q9QDH3 Q9QDH3 human papil

ALIGNMENTS

RESULT 1

Q81956 PRELIMINARY; PRT; 26 AA.
ID Q81956
AC Q81956;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6E7 (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Shippy R., Siwkowski A., Hampel A.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59900; AA03505.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 26 AA; 3208 MW; F06EBBE995EB67D5 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILECVYCK 9

Db 9 IILECVYCK 17

RESULT 2

Q919B2 PRELIMINARY; PRT; 99 AA.
ID Q919B2
AC Q919B2;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RL "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia."; Int. J. Cancer 97:868-874 (2002).
DR EMBL; AF404704; AAL01365.1; -.

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DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;
Query Match 100.0%; Score 51; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IILECVYCK 9
DB 2 IILECVYCK 10
RESULT 3
Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01363.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;
Query Match 100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IILECVYCK 9
DB 5 IILECVYCK 13
RESULT 4
Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01359.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
Query Match 100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IILECVYCK 9
DB 5 IILECVYCK 13
RESULT 5
Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
Query Match 100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IILECVYCK 9
DB 5 IILECVYCK 13
RESULT 6
Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01355.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
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Query Match      100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
Db 5 IILECVYCK 13

RESULT 7
Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404696; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
DR NON TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match      100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
Db 5 IILECVYCK 13

RESULT 8
Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404695; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
DR NON TER 1
SQ SEQUENCE 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;

Query Match      100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.22;

Qy 1 IILECVYCK 9
Db 5 IILECVYCK 13

RESULT 9
Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404694; AAL01345.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
DR NON TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481ESA90895FC2 CRC64;

Query Match      100.0%; Score 51; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
Db 13 IILECVYCK 21

RESULT 10
Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404702; AAL01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
DR NON TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match      100.0%; Score 51; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
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Db 18 IILECVYCK 26
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RESULT 11

Q919C4 PRELIMINARY; PRT; 143 AA.
ID Q919C4
AC Q919C4
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404698; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.24; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
|||||

Db 18 IILECVYCK 26
|||||

RESULT 12

O12335 PRELIMINARY; PRT; 151 AA.
ID O12335
AC O12335
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003015; AAB70732.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;

Query Match 100.0%; Score 51; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.26; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
|||||

Db 26 IILECVYCK 34
|||||

RESULT 13

O12336 PRELIMINARY; PRT; 151 AA.
ID O12336
AC O12336
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003016; AAB70733.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match 100.0%; Score 51; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.26; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
|||||

Db 26 IILECVYCK 34
|||||

RESULT 14

Q76TSO PRELIMINARY; PRT; 151 AA.
ID Q76TSO
AC Q76TSO
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34114; AAA91661.1; -.
DR EMBL; U34125; AAA91672.1; -.
DR EMBL; U34130; AAA91677.1; -.
DR EMBL; U34131; AAA91678.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.26; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
|||||

Db 26 IILECVYCK 34
|||||

Query Match 100.0%; Score 51; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILECVYCK 9
|||
Db 26 IILECVYCK 34

RESULT 15

Q77816 PRELIMINARY; PRT; 151 AA.
AC Q77816;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388056; CAB45104.1; -;
DR EMBL; AJ388061; CAB45114.1; -;
DR EMBL; AJ388066; CAB45124.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCBBA6C02 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILECVYCK 9
|||
Db 26 IILECVYCK 34

Search completed: June 28, 2005, 23:28:09
Job time : 56.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)
78.367 Million cell updates/sec

Title: US-08-170-344-41
Perfect score: 51
Sequence: 1 ILLECYCK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	158	1 W6WLS3	protein E6 - human
2	41	80.4	149	1 W6WLS3	E6 protein - human
3	41	80.4	445	2 T01214	hypothetical prote
4	40	78.4	153	2 S36503	E6 protein - human
5	40	78.4	477	2 T46125	calmodulin-binding
6	38	74.5	149	1 W6WLS3	E6 protein - human
7	38	74.5	155	1 W6WLS6	E6 protein - human
8	38	74.5	155	2 A44890	E6 protein - human
9	38	74.5	191	1 W6WLR1	E6 protein - rhesu
10	38	74.5	343	2 AF1407	polyol dehydrogena
11	38	74.5	343	2 AF1783	polyol dehydrogena
12	38	74.5	344	2 S42383	hypothetical prote
13	38	74.5	2251	2 T24490	hypothetical prote
14	37	72.5	76	2 E96619	protein T30E16.11
15	37	72.5	148	2 S36515	E6 protein - human
16	37	72.5	150	2 S36544	E6 protein - human
17	37	72.5	158	1 W6WLPK	E6 protein - human
18	37	72.5	809	2 T16448	hypothetical prote
19	36	70.6	57	2 I56705	E6 protein - human
20	36	70.6	158	1 W6WLR1	E6 protein - human
21	36	70.6	158	2 S36561	E6 protein - human
22	36	70.6	229	2 T25302	hypothetical prote
23	36	70.6	232	2 T23639	hypothetical prote
24	36	70.6	250	2 T16631	hypothetical prote
25	36	70.6	254	2 D82941	hypothetical prote
26	36	70.6	432	2 S51474	hypothetical prote
27	36	70.6	538	2 E81435	probable iron-upra
28	36	70.6	630	2 T43460	hypothetical prote
29	36	70.6	1145	2 T33606	hypothetical prote

ALIGNMENTS

RESULT 1

W6WLS3

protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C>Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virolology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

J.Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10427

A>Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C:Genetics:

A:Gene: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 51; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.23; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILLECYCK 9

Db 33 ILLECYCK 41

RESULT 2

W6WLS3

E6 protein - human papillomavirus type 35

C:Species: human papillomavirus type 35

A:Note: host Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: E40824; S36521

R:Marich, J.E.; Pontaler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.

Virolology 186, 770-776, 1992

A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillon

A:Reference number: A40824; MUID:92124753; PMID:1310198

A:Accession: E40824

A>Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-149 <MAR>
A:Cross-references: UNIPROT:P27228; GB:M74117; NID:G333050; PIDN:AAA46966.1; PID:G333051
R:Delius, H.; Hofmann, B.
A:Submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36521
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149
A:Cross-references: EMBL:X74477; NID:G396997; PIDN:CAA52561.1; PID:G396998
A:Experimental source: strain 35H
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 80.4%; Score 41; DB 1; Length 149;
Best Local Similarity 77.8%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ILECYVCK 9
| | | | |
DB 26 ICLNCVCK 34

RESULT 3
T01214
hypothetical protein F6N23.21 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01214
R:Geisel, C.
A:Submitted to the EMBL Data Library, April 1998
A:Description: The sequence of A. thaliana F6N23.
A:Reference number: Z14281
A:Accession: T01214
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-445 <GEI>
A:Cross-references: UNIPROT:O65259; EMBL:AF058919; NID:G3047100; PID:G3047111; GSPDB:GNC
C:Genetics:
A:Gene: AISP:F6N23.21
A:Map position: 5
A:Introns: 235/3; 255/2; 298/2; 343/3

Query Match 80.4%; Score 41; DB 2; Length 445;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ILECYVC 8
| | | | |
DB 9 VLECYVC 15

RESULT 4
S36503
E6 protein - human papillomavirus type 30
C:Species: human papillomavirus type 30
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36503
R:Delius, H.; Hofmann, B.
A:Submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36503
A:Molecule type: DNA
A:Residues: 1-153
A:Cross-references: UNIPROT:P36809; EMBL:X74474; NID:G396973; PIDN:CAA52543.1; PID:G3969
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 78.4%; Score 40; DB 2; Length 153;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LECVYCK 9
| | | | |
DB 31 LQCVYCK 37

RESULT 5
T46125
calmodulin-binding heat-shock-like protein - Arabidopsis thaliana
N:Alternate names: protein T2J13.110
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46125
R:Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Mayer, K.
A:Submitted to the Protein Sequence Database, November 1999
A:Reference number: Z23023
A:Accession: T46125
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-477 <RIE>
A:Cross-references: UNIPROT:Q9SMU2; EMBL:AL132967
A:Experimental source: cultivar Columbia; BAC clone T2J13
C:Genetics:
A:Map position: 3
A:Introns: 236/3; 256/2; 299/2; 344/3
A>Note: T2J13.110

Query Match 78.4%; Score 40; DB 2; Length 477;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ILECYVC 8
| | | | |
DB 10 LLECYVC 16

RESULT 6
W6WL31
E6 protein - human papillomavirus type 31
C:Species: human papillomavirus type 31
A>Note: host Homo sapiens (man)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: A32444
R:Goldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associ
A:Reference number: A94398; MUID:89299478; PMID:2545036
A:Accession: A32444
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-149 <GOL>
A:Cross-references: UNIPROT:P17386; GB:J04353; NID:G333048; PIDN:AAA46950.1; PID:G459916
C:Comment: This protein may be involved in the oncogenic potential of this virus.
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 74.5%; Score 38; DB 1; Length 149;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LECVYCK 9
| | | | |
DB 28 LNCVYCK 34

RESULT 7
W6WL56
E6 protein - human papillomavirus type 56

C:Species: human papillomavirus type 56
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C:Accession: A33377; S36579
 R:Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; McAllister, P.; Temple, G.F.
 J. Gen. Virol. 70, 3099-3104, 1989
 A:Title: Human papillomavirus type 56: a new virus detected in cervical cancers.
 A:Reference number: A33377; MUID:9063558; PMID:2555440
 A:Accession: A33377
 A:Molecule type: DNA
 A:Residues: 1-155 <LOE>
 A:Cross-references: UNIPROT:P24836
 R:Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A:Description: Primer-directed sequencing of human papillomavirus types.
 A:Reference number: S36469
 A:Accession: S36579
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-155
 A:Cross-references: EMBL:X74483; NID:g9397053; PIDN:CAAS2596.1; PID:g9397054
 C:Superfamily: papillomavirus E6 protein
 C:Keywords: DNA binding; early protein; transforming protein; zinc finger
 F:33-69/Region: zinc finger CCCC motif
 F:106-142/Region: zinc finger CCCC motif

Query Match 74.5%; Score 38; DB 1; Length 155;
 Best Local Similarity 85.7%; Pred. No. 28;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LECVYCK 9
 | | | | |
 DB 31 LSCVYCK 37

RESULT 8
 A44890
 E6 protein - human papillomavirus type 66
 C:Species: human papillomavirus type 66
 C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
 C:Accession: A44890
 R:Tawheed, A.R.; Beaudenon, S.; Favre, M.; Orth, G.
 J. Clin. Microbiol. 29, 2856-2860, 1991
 A:Title: Characterization of human papillomavirus type 66 from an invasive carcinoma of
 A:Reference number: A44890; MUID:92129556; PMID:1663515
 A:Accession: A44890
 A:Molecule type: DNA
 A:Residues: 1-155 <TAW>
 A:Cross-references: UNIPROT:Q80955
 A>Note: sequence extracted from NCBI backbone (NCBIN:78637, NCBIP:78638)
 C:Superfamily: papillomavirus E6 protein
 C:Keywords: DNA binding; early protein; transforming protein; zinc finger
 F:33-69/Region: zinc finger CCCC motif
 F:106-142/Region: zinc finger CCCC motif

Query Match 74.5%; Score 38; DB 2; Length 155;
 Best Local Similarity 85.7%; Pred. No. 28;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LECVYCK 9
 | | | | |
 DB 31 LSCVYCK 37

RESULT 9
 W6WLRI
 E6 protein - rhesus papillomavirus (type 1)
 C:Species: rhesus papillomavirus
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C:Accession: A38503
 R:Ostrow, R.S.; Labresh, K.V.; Faras, A.J.
 Virology 181, 424-429, 1991
 A:Title: Characterization of the complete RHPV 1 genomic sequence and an integration loc
 A:Reference number: A38503; MUID:91135018; PMID:1847267

A:Accession: A38503
 A>Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-191 <OST>
 A:Cross-references: UNIPROT:P22159; EMBL:M37717
 C:Superfamily: papillomavirus E6 protein
 C:Keywords: DNA binding; early protein; transforming protein; zinc finger
 F:60-96/Region: zinc finger CCCC motif
 F:133-169/Region: zinc finger CCCC motif

Query Match 74.5%; Score 38; DB 1; Length 191;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LECVYCK 8
 | | | | |
 DB 58 LECVYCK 63

RESULT 10
 AF1407
 polyol dehydrogenase homolog lmo2663 [imported] - Listeria monocytogenes (strain EGD-e)
 C:Species: Listeria monocytogenes
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AF1407
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
 ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AF1407
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-343 <GLA>
 A:Cross-references: UNIPROT:Q8Y414; GB:NC_003210; PIDN:CAD00876.1; PID:g16412163; GSPDB:G
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: lmo2663
 C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

Query Match 74.5%; Score 38; DB 2; Length 343;
 Best Local Similarity 83.3%; Pred. No. 50;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 ECVYCK 9
 | | | | |
 DB 94 ECIYCK 99

RESULT 11
 AF1783
 polyol dehydrogenase homolog lin2812 [imported] - Listeria innocua (strain Clip11262)
 C:Species: Listeria innocua
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AF1783
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
 ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AF1783
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-343 <GLA>
 A:Cross-references: UNIPROT:Q927H6; GB:AL592022; PIDN:CAC98038.1; PID:g16415348; GSPDB:G
 A:Experimental source: strain Clip11262
 C:Genetics:

A:Gene: lin2812

C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

Query Match 74.5%; Score 38; DB 2; Length 343;
Best Local Similarity 83.3%; Pred. No. 50;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 ECVYCK 9
||:||||
Db 94 ECIYCK 99

RESULT 12

S42383

Hypothetical protein T16H12.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S42383

R:Smith, A.

submitted to the EMBL Data Library, March 1994

A:Reference number: S42368

A:Accession: S42383

A:Molecule type: DNA

A:Residues: 1-344 <SMI>

A:Cross-references: UNIPROT:P34564; EMBL:Z30662; NID:G459581; PID:G459586

C:Genetics: 30/2; 65/3; 113/3; 129/3; 152/1; 174/2; 218/1; 219/3

C:Superfamily: Caenorhabditis elegans hypothetical protein T16H12.1

Query Match 74.5%; Score 38; DB 2; Length 344;
Best Local Similarity 71.4%; Pred. No. 50;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LECVYCK 9
||:||||
Db 116 LECIFCK 122

RESULT 13

T24490

Hypothetical protein T05A10.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T24490

R:Stietson, J.

submitted to the EMBL Data Library, November 1995

A:Reference number: Z19898

A:Accession: T24490

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-2251 <WIL>

A:Cross-references: UNIPROT:Q22190; EMBL:Z68108; PIDN:CAA92133.1; GSPDB:GN00028; CESP:T0

A:Experimental source: clone T05A10

C:Genetics:

A:Gene: CESP.T05A10.1

A:Map position: X

A:Introns: 188/3; 240/3; 420/1; 570/3; 596/1; 732/3; 778/3; 851/3; 1359/2; 1394/2; 1434/

Query Match 74.5%; Score 38; DB 2; Length 2251;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 ECVYCK 9
||:||||
Db 653 ECIYCK 658

RESULT 14

E96619

protein T30E16.11 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: E96619

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: E96619

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-76 <STO>

A:Cross-references: UNIPROT:Q9LQ60; GB:AE005173; NID:G8778740; PIDN:AAF79748.1; GSPDB:GN

C:Genetics:

A:Gene: T30E16.11

A:Map position: 1

Query Match 72.5%; Score 37; DB 2; Length 76;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IILECVYC 8
||||:|
Db 58 IILECIIC 65

RESULT 15

S36515

E6 protein - human papillomavirus type 34

C:Species: human papillomavirus type 34

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S36515

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A>Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36515

A:Molecule type: DNA

A:Residues: 1-148

A:Cross-references: UNIPROT:P36811; EMBL:X74476; NID:G396989; PIDN:CAAS2555.1; PID:G3969

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 72.5%; Score 37; DB 2; Length 148;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 IILECVYCK 9
||:||||
Db 27 IELDCVYCE 35

Search completed: June 28, 2005, 23:31:57

Job time : 12.05 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-41
Perfect score: 51
Sequence: 1 IILECVYCK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCT05_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	15	16	US-10-476-570-23
2	51	100.0	15	16	US-10-476-570-24
3	51	100.0	21	16	US-10-476-570-10
4	51	100.0	30	16	US-10-476-570-53
5	51	100.0	30	17	US-10-858-384-4
6	51	100.0	32	16	US-10-476-570-9
7	51	100.0	33	16	US-10-476-570-19
8	51	100.0	151	14	US-10-177-390-6
9	51	100.0	151	17	US-10-484-063-20
10	51	100.0	151	17	US-10-484-063-27
11	51	100.0	158	17	US-10-858-384-2

12	51	100.0	158	17	US-10-367-057-16	Sequence 16, Appl
13	51	100.0	171	16	US-10-472-724-2	Sequence 2, Appl
14	51	100.0	266	9	US-09-367-309A-1	Sequence 1, Appl
15	51	100.0	273	13	US-10-000-903-4	Sequence 4, Appl
16	51	100.0	273	17	US-10-899-771-4	Sequence 4, Appl
17	51	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
18	51	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
19	51	100.0	371	13	US-10-000-903-6	Sequence 6, Appl
20	51	100.0	371	17	US-10-899-771-6	Sequence 6, Appl
21	51	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
22	51	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
23	51	100.0	536	15	US-10-367-095-10	Sequence 10, Appl
24	51	100.0	536	15	US-10-368-046-10	Sequence 10, Appl
25	51	100.0	536	16	US-10-367-367-10	Sequence 10, Appl
26	51	100.0	536	17	US-10-918-337-10	Sequence 10, Appl
27	42	82.4	236	15	US-10-424-599-250987	Sequence 250987,
28	40	78.4	455	15	US-10-425-115-297879	Sequence 297879,
29	39	76.5	15	16	US-10-476-570-25	Sequence 25, Appl
30	39	76.5	89	15	US-10-424-599-251182	Sequence 251182,
31	39	76.5	149	15	US-10-369-493-13518	Sequence 13518, A
32	38	74.5	69	16	US-10-425-115-318856	Sequence 318856,
33	38	74.5	98	15	US-10-767-701-56715	Sequence 56715, A
34	38	74.5	147	15	US-10-369-493-11069	Sequence 11069, A
35	38	74.5	225	9	US-09-811-284-212	Sequence 212, App
36	38	74.5	343	15	US-10-282-122A-60799	Sequence 60799, A
37	37	72.5	82	15	US-10-424-599-250479	Sequence 250479,
38	37	72.5	151	15	US-10-369-493-18168	Sequence 18168, A
39	37	72.5	173	16	US-10-767-701-61472	Sequence 61472, A
40	36	70.6	42	17	US-10-751-845-152	Sequence 152, App
41	36	70.6	66	16	US-10-437-363-167456	Sequence 167456,
42	36	70.6	67	15	US-10-424-599-239259	Sequence 239259,
43	36	70.6	80	16	US-10-425-115-206533	Sequence 206533,
44	36	70.6	94	15	US-10-424-599-146113	Sequence 146113,
45	36	70.6	101	15	US-10-424-599-254488	Sequence 254488,

ALIGNMENTS

RESULT 1

- US-10-476-570-23
- Sequence 23, Application US/10476570
- Publication No. US20040170644A1
- GENERAL INFORMATION:
- APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
- APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
- APPLICANT: MAILLIERE, Bernard
- APPLICANT: BOURGAULT-VILLADA, Isabelle
- APPLICANT: POUVELLE-MORATILLE, Sandra
- APPLICANT: GUILLET, Jean-Gerard
- TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7 papillomavirus proteins and uses thereof
- FILE REFERENCE: 45636-5071-US
- CURRENT APPLICATION NUMBER: US/10/476,570
- CURRENT FILING DATE: 2003-11-04
- PRIOR APPLICATION NUMBER: PCT/FR02/01533
- PRIOR FILING DATE: 2002-05-03
- PRIOR APPLICATION NUMBER: FR 01 05980
- PRIOR FILING DATE: 2001-05-04
- NUMBER OF SEQ ID NOS: 63
- SOFTWARE: PatentIn Ver. 2.1
- SEQ ID NO 23
- LENGTH: 15
- TYPE: PRT
- ORGANISM: artificial sequence
- FEATURE:
- OTHER INFORMATION: Description of the artificial sequence: peptide E6 28-42

Query Match 100.0%; Score 51; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 IILECVYCK 9
      |||||
Db      6 IILECVYCK 14

RESULT 2
US-10-476-570-24
; Sequence 24, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 31-45
US-10-476-570-24

Query Match      100.0%; Score 51; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 IILECVYCK 9
      |||||
Db      3 IILECVYCK 11

RESULT 3
US-10-476-570-10
; Sequence 10, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 21
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 30-50
US-10-476-570-10

Query Match      100.0%; Score 51; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 IILECVYCK 9
      |||||
Db      3 IILECVYCK 11

RESULT 4
US-10-476-570-53
; Sequence 53, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 30
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 15-44
US-10-476-570-53

Query Match      100.0%; Score 51; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 IILECVYCK 9
      |||||
Db      19 IILECVYCK 27

RESULT 5
US-10-858-384-4
; Sequence 4, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HEV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
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FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E6 of HPV
US-10-858-384-4

Query Match 100.0%; Score 51; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.35; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 IILECVYCK 9

Db 19 IILECVYCK 27

RESULT 6

US-10-476-570-9
; Sequence 9, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 32
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-45
US-10-476-570-9

Query Match 100.0%; Score 51; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.37; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 IILECVYCK 9

Db 20 IILECVYCK 28

RESULT 7

US-10-476-570-19
; Sequence 19, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-46
US-10-476-570-19

Query Match 100.0%; Score 51; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.38; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 IILECVYCK 9

Db 20 IILECVYCK 28

RESULT 8

US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match 100.0%; Score 51; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.5; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 IILECVYCK 9

Db 26 IILECVYCK 34

RESULT 9

US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match 100.0%; Score 51; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
Db 26 IILECVYCK 34

RESULT 10
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match 100.0%; Score 51; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
Db 26 IILECVYCK 34

RESULT 11
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 100.0%; Score 51; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
Db 33 IILECVYCK 41

RESULT 12
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 100.0%; Score 51; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
Db 33 IILECVYCK 41

RESULT 13
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Zur Hausen, Harald
; APPLICANT: Cid-Arregui, Angel
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 100.0%; Score 51; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
Db 38 IILECVYCK 46

RESULT 14
US-09-367-309A-1

; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 51; DB 9; Length 266;
Best Local Similarity 100.0%; Pred No. 2.4; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
Db 33 IILECVYCK 41

RESULT 15
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match 100.0%; Score 51; DB 13; Length 273;
Best Local Similarity 100.0%; Pred No. 2.5; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
Db 139 IILECVYCK 147

Search completed: June 29, 2005, 05:18:09
Job time : 118.15 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-41
Perfect score: 51
Sequence: 1 IILECVCK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	9	US-08-159-339A-570	Sequence 570, App
2	51	100.0	10	US-08-159-339A-573	Sequence 573, App
3	51	100.0	20	US-08-934-915-160	Sequence 160, App
4	51	100.0	30	US-09-980-523A-4	Sequence 4, Appli
5	51	100.0	158	US-09-980-523A-2	Sequence 2, Appli
6	51	100.0	162	US-08-316-239B-3	Sequence 3, Appli
7	51	100.0	162	US-08-316-239B-4	Sequence 4, Appli
8	51	100.0	172	US-08-860-165-14	Sequence 14, Appl
9	51	100.0	172	US-09-359-382-14	Sequence 14, Appl
10	51	100.0	182	US-08-117-083-10	Sequence 10, Appl
11	51	100.0	266	US-08-860-165-10	Sequence 10, Appl
12	51	100.0	266	US-09-359-382-10	Sequence 10, Appl
13	51	100.0	266	US-09-367-309A-1	Sequence 1, Appli
14	51	100.0	273	US-09-485-885-4	Sequence 4, Appli
15	51	100.0	292	US-09-485-885-10	Sequence 10, Appl
16	51	100.0	371	US-09-485-885-6	Sequence 6, Appli
17	51	100.0	390	US-09-485-885-14	Sequence 14, Appl
18	37	72.5	10	US-08-159-339A-73	Sequence 73, Appl
19	37	72.5	986	US-09-248-796A-19088	Sequence 19088, A
20	36	70.6	15	US-08-159-339A-1176	Sequence 1176, Ap
21	36	70.6	32	US-08-466-285-2	Sequence 2, Appli
22	36	70.6	32	US-08-164-768-2	Sequence 2, Appli
23	36	70.6	158	US-08-247-904B-10	Sequence 10, Appl
24	36	70.6	158	US-08-767-942A-19	Sequence 19, Appl
25	36	70.6	271	US-08-117-083-14	Sequence 14, Appl
26	36	70.6	278	US-09-485-885-21	Sequence 21, Appl
27	36	70.6	383	US-09-485-885-23	Sequence 23, Appl

28	36	70.6	959	4	US-09-270-767-39036	Sequence 39036, A
29	36	70.6	959	4	US-09-270-767-54253	Sequence 54253, A
30	35	68.6	65	4	US-09-732-210-490	Sequence 490, App
31	35	68.6	102	4	US-09-732-210-1066	Sequence 1066, Ap
32	35	68.6	105	4	US-09-732-210-1058	Sequence 1058, Ap
33	35	68.6	105	4	US-09-732-210-1067	Sequence 1067, Ap
34	35	68.6	106	2	US-08-557-128-6	Sequence 6, Appli
35	35	68.6	106	3	US-09-242-690A-39	Sequence 39, Appl
36	35	68.6	106	4	US-09-732-210-370	Sequence 370, Appl
37	35	68.6	106	4	US-09-908-855-39	Sequence 39, Appl
38	35	68.6	106	4	US-09-674-826B-2	Sequence 2, Appli
39	35	68.6	111	4	US-09-248-796A-19756	Sequence 19756, A
40	35	68.6	144	4	US-09-270-767-61408	Sequence 61408, A
41	35	68.6	193	4	US-09-248-796A-14192	Sequence 14192, A
42	35	68.6	341	4	US-09-270-767-45876	Sequence 45876, A
43	35	68.6	486	3	US-08-904-452-2	Sequence 2, Appli
44	35	68.6	486	4	US-09-517-639-2	Sequence 2, Appli
45	35	68.6	973	3	US-08-904-452-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-159-339A-570
; Sequence 570, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 570:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-570

Query Match 100.0%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVCK 9
| | | | |
Db 1 IILECVCK 9

RESULT 2

US-08-159-339A-573

; Sequence 573, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993

; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:

INFORMATION FOR SEQ ID NO: 573:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-573

Query Match 100.0%; Score 51; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVCK 9
| | | | |
Db 2 IILECVCK 10

RESULT 3

US-08-934-915-160

; Sequence 160, Application US/08934915
; Patent No. 5932412

; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:

INFORMATION FOR SEQ ID NO: 160:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-934-915-160

Query Match 100.0%; Score 51; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVCK 9
| | | | |
Db 2 IILECVCK 10

RESULT 4

US-09-980-523A-4

; Sequence 4, Application US/09980523A
; Patent No. 6783763

; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE B6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WOBI AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513


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; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 162 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: not relevant
;   TOPOLOGY: not relevant
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
US-08-316-239B-4

Query Match      100.0%; Score 51; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILECVYCK 9
DB 33 IILECVYCK 41

RESULT 8
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match      100.0%; Score 51; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILECVYCK 9
DB 102 IILECVYCK 110

RESULT 9
US-08-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; EARLIER FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 162 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: not relevant
;   TOPOLOGY: not relevant
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
US-08-316-239B-4

Query Match      100.0%; Score 51; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILECVYCK 9
DB 33 IILECVYCK 41

RESULT 8
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match      100.0%; Score 51; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILECVYCK 9
DB 102 IILECVYCK 110

RESULT 9
US-08-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; EARLIER FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94

; INFORMATION FOR SEQ ID NO: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match      100.0%; Score 51; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILECVYCK 9
DB 102 IILECVYCK 110

RESULT 10
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 182 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   FEATURE:
;   NAME/KEY: Protein
;   LOCATION: 1..182
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-10

Query Match      100.0%; Score 51; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILECVYCK 9
DB 111 IILECVYCK 111
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Db 34 IILECVYCK 42

RESULT 11
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PNO157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 51; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
Db 33 IILECVYCK 41

RESULT 12
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PNO157/94
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 51; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
Db 33 IILECVYCK 41

RESULT 13
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU P0 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 51; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
Db 33 IILECVYCK 41

RESULT 14
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 51; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILECVYCK 9
Db 139 IILECVYCK 147

RESULT 15
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224

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; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match      100.0%; Score 51; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IILECVYCK 9
Db      158 IILECVYCK 166

Search completed: June 28, 2005, 23:37:44
Job time : 18.05 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-40
Perfect score: 47
Sequence: 1 HVDIRTLSD 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	93	2 Q90DH2	Q9qdh2 human papil
2	47	100.0	93	2 Q9QDH4	Q9qdh4 human papil
3	47	100.0	93	2 Q9QDH6	Q9qdh6 human papil
4	47	100.0	93	2 Q9QDH8	Q9qdh8 human papil
5	47	100.0	94	2 Q8B5P6	Q8B5p6 human papil
6	47	100.0	98	1 VE7_HPV16	P03129 human papil
7	47	100.0	98	2 O11650	O11650 human papil
8	47	100.0	98	2 O12337	O12337 human papil
9	47	100.0	98	2 Q8ORD2	Q8ord2 human papil
10	47	100.0	98	2 Q8ORD3	Q8ord3 human papil
11	47	100.0	98	2 Q8ORD4	Q8ord4 human papil
12	47	100.0	98	2 Q778H3	Q778h3 human papil
13	47	100.0	98	2 Q778H5	Q778h5 human papil
14	42	89.4	158	2 Q6CLZ3	Q6clz3 kluyveromyc
15	40	85.1	99	1 VE7_HPV35	P27230 human papil
16	40	85.1	99	2 Q76WP2	Q76wp2 human papil
17	39	83.0	26	2 Q84267	Q84267 human papil
18	39	83.0	75	2 Q6MSX5	Q6msx5 mycoplasma
19	39	83.0	98	2 O12338	O12338 human papil
20	39	83.0	98	2 Q8V1J0	Q8v1j0 human papil
21	38	80.9	83	2 Q92GF7	Q92gf7 rickettsia
22	37	78.7	273	2 Q8U4J4	Q8u4j4 pyrococcus
23	37	78.7	417	2 Q8G4V6	Q8g4v6 bifidobacte
24	37	78.7	582	2 Q8B6E7	Q8b6e7 pseudomonas
25	37	78.7	588	2 Q7B6G6	Q7b6g6 streptomyce
26	36	76.6	478	1 YBAR_BACSU	P55189 bacillus su
27	36	76.6	650	1 ACSA_VIBPA	Q87ku7 vibrio para
28	36	76.6	650	1 ACSA_VIBVU	Q84cz9 vibrio vuln
29	36	76.6	670	2 Q7MGU3	Q7mgus vibrio vuln
30	36	76.6	894	1 SEC5_DROME	Q9vqq9 drosophila
31	36	76.6	1105	2 Q949K1	Q949k1 lycopersico

32	35	74.5	84	2 Q97VJ7	Q97vj7 sulfolobus
33	35	74.5	131	2 Q7ZAA1	Q7zaa1 sulfolobus
34	35	74.5	145	2 Q27766	Q27766 methanobact
35	35	74.5	194	1 Y917_PYRAB	Q9v074 pyrococcus
36	35	74.5	245	2 Q8ED35	Q8ed35 shewanella
37	35	74.5	248	2 Q8R7X5	Q8r7x5 thermocaneer
38	35	74.5	251	1 Y761_METJA	Q58171 methanococc
39	35	74.5	255	2 Q9H1N5	Q9h1n5 homo sapien
40	35	74.5	332	2 Q92P29	Q92p29 rhizobium m
41	35	74.5	336	2 Q8UGZ0	Q8ugz0 agrobacteri
42	35	74.5	509	2 Q96SQ1	Q96sq1 homo sapien
43	35	74.5	510	2 Q6IE84	Q6ie84 mus musculu
44	35	74.5	547	2 Q9F5G2	Q9f5g2 agrobacteri
45	35	74.5	649	1 ACSA_VIBCH	Q9kv59 vibrio chol

ALIGNMENTS

RESULT 1

Q9QDH2 PRELIMINARY; PRT; 93 AA.
AC Q9QDH2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SRP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187869; AAF1339.1; -
DR InterPro; IPR000148; Papvi_E7.
FT Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 47; DB 2; Length 93;

Best Local Similarity 100.0%; Pred. No. 0.15;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLSD 9

Db 73 HVDIRTLSD 81

RESULT 2

Q9QDH4 PRELIMINARY; PRT; 93 AA.
AC Q9QDH4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SRP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187868; AAF1339.1; -
DR InterPro; IPR000148; Papvi_E7.
FT Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 47; DB 2; Length 93;

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Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVDIRTLTD 9
Db 73 HVDIRTLTD 81

RESULT 3
Q9QDH6 PRELIMINARY; PRT; 93 AA.
AC Q9QDH6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE E7 oncprotein (Fragment).
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187867; AAF13395.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON_TER 93
FT SEQUENCE 93 AA; 10513 MW; 92C7054341326A1F CRC64;

Query Match 100.0%; Score 47; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVDIRTLTD 9
Db 73 HVDIRTLTD 81

RESULT 4
Q9QDH8 PRELIMINARY; PRT; 93 AA.
AC Q9QDH8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187866; AAF13393.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON_TER 93
FT SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 47; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVDIRTLTD 9
Db 73 HVDIRTLTD 81

RESULT 5
Q8B5P6 PRELIMINARY; PRT; 94 AA.
AC Q8B5P6;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE E7 oncprotein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469197; AAO15692.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON_TER 94
FT SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;

Query Match 100.0%; Score 47; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVDIRTLTD 9
Db 73 HVDIRTLTD 81

RESULT 6
VE7 HPV16 STANDARD; PRT; 98 AA.
AC P03I29;
DT 21-JUL-1996 (Rel. 01, Created)
DT 21-JUL-1996 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85246220; PubMed=2990099;
RA Sedorf K., Krammer G., Durst M., Suhai S., Rowekamp W.G.;
RL "Human papillomavirus type 16 DNA sequence.";
RT Virology 145:181-185(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90218027; PubMed=2157796;
RA Schneider-Maunoury S., Pehau-Arnaudet G., Breitburd F., Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-v cells, a line derived from a vulvar intraepithelial neoplasia.";
RL J. Gen. Virol. 71:809-817(1990).
RN [3]
RP SEQUENCE FROM N.A.
RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP FUNCTION.
RX MEDLINE=88223347; PubMed=2836062;
RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;
RT "The human papillomavirus type 16 E7 gene encodes transactivation and transformation functions similar to those of adenovirus E1A.";
RL Cell 53:539-547(1988).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating activities.

```

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DR EMBL; K02718; AAA46940.1; -
DR EMBL; D00735; BAA00633.1; -
DR EMBL; U76411; AAB18962.1; -
DR EMBL; U76412; AAB18963.1; -
DR EMBL; U76413; AAB18964.1; -
DR EMBL; AF003020; AAB70737.1; -
DR EMBL; AF003023; AAB70740.1; -
DR EMBL; AF003024; AAB70741.1; -
DR EMBL; AF003025; AAB70742.1; -
DR EMBL; AF003026; AAB70743.1; -
DR PIR; A03688; W7WLHS.
DR InterPro; IPR00148; Papvi_E7.
KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW Transcription regulation.
FT SITE 58 61 C-XX-C motif-1.
FT SITE 91 94 C-XX-C motif-2.
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 100.0%; Score 47; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.15; Length 98;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVDIETLED 9
Db |||||
73 HVDIETLED 81

RESULT 7
ID O11650 PRELIMINARY; PRT; 98 AA.
AC O11650;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative transforming protein E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
RA Lee H.P.;
RT "Major sequence variants in E7 gene of human papillomavirus type 16
RT from cervical cancerous and noncancerous lesions of Korean women.";
RL Gynecol. Oncol. 66:275-281(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
RA Lee H.-P.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Terai M., Ma Z., Burk R.D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheng T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China."
RL J. Infect. Dis. 186:696-700(2002).

RN [5]
RP SEQUENCE FROM N.A.
RA Terai M., Fu L., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U76404; AAC58243.1; -
DR EMBL; AF472509; AAO15706.1; -
DR EMBL; AF486326; AAL96631.1; -
DR EMBL; AF486327; AAL96632.1; -
DR EMBL; AF486330; AAL96635.1; -
DR EMBL; AF486331; AAL96636.1; -
DR EMBL; AF486332; AAL96637.1; -
DR EMBL; AF486333; AAL96638.1; -
DR EMBL; AF486334; AAL96639.1; -
DR EMBL; AF486336; AAL96641.1; -
DR EMBL; AF486338; AAL96643.1; -
DR EMBL; AF486346; AAL96651.1; -
DR EMBL; AF486350; AAL96655.1; -
DR EMBL; AF486351; AAL96656.1; -
DR EMBL; AF534061; AAQ10404.1; -
DR InterPro; IPR00148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 47; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVDIETLED 9
Db |||||
73 HVDIETLED 81

RESULT 8
ID O12337 PRELIMINARY; PRT; 98 AA.
AC O12337;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Girardo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients."
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003021; AAB70738.1; -
DR InterPro; IPR00148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVDIETLED 9
Db |||||
73 HVDIETLED 81

RESULT 9
Q8QRD2
ID Q8QRD2 PRELIMINARY; PRT; 98 AA.
AC Q8QRD2;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)

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DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
ON NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486344; AAL96650.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 100.0%; Score 47; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVDIRTLED 9
Db 73 HVDIRTLED 81

RESULT 10
Q8QRD3 PRELIMINARY; PRT; 98 AA.
AC Q8QRD3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486344; AAL96649.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVDIRTLED 9
Db 73 HVDIRTLED 81

RESULT 11
Q8QRD4 PRELIMINARY; PRT; 98 AA.
AC Q8QRD4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486344; AAL96634.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11025 MW; 86E24B234CC3281B CRC64;

Query Match 100.0%; Score 47; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVDIRTLED 9
Db 73 HVDIRTLED 81

RESULT 12
Q778H3 PRELIMINARY; PRT; 98 AA.
ID Q778H3
AC Q778H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RL p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388063; CAB45119.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 98
SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 47; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVDIRTLED 9
Db 73 HVDIRTLED 81

RESULT 13
Q778H5 PRELIMINARY; PRT; 98 AA.
ID Q778H5
AC Q778H5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,

```


RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 RL p53 codon 72 polymorphism genotypes in cervical carcinogenesis."; J. Gen. Virol. 81:317-325(2000).
 DR EMBL: AJ388062; CAB45117.1; -
 DR InterPro: IPR000148; Papvi_E7.
 FT Pfam: PF00527; E7; 1.
 FT NON_TER 98
 SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 47; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.15; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

OY 1 HVDIETLED 9
 Db 73 HVDIETLED 81

RESULT 14
 O6CLZ3 PRELIMINARY; PRT; 158 AA.
 AC O6CLZ3;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE Similar to sgdlS0006020 Saccharomyces cerevisiae YPL099c.
 OS ORFNames=KLA0E243329;
 GN Kluyveromyces lactis NRRL Y-1140.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=284590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
 RA Goffard N., Franquell L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boissane A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.M., Nikolski M., Oztas G., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swennens D., Tekcia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissbach J.,
 RT Wincker P., Souciet J.L.;
 RL "Genome evolution in yeasts.";
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: CR382125; CAH00133.1; -
 SQ SEQUENCE 158 AA; 18707 MW; 0EF238575748B148 CRC64;

Query Match 89.4%; Score 42; DB 2; Length 158;
 Best Local Similarity 77.8%; Pred. No. 2.6;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 HVDIETLED 9
 Db 24 HIEIETLED 32

RESULT 15
 VE7_HPV35 STANDARD; PRT; 99 AA.
 ID VE7_HPV35
 AC P27230;

DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE E7 protein.
 GN Name=E7;
 OS Human papillomavirus type 35.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10587;
 RN [1]
 RP SEQUENCE FROM N.A.
 EX MEDLINE=94265501; PubMed=8205838;
 RA Delius H., Hofmann B.;
 RL "Primer-directed sequencing of human papillomavirus types."; Curr. Top. Microbiol. Immunol. 186:13-31(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92124753; PubMed=1310198;
 RA Marich J.E., Pontsler A.V., Rice S.M., McGraw K.A., Dubensky T.W.;
 RL "The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35."; Virol. 186:770-776(1992).
 CC -!- FUNCTION: E7 protein has both transforming and trans-activating activities.
 CC -----
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 CC -----
 DR EMBL: M74117; AAA46967.1; -
 DR EMBL: X74477; CAA52562.1; -
 DR PIR: F40824; W7WL35.
 DR InterPro: IPR000148; Papvi_E7.
 KW Pfam: PF00527; E7; 1.
 KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
 KW Transcription regulation.
 FT SITE 59 62 C-XX-C motif-1.
 FT SITE 92 95 C-XX-C motif-2.
 SQ SEQUENCE 99 AA; 10954 MW; 8EAA8F248051E226 CRC64;
 Query Match 85.1%; Score 40; DB 1; Length 99;
 Best Local Similarity 77.8%; Pred. No. 4;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HVDIETLED 9
 Db 74 HIDIKLED 82

Search completed: June 28, 2005, 21:24:12
 Job time : 57.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-40

Perfect score: 47

Sequence: 1 HVDIITLED 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	98	1 W7WLHS	E7 protein - human
2	40	85.1	99	1 W7WL35	E7 protein - human
3	38	80.9	83	2 F97845	hypothetical prote
4	36	76.6	478	2 C69743	conserved hypothet
5	35	74.5	84	2 D90436	coA-ligase / coenz
6	35	74.5	145	2 G69098	hypothetical prote
7	35	74.5	194	2 F75139	hypothetical prote
8	35	74.5	251	2 A64395	hypothetical prote
9	35	74.5	336	2 AG2686	ABC transporter, s
10	35	74.5	336	2 D97468	hypothetical prote
11	35	74.5	666	2 D82339	acetyl-CoA synthas
12	35	74.5	756	2 AC2378	penicillin-binding
13	34	72.3	330	2 E81717	Holliday junction
14	34	72.3	334	2 T15565	DNA-binding protei
15	34	72.3	1135	2 T14699	DNA polymerase III
16	34	72.3	1174	2 T15021	probable DNA polym
17	34	72.3	2178	2 S29237	calcium channel pr
18	34	72.3	2222	2 A37490	voltage-dependent
19	34	72.3	2251	2 B54972	voltage-dependent
20	34	72.3	2259	2 S29236	calcium channel pr
21	34	72.3	2270	2 A54972	voltage-dependent
22	34	72.3	2288	2 T29999	hypothetical prote
23	33	70.2	87	2 AH1828	hypothetical prote
24	33	70.2	144	2 A10008	probable membrane
25	33	70.2	204	2 T45270	superoxide dismuta
26	33	70.2	211	2 B75415	superoxide dismuta
27	33	70.2	234	2 T13275	hypothetical prote
28	33	70.2	250	2 D75054	hypothetical prote
29	33	70.2	319	2 A83898	formiminoglutamase

30	33	70.2	521	2 T01563	hypothetical prote
31	33	70.2	524	2 AH2427	phosphodiesterase/
32	33	70.2	557	1 S43322	phosphoribosylamin
33	33	70.2	645	2 T02535	phosphoribosylamin
34	33	70.2	807	2 T28279	ORF MSV119 probabl
35	33	70.2	1171	2 T17454	diaphanous-related
36	32	68.1	86	2 S36533	E7 protein - human
37	32	68.1	188	2 A84383	probable acetyltra
38	32	68.1	200	2 B71101	hypothetical prote
39	32	68.1	267	2 S21399	hypothetical prote
40	32	68.1	283	2 G64101	thymidylate syntha
41	32	68.1	290	2 F69897	transcription regu
42	32	68.1	337	2 D72084	holliday junction
43	32	68.1	337	2 D86539	holliday junction
44	32	68.1	337	2 A81586	Holliday junction
45	32	68.1	338	2 T04891	hyc protein homol

ALIGNMENTS

RESULT 1

W7WLHS

E7 protein - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03688: S12367; T10428

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03688

A:Molecule type: DNA

A:Residues: 1-98 <SEE>

A:Cross-references: UNIPROT:P03129; GB:K02718; NID:G333031; PIDN:AAA46940.1; PID:G333033

R:Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vousden, K.H.

EMBO J. 9, 153-160, 1990

A:Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 large

A:Reference number: S12367; MUID:90107938; PMID:2153075

A:Accession: S12367

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-98 <BAR>

R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human papillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10428

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-98 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46940.1; PID:G333033

C:Genetics:

A:Gene: E7

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:58-94/Region: zinc finger CCCC motif

Query Match 100.0%; Score 47; DB 1; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.027;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIITLED 9

Db 73 HVDIITLED 81

RESULT 2

W7WL35

E7 protein - human papillomavirus type 35

C:Species: human papillomavirus type 35

A:Note: host Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Accession: F40824; S36522
B;Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A;Title: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 16
A;Reference number: A40824; MUID:92124753; PMID:1310198
A;Accession: F40824
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-99 <VAR>
A;Cross-references: UNIPROT:P27230; GB:M74117; NID:G333050; PIDN:AAA46967.1; PID:G333052
R;Deilus, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36522
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99
A;Cross-references: EMBL:X74477; NID:G396997; PIDN:CAA52562.1; PID:G396999
A;Experimental source: strain 35H
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;59-95/Region: zinc finger CCCC motif

Query Match 85.1%; Score 40; DB 1; Length 99;
Best Local Similarity 77.8%; Pred. No. 0.71; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HVDIIRLTLED 9
|:|||||
DB 74 HIDIKRLD 82

RESULT 3
F97845
hypothetical protein RC1166 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97845
R;Ogata, H.; Audic, S.; Reneato-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: F97845
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <KUR>
A;Cross-references: UNIPROT:Q92GF7; GB:AE006914; PIDN:AAL03704.1; PID:G15620293; GSPDB:G
C;Genetics:
A;Gene: RC1166

Query Match 80.9%; Score 38; DB 2; Length 83;
Best Local Similarity 66.7%; Pred. No. 1.5; Mismatches 3; Indels 0; Gaps 0;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVDIIRLTLED 9
|:|||||
DB 26 HLDIIRTKD 34

RESULT 4
C69743
conserved hypothetical protein ybaR - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69743
R;Kunet, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Enfrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallex
ich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivoita, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptratr, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: C69743
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-478 <KUN>
A;Cross-references: UNIPROT:P55189; GB:Z99104; GB:AL009126; NID:G2632267; PIDN:CAB11934.1
A;Experimental source: strain 168
C;Genetics:
A;Gene: ybaR
C;Superfamily: integral membrane protein HP0228

Query Match 76.6%; Score 36; DB 2; Length 478;
Best Local Similarity 66.7%; Pred. No. 26; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HVDIIRLTLED 9
|:|||||
DB 187 HVDIIRTVCD 195

RESULT 5
D90436
coA-ligase / coenzyme F390 synthetase, probable [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: D90436
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: D90436
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-84 <KUR>
A;Cross-references: UNIPROT:Q97VJ7; GB:AE006641; NID:G13815935; PIDN:AAK42747.1; GSPDB:G
C;Genetics:
A;Gene: SSO10784

Query Match 74.5%; Score 35; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 6; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DIRTLED 9
|:|||||
DB 55 DIRTLED 61

RESULT 6
G69098
hypothetical protein MTH1733 - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: G69098
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; I
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
kl, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: G69098
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-145 <MTH>

A;Cross-references: UNIPROT:O27766; GB:AE000666; NID:G2622853; PIDN:AA88630
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1733

Query Match 74.5%; Score 35; DB 2; Length 145;
Best Local Similarity 55.6%; Pred. No. 11;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HVDIIRTLED 9
Db 50 HIDLNTLEE 58
|.:|:|:|:|

RESULT 7
F75139
hypothetical protein PAB0615 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: F75139
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A;Reference number: A75001
A;Accession: F75139
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-194 <KAW>
A;Cross-references: UNIPROT:Q9V074; GB:AJ248285; GB:AL096836; NID:G5458067; PIDN:CAB4983
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB0615
C;Superfamily: Pyrococcus abyssi hypothetical protein PAB2159

Query Match 74.5%; Score 35; DB 2; Length 194;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HVDIIRTLED 9
Db 105 HVGARTLED 113
|:|:|:|:|

RESULT 8
A64395
hypothetical protein MJ0761 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: A64395
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Raich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: A64395
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-251 <BUJ>
A;Cross-references: UNIPROT:Q58171; GB:U67521; GB:L77117; NID:gl591463; PIDN:AA898752.1
C;Genetics:
A;Map position: REV684826-684071
C;Superfamily: metal-dependent hydrolase related to TatD DNase

Query Match 74.5%; Score 35; DB 2; Length 251;
Best Local Similarity 55.6%; Pred. No. 20;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HVDIIRTLED 9
Db 7 HLDVRSFED 15
|:|:|:|:|

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: D82339

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-666 <HEI>

A;Cross-references: UNIPROT:Q9KV59; GB:AE004119; GB:AE003852; NID:g9654718; PIDN:AAF9347

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC0298

A;Map position: 1

C;Superfamily: acetate-CoA ligase; acetate-CoA ligase homology

P;145-633/Domain: acetate-CoA ligase homology <ACL>

Query Match 74.5%; Score 35; DB 2; Length 666;

Best Local Similarity 66.7%; Pred. No. 60;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HVDIRTLTD 9

|:|||||

Db 81 HIDIWFED 89

RESULT 12

AC2378

penicillin-binding protein [imported] - *Nostoc* sp. (strain PCC 7120)

C;Species: *Nostoc* sp. PCC 7120

A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AC2378

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S

DNA Res. 8, 203-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AC2378

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-756 <KUR>

A;Cross-references: UNIPROT:Q8YNI6; GB:BA000019; PIDN:BA876278.1; PID:g17133715; GSPDB:G

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: alr4579

C;Superfamily: penicillin-binding protein

Query Match 74.5%; Score 35; DB 2; Length 756;

Best Local Similarity 66.7%; Pred. No. 69;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HVDIRTLTD 9

|:|||||

Db 212 HVDIMKRLTD 220

RESULT 13

EB1717

Holliday junction DNA helicase RuvB TC0310 [imported] - *Chlamydia muridarum* (strain Nigg

C;Species: *Chlamydia muridarum*, *Chlamydia trachomatis* MoPn

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: EB1717

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,

C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1405, 2000

A;Title: Genome sequences of *Chlamydia trachomatis* MoPn and *Chlamydia pneumoniae* AR39.

A;Reference number: AB1500; MUID:20150255; PMID:10684935

A;Accession: EB1717

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-330 <TET>

A;Cross-references: UNIPROT:Q9PKZ8; GB:AE002298; GB:AE002160; NID:g7190343; PIDN:AAF3917

A;Experimental source: strain Nigg (MoPn)

C;Genetics:

A;Gene: TC0310

C;Superfamily: ruvB protein

Query Match 72.3%; Score 34; DB 2; Length 330;

Best Local Similarity 85.7%; Pred. No. 44;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DIRTLED 9

|:|||||

Db 288 DVRTLED 294

RESULT 14

C71565

DNA-binding protein ruvB - *Chlamydia trachomatis* (serotype D, strain UW3/Cx)

N;Alternate names: Holliday junction helicase

C;Species: *Chlamydia trachomatis*

C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C;Accession: C71565

R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Atavind, L.; Mitchell,

Science 282, 754-759, 1998

A;Title: Genome sequence of an obligate intracellular pathogen of humans: *Chlamydia trach*

A;Reference number: A71570; MUID:9900809; PMID:9784136

A;Accession: C71565

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-334 <ARN>

A;Cross-references: UNIPROT:O84044; GB:AE001278; GB:AE001273; NID:g3328423; PIDN:AA67630

A;Experimental source: serotype D, strain UW-3/Cx

C;Genetics:

A;Gene: ruvB

C;Function:

A;Description: involved in late stages of homologous genetic recombination and DNA repair;

C;Superfamily: ruvB protein

C;Keywords: ATP; DNA binding; DNA recombination; DNA repair; magnesium; nucleotide bindir

F;57-64/Region: nucleotide-binding motif A (P-loop)

F;104-109/Region: nucleotide-binding motif B

Query Match 72.3%; Score 34; DB 2; Length 334;

Best Local Similarity 85.7%; Pred. No. 44;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DIRTLED 9

|:|||||

Db 288 DVRTLED 294

RESULT 15

T14699

DNA polymerase III alpha chain homolog - *Yersinia pestis* plasmid pMT1

C;Species: *Yersinia pestis*

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T14699

R;Hu, P.; Elliott, J.; McCreedy, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Carrano,

submitted to the EMBL Data Library, March 1998

A;Description: Structural organization of virulence determinants in three *Yersinia pestis*

A;Reference number: Z18168

A;Accession: T14699

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1135 <HUP>

A;Cross-references: UNIPROT:O68770; EMBL:AF053947; NID:g2996286; PID:g2996335; PIDN:AA61:

C;Genetics:

A;Genome: plasmid pMT1

C;Superfamily: DNA-directed DNA polymerase III alpha chain

Query Match 72.3%; Score 34; DB 2; Length 1135;

Best Local Similarity 75.0%; Pred. No. 1.7e+02;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDITRTLED 9

|:|||||

Db 842 IEITRTLED 849

Search completed: June 28, 2005, 21:27:55
Job time : 12.15 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds
(without alignments)
59.826 Million cell updates/sec

Title: US-08-170-344-40
Perfect score: 47
Sequence: 1 HVDIRTLTD 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCT05_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	10	9	US-09-891-823-43
2	47	100.0	10	14	US-10-365-908-43
3	47	100.0	10	16	US-10-871-138-43
4	47	100.0	15	16	US-10-476-570-49
5	47	100.0	15	16	US-10-476-570-50
6	47	100.0	15	16	US-10-306-541-68
7	47	100.0	15	16	US-10-306-541-78
8	47	100.0	15	16	US-10-306-541-90
9	47	100.0	15	16	US-10-306-541-97
10	47	100.0	20	15	US-10-432-465-50
11	47	100.0	20	16	US-10-890-526-75

12	47	100.0	23	16	US-10-476-570-17	Sequence 17, Appl
13	47	100.0	98	9	US-09-728-466-1	Sequence 1, Appl
14	47	100.0	98	9	US-09-820-765-4	Sequence 4, Appl
15	47	100.0	98	9	US-09-824-017-4	Sequence 4, Appl
16	47	100.0	98	10	US-09-986-118A-4	Sequence 4, Appl
17	47	100.0	98	14	US-10-267-311-8	Sequence 8, Appl
18	47	100.0	98	14	US-10-177-390-8	Sequence 8, Appl
19	47	100.0	98	14	US-10-201-764-19	Sequence 19, Appl
20	47	100.0	98	15	US-10-654-129-4	Sequence 4, Appl
21	47	100.0	98	15	US-10-681-410-19	Sequence 19, Appl
22	47	100.0	98	16	US-10-772-988-3	Sequence 3, Appl
23	47	100.0	98	16	US-10-479-541-5	Sequence 5, Appl
24	47	100.0	98	17	US-10-042-526A-4	Sequence 4, Appl
25	47	100.0	98	17	US-10-657-399-1	Sequence 1, Appl
26	47	100.0	98	17	US-10-858-384-12	Sequence 12, Appl
27	47	100.0	98	17	US-10-484-063-26	Sequence 26, Appl
28	47	100.0	98	17	US-10-343-448-5	Sequence 5, Appl
29	47	100.0	98	17	US-10-679-956-8	Sequence 8, Appl
30	47	100.0	98	17	US-10-367-057-17	Sequence 17, Appl
31	47	100.0	99	15	US-10-115-440-7	Sequence 7, Appl
32	47	100.0	111	16	US-10-472-724-4	Sequence 4, Appl
33	47	100.0	121	14	US-10-267-311-12	Sequence 12, Appl
34	47	100.0	121	17	US-10-679-956-12	Sequence 12, Appl
35	47	100.0	198	14	US-10-267-311-35	Sequence 35, Appl
36	47	100.0	198	17	US-10-679-956-35	Sequence 35, Appl
37	47	100.0	220	13	US-10-000-903-1	Sequence 1, Appl
38	47	100.0	220	13	US-10-000-903-8	Sequence 8, Appl
39	47	100.0	220	17	US-10-899-771-1	Sequence 1, Appl
40	47	100.0	220	17	US-10-899-771-8	Sequence 8, Appl
41	47	100.0	239	13	US-10-000-903-12	Sequence 12, Appl
42	47	100.0	239	17	US-10-899-771-12	Sequence 12, Appl
43	47	100.0	266	9	US-09-367-309A-1	Sequence 1, Appl
44	47	100.0	289	15	US-10-115-440-5	Sequence 5, Appl
45	47	100.0	295	14	US-10-267-311-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-09-891-823-43
; Sequence 43, Application US/09891823
; Publication No. US20020110566A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/09/891,823
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-891-823-43

Query Match 100.0%; Score 47; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLTD 9
Db 1 HVDIRTLTD 9

RESULT 2

```

US-10-365-908-43
; Sequence 43, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
; OTHER INFORMATION: Description of the artificial sequence: peptide E7 67-81
US-10-365-908-43

Query Match      100.0%; Score 47; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLTD 9
Db 1 HVDIRTLTD 9

RESULT 3
US-10-871-138-43
; Sequence 43, Application US/10871138
; Publication No. US20040235741A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/871,138
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
; OTHER INFORMATION: Description of the artificial sequence: peptide E7 72-86
US-10-871-138-43

Query Match      100.0%; Score 47; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLTD 9
Db 1 HVDIRTLTD 9

RESULT 4
US-10-476-570-49
; Sequence 49, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E7 67-81
US-10-476-570-49

Query Match      100.0%; Score 47; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLTD 9
Db 7 HVDIRTLTD 15

RESULT 5
US-10-476-570-50
; Sequence 50, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E7 72-86
US-10-476-570-50

Query Match      100.0%; Score 47; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLTD 9
Db 2 HVDIRTLTD 10

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RESULT 6
US-10-306-541-68
; Sequence 68, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 68
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-68

Query Match
Best Local Similarity 100.0%; Score 47; DB 16; Length 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLTD 9
Db 2 HVDIRTLTD 10

RESULT 7
US-10-306-541-78
; Sequence 78, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 78
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-78

Query Match
Best Local Similarity 100.0%; Score 47; DB 16; Length 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLTD 9
Db 1 HVDIRTLTD 9

RESULT 8
US-10-306-541-90
; Sequence 90, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 90
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-90

Query Match
Best Local Similarity 100.0%; Score 47; DB 16; Length 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLTD 9
Db 1 HVDIRTLTD 9

RESULT 9
US-10-306-541-97
; Sequence 97, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 97
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-97

Query Match
Best Local Similarity 100.0%; Score 47; DB 16; Length 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLTD 9
Db 3 HVDIRTLTD 11

RESULT 10
US-10-432-465-50
; Sequence 50, Application US/10432465
; Publication No. US20040091479A1
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, John
; APPLICANT: Kaufmann, Andreas
; APPLICANT: Kather, Angela
; APPLICANT: Schinz, Manuela
; TITLE OF INVENTION: T-Cell Epitopes of the Papillomavirus L1
; TITLE OF INVENTION: Protein and E7 Protein and Their Use in Diagnosis and
; FILE REFERENCE: 50125/077001
; CURRENT APPLICATION NUMBER: US/10/432,465
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/14037
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 10059631.2
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-432-465-50
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US-10-432-465-50
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; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E7 6S-87
US-10-476-570-17
;
Query Match          100.0%; Score 47; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLTD 9
   |||||
Db 7 HVDIRTLTD 15

RESULT 11
US-10-890-526-75
; Sequence 75, Application US/10890526
; Publication No. US20040258708A1
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; APPLICANT: Nienland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus Li-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/10/890,526
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: US/09/980,177
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-890-526-75

Query Match          100.0%; Score 47; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLTD 9
   |||||
Db 7 HVDIRTLTD 15

RESULT 12
US-10-476-570-17
; Sequence 17, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 23
; TYPE: PRT
; ORGANISM: artificial sequence

US-10-432-465-50
;
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E7 6S-87
US-10-476-570-17
;
Query Match          100.0%; Score 47; DB 16; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLTD 9
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Db 9 HVDIRTLTD 17

RESULT 13
US-09-728-466-1
; Sequence 1, Application US/09728466
; Patent No. US20010029022A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Christopher
; APPLICANT: He, Wanxia
; TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
; FILE REFERENCE: 26341/6216
; CURRENT APPLICATION NUMBER: US/09/728,466
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/382,616
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Papillomavirus sylvilagi
US-09-728-466-1

Query Match          100.0%; Score 47; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLTD 9
   |||||
Db 73 HVDIRTLTD 81

RESULT 14
US-09-820-765-4
; Sequence 4, Application US/09820765
; Publication No. US2002039584A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; APPLICANT: HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/820,765
; FILING DATE: 30-Mar-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:

```

NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-765-4

Query Match 100.0%; Score 47; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLED 9
Db 73 HVDIRTLED 81

RESULT 15
US-09-824-017-4
; Sequence 4, Application US/09824017
; Publication No. US20020197668A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/824,017
; FILING DATE: 03-Apr-2001
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/026,896
; FILING DATE: 1998-02-20
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-824-017-4

Query Match 100.0%; Score 47; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLED 9
Db 73 HVDIRTLED 81

Search completed: June 29, 2005, 04:19:29
Job time : 57.85 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-40

Perfect score: 47

Sequence: 1 HVDIRTLTD 9

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	9	US-08-159-339A-217	Sequence 217, Appl
2	47	100.0	10	US-10-365-908-43	Sequence 43, Appl
3	47	100.0	20	US-08-075-541D-49	Sequence 49, Appl
4	47	100.0	20	US-09-980-177A-75	Sequence 75, Appl
5	47	100.0	21	US-08-934-915-49	Sequence 49, Appl
6	47	100.0	26	US-08-075-541D-40	Sequence 40, Appl
7	47	100.0	28	US-09-486-394-5	Sequence 5, Appl
8	47	100.0	30	US-08-934-915-53	Sequence 53, Appl
9	47	100.0	30	US-08-934-915-54	Sequence 54, Appl
10	47	100.0	30	US-09-486-394-4	Sequence 4, Appl
11	47	100.0	98	US-08-406-248-6	Sequence 6, Appl
12	47	100.0	98	US-08-075-541D-42	Sequence 42, Appl
13	47	100.0	98	US-09-382-616A-1	Sequence 1, Appl
14	47	100.0	98	US-08-944-368A-4	Sequence 4, Appl
15	47	100.0	98	US-09-820-764-4	Sequence 4, Appl
16	47	100.0	98	US-09-613-303-8	Sequence 8, Appl
17	47	100.0	98	US-09-566-420-19	Sequence 19, Appl
18	47	100.0	98	US-09-986-118A-4	Sequence 4, Appl
19	47	100.0	98	US-09-728-466-1	Sequence 1, Appl
20	47	100.0	98	US-09-824-017-4	Sequence 4, Appl
21	47	100.0	98	US-10-267-311-8	Sequence 8, Appl
22	47	100.0	98	US-10-201-764-19	Sequence 19, Appl
23	47	100.0	98	US-09-637-746-3	Sequence 3, Appl
24	47	100.0	98	US-09-501-097A-7	Sequence 7, Appl
25	47	100.0	98	US-09-980-523A-12	Sequence 12, Appl
26	47	100.0	121	US-09-613-303-12	Sequence 12, Appl
27	47	100.0	121	US-10-267-311-12	Sequence 12, Appl

28 47 100.0 172 3 US-08-860-165-14 Sequence 14, Appl
29 47 100.0 172 3 US-09-359-382-14 Sequence 14, Appl
30 47 100.0 198 4 US-09-613-303-35 Sequence 35, Appl
31 47 100.0 198 4 US-10-267-311-35 Sequence 35, Appl
32 47 100.0 220 3 US-09-485-885-1 Sequence 1, Appl
33 47 100.0 220 3 US-09-485-885-8 Sequence 8, Appl
34 47 100.0 239 3 US-09-485-885-12 Sequence 12, Appl
35 47 100.0 253 2 US-08-459-818-20 Sequence 20, Appl
36 47 100.0 253 2 US-08-889-666-20 Sequence 20, Appl
37 47 100.0 253 2 US-08-465-078-20 Sequence 20, Appl
38 47 100.0 253 2 US-08-725-776-20 Sequence 20, Appl
39 47 100.0 253 2 US-08-488-062-20 Sequence 20, Appl
40 47 100.0 263 1 US-08-117-083-9 Sequence 9, Appl
41 47 100.0 266 3 US-08-860-165-10 Sequence 10, Appl
42 47 100.0 266 3 US-09-359-382-10 Sequence 10, Appl
43 47 100.0 266 4 US-09-367-309A-1 Sequence 1, Appl
44 47 100.0 287 4 US-09-501-097A-25 Sequence 25, Appl
45 47 100.0 295 4 US-09-613-303-33 Sequence 33, Appl

ALIGNMENTS

RESULT 1

US-08-159-339A-217

; Sequence 217, Application US/08159339A

; Patent No. 6037135

; GENERAL INFORMATION:

; APPLICANT: Kubo, Ralph T.

; APPLICANT: Grey, Howard M.

; APPLICANT: Sette, Alessandro

; APPLICANT: Cellis, Esteban

; TITLE OF INVENTION: HLA Binding peptides and Their

; NUMBER OF SEQUENCES: 1254

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08159,339A

; FILING DATE: 29-NOV-1993

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/926,666

; FILING DATE: 07-AUG-1992

; APPLICATION NUMBER: US 08/027,746

; FILING DATE: 05-MAR-1993

; APPLICATION NUMBER: US 08/103,396

; FILING DATE: 06-AUG-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Ellen Lauver

; REGISTRATION NUMBER: 32,762

; REFERENCE/DOCKET NUMBER: 018623-005030US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; TELEX:

; INFORMATION FOR SEQ ID NO: 217:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-159-339A-217

Query Match 100.0%; Score 47; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDI RTLED 9
| | | | | | | | |
Db 1 HVDI RTLED 9

RESULT 2

US-10-365-908-43

; Sequence 43, Application US/10365908

; Patent No. 6797491

; GENERAL INFORMATION:

; APPLICANT: Neefe, John R.

; APPLICANT: Boux, Leslie J.

; APPLICANT: Winnett, Mark T.

; APPLICANT: Goldstone, Stephen E.

; APPLICANT: Siegel, Marvin

; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT

; FILE REFERENCE: 12071-003001

; CURRENT APPLICATION NUMBER: US/10/365,908

; CURRENT FILING DATE: 2003-02-13

; PRIOR APPLICATION NUMBER: US/09/891,823

; PRIOR FILING DATE: 2001-10-19

; PRIOR APPLICATION NUMBER: US 60/214,202

; PRIOR FILING DATE: 2000-06-26

; NUMBER OF SEQ ID NOS: 140

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 43

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Human papilloma virus

US-10-365-908-43

Query Match 100.0%; Score 47; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDI RTLED 9
| | | | | | | | | |
Db 1 HVDI RTLED 9

RESULT 3

US-08-075-541D-49

; Sequence 49, Application US/08075541D

; Patent No. 6183745

; GENERAL INFORMATION:

; APPLICANT: TINDLE, ROBERT

; APPLICANT: FERNANDO, GERMAIN

; APPLICANT: FRAZER, IAN

; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND

; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESS: PANITCH SCHWARZE JACOBS & NADEL, P.C.

; STREET: 1601 MARKET STREET, 36TH FLOOR

; CITY: PHILADELPHIA

; STATE: PENNSYLVANIA

; COUNTRY: USA

; ZIP: 19103-2398

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/075,541D

; FILING DATE: 10-JUN-1993

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-075-541D-49

Query Match 100.0%; Score 47; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDI RTLED 9
| | | | | | | | | |
Db 4 HVDI RTLED 12

RESULT 4

US-09-980-177A-75

; Sequence 75, Application US/09980177A

; Patent No. 6838084

; GENERAL INFORMATION:

; APPLICANT: Jochmus, Ingrid

; APPLICANT: Nicland, John

; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the

; TITLE OF INVENTION: Papilloma Virus LI-Protein and Use Thereof in Diagnosis and

; TITLE OF INVENTION: Therapy

; FILE REFERENCE: 50125/036001

; CURRENT APPLICATION NUMBER: US/09/980,177A

; PRIOR FILING DATE: 2001-11-29

; PRIOR APPLICATION NUMBER: PCT/EP00/05006

; PRIOR FILING DATE: 2000-05-31

; PRIOR APPLICATION NUMBER: DE 19925199.1

; PRIOR FILING DATE: 1999-06-01

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 75

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Human papillomavirus type 16

US-09-980-177A-75

Query Match 100.0%; Score 47; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDI RTLED 9
| | | | | | | | | |
Db 7 HVDI RTLED 15

RESULT 5

US-08-934-915-49

; Sequence 49, Application US/08934915

; Patent No. 5932412

; GENERAL INFORMATION:

; APPLICANT: DILLNER, JOAKIM

; APPLICANT: DILLNER, LENA

; APPLICANT: CHENG, HWEE-MING


```

; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. FOUTCH
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-49

Query Match 100.0%; Score 47; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLED 9
Db 12 HVDIRTLED 20

RESULT 6
US-08-075-541D-40
; Sequence 40, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SURUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-40

Query Match 100.0%; Score 47; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLED 9
Db 2 HVDIRTLED 10

RESULT 7
US-09-486-394-5
; Sequence 5, Application US/09486394
; Patent No. 6478749
; GENERAL INFORMATION:
; APPLICANT: Hopfl, Reinhard
; TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
; FILE REFERENCE: 032929-001
; CURRENT APPLICATION NUMBER: US/09/486,394
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/04773
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: DE 197 37 409.3
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 28
; TYPE: PPT
; ORGANISM: Human papillomavirus type 16
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(28)
; OTHER INFORMATION: E7 peptide.
US-09-486-394-5

Query Match 100.0%; Score 47; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLED 9
Db 3 HVDIRTLED 11

RESULT 8
US-08-934-915-53
; Sequence 53, Application US/08934915
; Patent No. 5932412

```

GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Fouch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-53

Query Match 100.0%; Score 47; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLED 9
Db 16 HVDIRTLED 24

RESULT 9
US-08-934-915-54
Sequence 54, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Fouch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-54

Query Match 100.0%; Score 47; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLED 9
Db 5 HVDIRTLED 13

RESULT 10
US-09-486-394-4
Sequence 4, Application US/09486394
Patent No. 6478749
GENERAL INFORMATION:
APPLICANT: Hopf, Reinhard
TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
FILE REFERENCE: 032929-001
CURRENT APPLICATION NUMBER: US/09/486,394
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/04773
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: DE 197 37 409.3
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 30
TYPE: PRT
ORGANISM: Human papillomavirus type 16
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(30)
OTHER INFORMATION: E7 peptide.
US-09-486-394-4

Query Match 100.0%; Score 47; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDIRTLED 9
Db 13 HVDIRTLED 21

RESULT 11

US-08-406-248-6
; Sequence 6, Application US/08406248
; Patent No. 5736318
; GENERAL INFORMATION:
; APPLICANT: Munger, Karl
; APPLICANT: Jones, D. Leanne
; TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
; TITLE OF INVENTION: TRANSFORMED CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Kusmer
; STREET: 200 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406:248
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: HAZ-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-406-248-6

Query Match 100.0%; Score 47; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDI RTLE 9
| | | | | | | |
Db 73 HVDI RTLE 81

RESULT 12
US-08-075-541D-42
; Sequence 42, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-42

Query Match 100.0%; Score 47; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDI RTLE 9
| | | | | | | |
Db 73 HVDI RTLE 81

RESULT 13
US-09-382-616A-1
; Sequence 1, Application US/09382616A
; Patent No. 6200746
; GENERAL INFORMATION:
; APPLICANT: Fisher, Christopher
; APPLICANT: He, Wanxia
; TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
; FILE REFERENCE: 28341/6216
; CURRENT APPLICATION NUMBER: US/09/382,616A
; CURRENT FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/382,616
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Papillomavirus sylvilagi
US-09-382-616A-1

Query Match 100.0%; Score 47; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVDI RTLE 9
| | | | | | | |
Db 73 HVDI RTLE 81

RESULT 14
US-08-944-368A-4
; Sequence 4, Application US/08944368A
; Patent No. 6228368
; GENERAL INFORMATION:
; APPLICANT: Gissman, et al.
; TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine
; TITLE OF INVENTION: Formulations and Methods of Use
; NUMBER OF SEQUENCES: 28

```
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
/ ADDRESSEE: Borun
/ STREET: 233 South Wacker Drive, 6300 Sears Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States of America
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/944,368A
/ FILING DATE:
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27013/34028
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 98 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-944-368A-4

Query Match 100.0%; Score 47; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HVDI RTLED 9
Db 73 HVDI RTLED 81

RESULT 15
US-09-820-764-4
/ Sequence 4, Application US/09820764
/ Patent No. 6352696
/ GENERAL INFORMATION:
/ APPLICANT: BURGER, Alexander
/ HALLEK, Michael
/ TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
/ FORMULATIONS AND METHODS OF USE
/ NUMBER OF SEQUENCES: 28
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: FOLEY & LARDNER
/ STREET: 3000 K Street, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20007-5109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/820,764
/ FILING DATE: 30-Mar-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 09/026,896
/ FILING DATE: 20-FEB-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sandercock, Colin G.
/ REGISTRATION NUMBER: 31,298
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/ REFERENCE/DOCKET NUMBER: 37067/102
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 672-5300
/ TELEFAX: (202) 672-5399
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 98 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-764-4

Query Match 100.0%; Score 47; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HVDI RTLED 9
Db 73 HVDI RTLED 81

Search completed: June 28, 2005, 21:33:32
Job time : 18 secs
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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-4
Perfect score: 46
Sequence: 1 LCTELQTTI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	46	100.0	138	2	Q919D2	Q919d2 human papil
2	46	100.0	143	2	Q919B6	Q919b6 human papil
3	46	100.0	143	2	Q919C4	Q919c4 human papil
4	46	100.0	151	2	O12335	O12335 human papil
5	46	100.0	151	2	O12336	O12336 human papil
6	46	100.0	151	2	O76TS0	O76ts0 human papil
7	46	100.0	151	2	Q77816	Q77816 human papil
8	46	100.0	151	2	Q77816	Q77816 human papil
9	46	100.0	151	2	Q77JCY	Q77jcy human papil
10	46	100.0	151	2	Q77ZJ5	Q77zj5 human papil
11	46	100.0	151	2	Q80963	Q80963 human papil
12	46	100.0	151	2	Q80966	Q80966 human papil
13	46	100.0	151	2	Q89640	Q89640 human papil
14	46	100.0	151	2	Q89648	Q89648 human papil
15	46	100.0	151	2	Q89708	Q89708 human papil
16	46	100.0	151	2	Q89755	Q89755 human papil
17	46	100.0	151	2	Q89852	Q89852 human papil
18	46	100.0	151	2	Q89887	Q89887 human papil
19	46	100.0	151	2	Q89887	Q89887 human papil
20	46	100.0	151	2	Q8B564	Q8b564 human papil
21	46	100.0	151	2	Q8BB19	Q8bb19 human papil
22	46	100.0	151	2	Q8BB20	Q8bb20 human papil
23	46	100.0	151	2	Q8BB21	Q8bb21 human papil
24	46	100.0	151	2	Q8W8C3	Q8w8c3 human papil
25	46	100.0	151	2	Q9W931	Q9w931 human papil
26	46	100.0	151	2	Q9WMP2	Q9wmp2 human papil
27	46	100.0	151	2	Q9WMP3	Q9wmp3 human papil
28	46	100.0	151	2	Q9WMP4	Q9wmp4 human papil
29	46	100.0	158	1	V86_HPV16	V03126 human papil
30	46	100.0	158	2	Q8JMU8	Q8jmu8 human papil
31	46	100.0	158	2	Q8QHN0	Q8qhn0 human papil

32 46 100.0 158 2 Q8QHPS human papil
33 46 100.0 158 2 Q8QHT0 human papil
34 46 100.0 158 2 Q8QRDS human papil
35 46 100.0 158 2 Q8QRD6 human papil
36 46 100.0 158 2 Q8QRD7 human papil
37 46 100.0 158 2 Q8QRD8 human papil
38 46 100.0 158 2 Q8QRD9 human papil
39 46 100.0 158 2 Q8QRE0 human papil
40 46 100.0 158 2 Q8QRE1 human papil
41 46 100.0 158 2 Q71BI7 human papil
42 46 100.0 158 2 Q9QDH3 human papil
43 46 100.0 158 2 Q9QDH5 human papil
44 46 100.0 158 2 Q9QDH7 human papil
45 46 100.0 158 2 Q9QDH9 human papil

ALIGNMENTS

RESULT 1

Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404694; AAL01345.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481ESA90895FC2 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 LCTELQTTI 9

Db 2 LCTELQTTI 10

RESULT 2

Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).

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DR EMBL; AF404702; AAL01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;
FT NON TER 1
Query Match 100.0%; Score 46; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTELQTTI 9
Db 7 LCTELQTTI 15
RESULT 3
Q919C4 PRELIMINARY; PRT; 143 AA.
AC Q919C4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Consart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404698; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;
Query Match 100.0%; Score 46; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTELQTTI 9
Db 7 LCTELQTTI 15
RESULT 4
Q12335 PRELIMINARY; PRT; 151 AA.
AC Q12335;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003015; AAB70732.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;
Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTELQTTI 9
Db 15 LCTELQTTI 23
RESULT 5
Q12336 PRELIMINARY; PRT; 151 AA.
AC Q12336;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003016; AAB70733.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;
Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTELQTTI 9
Db 15 LCTELQTTI 23
RESULT 6
Q76TS0 PRELIMINARY; PRT; 151 AA.
AC Q76TS0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
```

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DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;
Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTELQTTI 9
Db 15 LCTELQTTI 23
RESULT 5
Q12336 PRELIMINARY; PRT; 151 AA.
AC Q12336;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003016; AAB70733.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;
Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTELQTTI 9
Db 15 LCTELQTTI 23
RESULT 6
Q76TS0 PRELIMINARY; PRT; 151 AA.
AC Q76TS0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
```

RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34114; AAA91661.1; -;
DR EMBL; U34125; AAA91672.1; -;
DR EMBL; U34130; AAA91677.1; -;
DR EMBL; U34131; AAA91678.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTELOTTI 9
Db 15 LCTELOTTI 23

RESULT 7

Q77816 PRELIMINARY; PRT; 151 AA.
AC Q77816;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388056; CAB45104.1; -;
DR EMBL; AJ388061; CAB45114.1; -;
DR EMBL; AJ388066; CAB45124.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCBBA6C02 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTELOTTI 9
Db 15 LCTELOTTI 23

RESULT 8

Q77E16 PRELIMINARY; PRT; 151 AA.
AC Q77E16;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 oncoprotein (E6 protein).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.

RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AF469197; AA015691.1; -;
DR EMBL; AJ388063; CAB45118.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTELOTTI 9
Db 15 LCTELOTTI 23

RESULT 9

Q77JC7 PRELIMINARY; PRT; 151 AA.
AC Q77JC7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6 variant (transforming protein E6).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Xinjiang;
RA Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang F.;
RT "Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma Biopsies in Xinjiang."
RL Sheng Wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan 0:0-0(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=2224222; PubMed=12355268; DOI=10.1007/s00239-002-2344-y;
RA Defilippis V.R., Ayala F.J., Villarreal L.F.;
RT "Evidence of diversifying selection in human papillomavirus type 16 E6 but not E7 oncogenes."
RL J. Mol. Evol. 55:491-499(2002).
RN [4]
RP SEQUENCE FROM N.A.
RA Cruz Mr., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S., Martins C.R.F.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Cruz M.R., Martins C.R.F.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF327851; AAG45940.1; -;
DR EMBL; AJ388057; CAB45106.1; -;
DR EMBL; AJ388069; CAB451130.1; -;

DR EMBL; AY089951; AAM11875.1; -;
 DR EMBL; AY089954; AAM11881.1; -;
 DR EMBL; AY112663; AAM1854.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18320 MW; 617D2A2FDB4F8C17 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTELQTTI 9
 Db 15 LCTELQTTI 23

RESULT 10
 Q77ZJ5 PRELIMINARY; PRT; 151 AA.
 ID Q77ZJ5
 AC Q77ZJ5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus
 type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 DR EMBL; AF003019; AAB70735.1; -;
 DR EMBL; AF003018; AAB70735.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18221 MW; 60CD2A34DAF48CB7 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTELQTTI 9
 Db 15 LCTELQTTI 23

RESULT 11
 Q80963 PRELIMINARY; PRT; 151 AA.
 ID Q80963
 AC Q80963;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Early transforming protein E6.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96079021; PubMed=7494284;
 RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
 RA Jenison S.A.;
 RT "Human papillomavirus type 16 variant lineages in United States

RT populations characterized by nucleotide sequence analysis of the E6,
 RT L2, and L1 coding segments.";
 RT J. Virol. 69:7743-7753(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Farmer A.D.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U34122; AAA91669.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18291 MW; 97C7028D5169382D CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTELQTTI 9
 Db 15 LCTELQTTI 23

RESULT 12
 Q80966 PRELIMINARY; PRT; 151 AA.
 ID Q80966
 AC Q80966; O12650; O12651; O12652; O12925; O12926; O12927; Q80962;
 AC Q80964; Q80965;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus
 type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 DR EMBL; AF003019; AAB70735.1; -;
 DR EMBL; AF003018; AAB70735.1; -;
 DR EMBL; AF003017; AAB70734.1; -;
 DR EMBL; AF472508; AAO15697.1; -;
 DR EMBL; AJ388068; CAB45128.1; -;
 DR EMBL; AF003013; AAB70730.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTELQTTI 9
 Db 15 LCTELQTTI 23

RESULT 13
 Q80963 PRELIMINARY; PRT; 151 AA.
 ID Q80963
 AC Q80963;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Early transforming protein E6.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96079021; PubMed=7494284;
 RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
 RA Jenison S.A.;
 RT "Human papillomavirus type 16 variant lineages in United States


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Db          15 LCTELQTTI 23

RESULT 13
Q89640      PRELIMINARY;          PRT; 151 AA.
ID Q89640
AC Q89640
DR EMBL; U34110; AAA91657.1; -.
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
[1]
RN SEQUENCE FROM N.A.
RP Farmer A.D.;
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
[2]
RN SEQUENCE FROM N.A.
RP Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP Fonglittmongkol M., Vateewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34129; AAA91676.1; -.
DR EMBL; AF469198; AAO15693.1; -.
DR EMBL; U34115; AAA91662.1; -.
DR EMBL; U34120; AAA91667.1; -.
DR EMBL; U34124; AAA91671.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18348 MW; FE3F2A2FCF0A6CB2 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LCTELQTTI 9
Db          15 LCTELQTTI 23

RESULT 14
Q89648      PRELIMINARY;          PRT; 151 AA.
ID Q89648
AC Q89648; O12653; O12654; O12928; O12929;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
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RN SEQUENCE FROM N.A.
RP Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34110; AAA91657.1; -.
DR EMBL; U34109; AAA91656.1; -.
DR EMBL; U34113; AAA91660.1; -.
DR EMBL; U34135; AAA91682.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18221 MW; 60CD2A34DAF48CB7 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LCTELQTTI 9
Db          15 LCTELQTTI 23

RESULT 15
Q89708      PRELIMINARY;          PRT; 151 AA.
ID Q89708
AC Q89708;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
[2]
RN SEQUENCE FROM N.A.
RP Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34128; AAA91675.1; -.
DR EMBL; U34117; AAA91664.1; -.
DR EMBL; U34118; AAA91665.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LCTELQTTI 9
Db          15 LCTELQTTI 23

Search completed: June 28, 2005, 19:19:20
Job time : 55.3 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 Seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-4
Perfect score: 46
Sequence: 1 LCTELQTTI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	158	1 W6WLHS	protein E6 - human
2	38	82.6	239	1 LNMSWA	mannose-binding le
3	37	80.4	158	2 E89818	hypothetical prote
4	37	80.4	187	2 A90126	hypothetical prote
5	36	78.3	511	2 T23189	hypothetical prote
6	36	78.3	527	2 F89240	protein K01D12.6 l
7	35	76.1	57	2 I56705	E6 protein - human
8	35	76.1	158	1 W6WL18	E6 protein - human
9	35	76.1	158	2 S36561	E6 protein - human
10	34	73.9	244	1 LNRTMC	mannose-binding le
11	34	73.9	455	2 AE0181	hypothetical prote
12	34	73.9	587	2 S54061	probable inorganic
13	34	73.9	980	2 T39630	valine-tRNA ligase
14	34	73.9	2344	1 RWRWRH	genome polyprotein
15	33	71.7	138	2 T39504	hypothetical prote
16	33	71.7	158	1 W6WL39	E6 protein - human
17	33	71.7	243	2 D84629	hypothetical prote
18	33	71.7	342	2 AB3116	transcription regu
19	33	71.7	356	2 C98171	hypothetical prote
20	33	71.7	492	1 T03271	calcium-dependent
21	33	71.7	768	2 D86404	unknown protein [i
22	33	71.7	819	2 T10355	hypothetical prote
23	33	71.7	905	2 S55059	fertilin alpha-I -
24	33	71.7	1374	2 D85390	myosin-like protei
25	33	71.7	1375	2 T05200	myosin heavy chain
26	32	69.6	147	2 JC7263	receptor activity
27	32	69.6	147	2 JCT237	receptor activity
28	32	69.6	182	2 A12373	hypothetical prote
29	32	69.6	391	2 T35698	hypothetical prote

ALIGNMENTS

RESULT 1

W6WLHS

protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C>Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowe, W. G.

Virology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human papillomavirus type 16 genome acts at the level

A:Reference number: 217014; MUID:91162763; PMID:1848319

A:Accession: T10427

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C:Genetics: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 46; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.062;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9

Db 22 LCTELQTTI 30

RESULT 2

LNMSWA

mannose-binding lectin A precursor - mouse

N:Alternate names: RA-reactive factor P28b; serum mannan-binding protein

C:Species: Mus musculus (house mouse)

C>Date: 18-Jun-1993 #sequence_revision 02-Jun-1994 #text_change 09-Jul-2004

C:Accession: A46466; B42574; I48650

R:Sastry, K.; Zahedi, K.; Lelias, J.M.; Whitehead, A.S.; Ezekowitz, R.A.

J. Immunol. 147, 692-697, 1991

A:Title: Molecular characterization of the mouse mannose-binding proteins. The mannose-bi

A:Reference number: A46466; MUID:91302823; PMID:1712818

A:Accession: A46466

A:Molecule type: mRNA

```

A:Residues: 1-239 <SAS1>
A:Cross-references: UNIPROT:P39039; GB:S42292; NID:g1679939; PIDN:AA19342.1; PID:g23301
A:Experimental source: Inbred CBA/J, acute phase liver library, prz 19 vector
A:Note: sequence extracted from NCBI backbone (NCBIN:42292, NCBIP:42293)
R:Kuge, S.; Ihara, S.; Watanabe, E.; Watanabe, M.; Takishima, K.; Suga, T.; Mamiya, G.;
Biochemistry 31, 6943-6950, 1992
A:Title: cDNAs and deduced amino acid sequences of subunits in the binding component of
A:Reference number: A42574; MUID:92345256; PMID:1637828
A:Accession: B42574
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA; protein
A:Residues: 1-239 <KUG>
A:Cross-references: GB:D11441; NID:g220587; PIDN:BAA02006.1; PID:g220588
A:Experimental source: BALB/c, liver
A:Note: sequence extracted from NCBI backbone (NCBIP:110142)
R:Sastry, R.; Wang, J.S.; Brown, D.C.; Ezekowitz, R.A.; Tauber, A.I.; Sastry, K.N.
Mamm. Genome 6, 103-110, 1995
A:Title: Characterization of murine mannose-binding protein genes Mb11 and Mb12 reveals
A:Reference number: I48650; MUID:95284466; PMID:7766991
A:Accession: I48650
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-239 <SAS2>
A:Cross-references: EMBL:U09010; NID:g773278; PIDN:AAA92009.1; PID:g773280
A:Comment: Mannose-binding lectins are opsonins that are important in host defense against
C:Genetics:
A:Gene: Mb11
A:Introns: 52/1, 91/1, 116/1
C:Superfamily: mannose-binding lectin; C-type lectin homology
C:Keywords: acute phase; calcium; hydroxyproline; lectin; liver; plasma
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-238/Product: mannose-binding lectin A #status predicted <MAT>
F:36-88/Region: collagen-like
F:119-235/Domain: C-type lectin homology <LCH>

Query Match      82.6%; Score 38; DB 1; Length 239;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9
Db 145 LCTELQGTV 153

RESULT 3
E89818
hypothetical protein folk [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: E89818
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: E89818
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-158 <KUR>
A:Cross-references: UNIPROT:Q99W87; GB:BA0000018; PID:g13700406; PIDN:BA11704.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:
A:Gene: folk
C:Superfamily: 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase; 2-am

Query Match      80.4%; Score 37; DB 2; Length 158;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9
Db 57 LCTELQTTI 65

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RESULT 4
A90126
hypothetical protein orf187 [imported] - Guillardia theta nucleomorph
C:Species: nucleomorph Guillardia theta
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A90126
R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reit
Nature 410, 1091-1096, 2001
A:Title: The highly reduced genome of an enslaved algal nucleus.
A:Reference number: A99082; MUID:11323671; PMID:11323671
A:Accession: A90126
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-187 <DOU>
A:Cross-references: UNIPROT:Q98S81; GB:AF083031; NID:gl3794324; PIDN:AAK39701.1; GSPDB:G
C:Genetics:
A:Gene: orf187
A:Map position: 3
A:Genome: nucleomorph
C:Keywords: nucleomorph

Query Match      80.4%; Score 37; DB 2; Length 187;
Best Local Similarity 77.8%; Pred. No. 4.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9
Db 4 LCTELETLI 12

RESULT 5
T23189
hypothetical protein K01D12.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23189
R:Dobson, R.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19703
A:Accession: T23189
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-511 <WIL>
A:Cross-references: UNIPROT:Q21096; EMBL:Z75543; PIDN:CAA99873.2; GSPDB:GN00023; CESP:K01
A:Experimental source: clone K01D12
C:Genetics:
A:Gene: CESP:K01D12.6
A:Map position: 5
A:Introns: 55/2; 192/1; 297/3; 461/3

Query Match      78.3%; Score 36; DB 2; Length 511;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9
Db 132 LCTELRNTI 140

RESULT 6
F89240
protein K01D12.6 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: F89240
R:anonymous, the C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg

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A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A;Accession: F89240
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-527 <STO>
 A;Cross-references: UNIPROT:Q21096; GB:chr_V; PIDN:CAA99873.1; PID:g3878147; GSPDB:GN000
 C;Genetics:
 A;Gene: K01b12.6
 A;Map position: 5

Query Match 78.3%; Score 36; DB 2; Length 527;
 Best Local Similarity 77.8%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9
 |||||:
 Db 132 LCTELRKTII 140

RESULT 7
 I56705
 E6 protein - human papillomavirus type 18
 C;Species: human papillomavirus type 18
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C;Accession: I56705
 J;Inagaki, Y.; Tsunokawa, Y.; Takebe, N.; Nawa, H.; Nakanishi, S.; Terada, M.; Sugimura, J. Virol. 62, 1640-1646, 1988
 A;Title: Nucleotide sequences of cDNAs for human papillomavirus type 18 transcripts in H
 A;Reference number: I56705; MUID:88188247; PMID:2833614
 A;Accession: I56705
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-57 <RES>
 A;Cross-references: UNIPROT:Q90133; GB:M20324; NID:g183933; PIDN:AAA99512.1; PID:g306834
 C;Superfamily: papillomavirus E6 protein

Query Match 76.1%; Score 35; DB 2; Length 57;
 Best Local Similarity 66.7%; Pred. No. 3.8;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9
 |||||:
 Db 17 LCTELNTSL 25

RESULT 8
 W6WL18
 E6 protein - human papillomavirus type 18
 C;Species: human papillomavirus type 18
 C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
 C;Accession: A26165; G26251
 R;Seedorf, K.; Oltersdorf, T.; Kraemer, G.; Roewekamp, W. EMBO J. 6, 139-144, 1987
 A;Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16
 A;Reference number: A91068; MUID:87218459; PMID:3034571
 A;Accession: A26165
 A;Molecule type: DNA
 A;Residues: 1-158 <SEE>
 A;Cross-references: UNIPROT:P06463; GB:X04773; NID:g60876; PIDN:CAA28466.1; PID:g60877
 R;Cole, S.T.; Danos, O. J. Mol. Biol. 193, 599-608, 1987
 A;Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 1
 A;Reference number: A92937; MUID:87283882; PMID:3039146
 A;Accession: G26251
 A;Molecule type: DNA
 A;Residues: 1-158 <COL>
 A;Cross-references: GB:X05015; NID:g60975; PIDN:CAA28664.1; PID:g60976
 R;Matlashewski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pim, D.; Crawford, L. J. Gen. Virol. 67, 1909-1916, 1986
 A;Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the p
 A;Reference number: A92791; MUID:86306665; PMID:3018129
 A;Contents: annotation; identification of the protein
 C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; transforming protein; zinc finger
 F:32-68/Region: zinc finger CCCC motif
 F:105-141/Region: zinc finger CCCC motif

Query Match 76.1%; Score 35; DB 1; Length 158;
 Best Local Similarity 66.7%; Pred. No. 10;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9
 |||||:
 Db 17 LCTELNTSL 25

RESULT 9
 S36561
 E6 protein - human papillomavirus type 45
 C;Species: human papillomavirus type 45
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C;Accession: S36561
 R;Delius, H.; Hofmann, B. submitted to the EMBL Data Library, August 1993
 A;Description: Primer-directed sequencing of human papillomavirus types.
 A;Reference number: S36469
 A;Accession: S36561
 A;Molecule type: DNA
 A;Residues: 1-158
 A;Cross-references: UNIPROT:P21735; EMBL:X74479; NID:g397022; PIDN:CAA52573.1; PID:g39702
 C;Superfamily: papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 76.1%; Score 35; DB 2; Length 158;
 Best Local Similarity 66.7%; Pred. No. 10;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9
 |||||:
 Db 17 LCTELNTSL 25

RESULT 10
 LNRTMC
 mannose-binding lectin C precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
 C;Accession: A24791; A38322; JX0201; A26798
 R;Drickamer, K.; Dordal, M.S.; Reynolds, L. J. Biol. Chem. 261, 6878-6887, 1986
 A;Title: Mannose-binding proteins isolated from rat liver contain carbohydrate-recognitic
 rotein.
 A;Reference number: A24791; MUID:86196130; PMID:3009480
 A;Accession: A24791
 A;Molecule type: mRNA
 A;Residues: 1-244 <DRI>
 A;Cross-references: UNIPROT:P08661; GB:M14103
 A;Note: part of the sequence, including the amino end of the mature protein, was confirme
 R;Childs, R.A.; Feizi, T.; Yuen, C.T.; Drickamer, K.; Quesenberry, M.S. J. Biol. Chem. 265, 20770-20777, 1990
 A;Title: Differential recognition of core and terminal portions of oligosaccharide ligand
 A;Reference number: A38322; MUID:91065871; PMID:2249985
 A;Accession: A38322
 A;Molecule type: mRNA
 A;Residues: 86,'EL',89-97 <CHI>
 R;Wada, M.; Itoh, N.; Ohta, M.; Kawasaki, T. J. Biochem. 111, 66-73, 1992
 A;Title: Characterization of rat liver mannan-binding protein gene.
 A;Reference number: JX0201; MUID:92299655; PMID:1607365
 A;Accession: JX0201
 A;Molecule type: DNA
 A;Residues: 1-244 <WAD>
 A;Experimental source: liver
 A;Note: the authors translated the codon CCA for residue 43 as Phe
 R;Oka, S.; Itoh, N.; Kawasaki, T.; Yamashina, I. J. Biochem. 101, 135-144, 1987

A;Title: Primary structure of rat liver mannan-binding protein deduced from its cDNA seq
A;Reference number: A26798; MUID:87194686; PMID:3032924
A;Accession: A26798
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-244 <ORA>
A;Cross-references: GB:X05023; NID:G56634; PIDN:CAA28687.1; PID:G56635
C;Comment: The molecule contains six identical chains, occurring as disulfide-bonded dim
C;Comment: Mannan-binding proteins are calcium ion-dependent and are specific for mannose
C;Genetics:
A;Introns: 59/1; 98/1; 121/1
C;Superfamily: mannose-binding lectin; C-type lectin homology
C;Keywords: calcium; endoplasmic reticulum; Golgi apparatus; homohexamer; hydroxyproline
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-244/Product: mannose-binding lectin C #status experimental <MAT>
F;138-94/Region: collagen-like
F;124-240/Domain: C-type lectin homology <LCH>
F;29,34/Disulfide bonds: interchain #status predicted
F;69/Modified site: 4-hydroxyproline (Pro) #status experimental
Query Match 73.9%; Score 34; DB 1; Length 244;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LCTELQTTI 9
Db 150 LCTELQTTV 158
:::|||||:
RESULT 11
AE0181
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE0181
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AE0181
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-455 <KUP>
A;Cross-references: UNIPROT:Q8ZG30; GB:AL590842; PIDN:CAC90312.1; PID:G15979531; GSPDB:G
C;Genetics:
A;Gene: YPO1489
Query Match 73.9%; Score 34; DB 2; Length 455;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTELQTT 7
Db 142 LCTQLQT 148
:::|||||:
RESULT 12
S54061
probable inorganic phosphate transport protein PHO84 - Yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YN7056.03c; protein YML123c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S54061; A40260
R;Badcock, K.; Churcher, C.M.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54059
A;Accession: S54061
A;Molecule type: DNA
A;Residues: 1-587 <BAD>
A;Cross-references: UNIPROT:P25297; EMBL:249218; NID:G805016; PIDN:CAA89157.1; PID:G8050
A;Experimental source: strain AB972

R;Bun-Ya, M.; Nishimura, M.; Harashima, S.; Oshima, Y.
Mol. Cell. Biol. 11, 3229-3238, 1991
A;Title: The PHO84 gene of Saccharomyces cerevisiae encodes an inorganic phosphate transp
A;Reference number: A40260; MUID:91246191; PMID:2038328
A;Accession: A40260
A;Molecule type: DNA
A;Residues: 1-162, 'HSPAINFVA' 163-352, 'Y', 354-587 <BUN>
A;Cross-references: GB:D90346; NID:G218454; PIDN:BAAL4358.1; PID:G218455
C;Genetics:
A;Gene: SGD:PHO84
A;Cross-references: SGD:S0004592; MIPS:YML123c
A;Map position: 13L
C;Superfamily: probable inorganic phosphate transport protein PHO84
C;Keywords: transmembrane protein
F;137-153/Domain: transmembrane #status predicted <TM1>
F;160-176/Domain: transmembrane #status predicted <TM2>
F;207-223/Domain: transmembrane #status predicted <TM3>
F;250-266/Domain: transmembrane #status predicted <TM4>
F;395-411/Domain: transmembrane #status predicted <TM5>
F;423-439/Domain: transmembrane #status predicted <TM6>
F;527-543/Domain: transmembrane #status predicted <TM7>
Query Match 73.9%; Score 34; DB 2; Length 587;
Best Local Similarity 66.7%; Pred. No. 56;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LCTELQTTI 9
Db 144 VCTILOTTV 152
:::|||||:
RESULT 13
T39630
valine-tRNA ligase precursor, mitochondrial - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39630; T39665
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z21868
A;Accession: T39630
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-980 <LYN>
A;Cross-references: UNIPROT:O75005; EMBL:AL031852; PIDN:CAA21241.1; GSPDB:GN00067; SPDB:G
A;Experimental source: strain 972h-; cosmid ci709
A;Accession: T39665
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-980 <LY2>
A;Cross-references: EMBL:AL031856; PIDN:CAA21312.1; GSPDB:GN00067; SPDB:SPBC1734.18c
A;Experimental source: strain 972h-; cosmid ci734
C;Genetics:
A;Gene: SPBC1709.02c; SPBC1734.18c
A;Map position: 2
A;Genome: nuclear
A;Introns: 12/3; 30/1; 54/3
C;Superfamily: valine-tRNA ligase
C;Keywords: mitochondrion
Query Match 73.9%; Score 34; DB 2; Length 980;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CTELOTTTI 9
Db 273 CTALQTTTL 280
:::|||||:
RESULT 14
RRWRH
genome polyprotein - rabbit hemorrhagic disease virus
N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)

C:Species: rabbit hemorrhagic disease virus
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
 C:Accession: A41039
 R:Meyers, G.; Wirblich, C.; Thiel, H.J.
 Virology 184, 664-676, 1991
 A:Title: Rabbit hemorrhagic disease virus--molecular cloning and nucleotide sequencing
 A:Reference number: A41039; MUID:91361557; PMID:1840711
 A:Accession: A41039
 A:Molecule type: genomic RNA
 A:Residues: 1-2344 <MEY>
 A:Cross-references: UNIPROT:P27410; GB:M67473
 C:Superfamily: rabbit calicivirus RNA-directed RNA polymerase
 C:Keywords: nucleotidyltransferase

Query Match 73.9%; Score 34; DB 1; Length 2344;
 Best Local Similarity 55.6%; Pred. No. 2.1e+02;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTELQTTI 9
 ||:||||
 DB 464 LCSDELTTL 472

RESULT 15

T39504
 Hypothetical protein SPBC1604.10 - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T39504
 R:Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, December 1998
 A:Reference number: Z21859
 A:Accession: T39504
 A>Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-138 <BEC>
 A:Cross-references: UNIPROT:O94376; EMBL:AL034433; PIDN:CAA22343.1; GSPDB:GN000066; SPDB:
 A:Experimental source: strain 972h-; cosmid c1604
 C:Genetics:
 A:Gene: SPDB:SPBC1604.10
 A:Map position: 1
 A:Introns: 14/3; 46/1; 56/1

Query Match 71.7%; Score 33; DB 2; Length 138;
 Best Local Similarity 75.0%; Pred. No. 23;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTELOTTI 9
 ||:||||
 DB 5 CTQLQDTI 12

Search completed: June 28, 2005, 19:23:16
 Job time : 12.2 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 01:35:30 ; Search time 57.55 Seconds
(without alignments)
60.138 Million cell updates/sec

Title: US-08-170-344-4
Perfect score: 46
Sequence: 1 LCTELQTTI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*
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21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	46	100.0	15	16	US-10-476-570-21
3	46	100.0	20	16	US-10-476-570-8
4	46	100.0	30	16	US-10-476-570-53
5	46	100.0	30	17	US-10-858-384-4
6	46	100.0	32	16	US-10-476-570-9
7	46	100.0	33	16	US-10-476-570-19
8	46	100.0	151	14	US-10-177-390-6
9	46	100.0	151	17	US-10-484-063-20
10	46	100.0	151	17	US-10-484-063-27
11	46	100.0	158	17	US-10-858-384-2

12	46	100.0	158	17	US-10-367-057-16	Sequence 16, Appl
13	46	100.0	171	16	US-10-472-724-2	Sequence 2, Appl
14	46	100.0	266	9	US-09-367-309A-1	Sequence 1, Appl
15	46	100.0	273	13	US-10-000-903-4	Sequence 4, Appl
16	46	100.0	273	17	US-10-899-771-4	Sequence 4, Appl
17	46	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
18	46	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
19	46	100.0	371	13	US-10-000-903-6	Sequence 6, Appl
20	46	100.0	371	17	US-10-899-771-6	Sequence 6, Appl
21	46	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
22	46	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
23	46	100.0	536	15	US-10-367-095-10	Sequence 10, Appl
24	46	100.0	536	15	US-10-368-046-10	Sequence 10, Appl
25	46	100.0	536	16	US-10-367-367-10	Sequence 10, Appl
26	46	100.0	536	17	US-10-918-337-10	Sequence 10, Appl
27	37	80.4	48	9	US-09-925-399-1386	Sequence 1386, Ap
28	37	80.4	48	10	US-09-925-299-1386	Sequence 1386, Ap
29	37	80.4	158	15	US-10-282-122A-70249	Sequence 70249, A
30	37	80.4	158	17	US-10-857-625-567	Sequence 567, App
31	36	78.3	55	15	US-10-424-599-191823	Sequence 191823,
32	36	78.3	759	16	US-10-408-765A-748	Sequence 748, App
33	35	76.1	42	17	US-10-751-845-152	Sequence 152, App
34	35	76.1	82	16	US-10-437-963-175677	Sequence 175677,
35	35	76.1	119	17	US-10-751-845-159	Sequence 159, App
36	35	76.1	158	16	US-10-800-023-27	Sequence 27, Appl
37	35	76.1	172	16	US-10-472-724-6	Sequence 6, Appl
38	35	76.1	236	17	US-10-751-845-157	Sequence 157, App
39	35	76.1	237	17	US-10-751-845-158	Sequence 158, App
40	35	76.1	261	17	US-10-751-845-160	Sequence 160, App
41	35	76.1	278	13	US-10-000-903-21	Sequence 21, Appl
42	35	76.1	278	17	US-10-899-771-21	Sequence 21, Appl
43	35	76.1	383	13	US-10-000-903-23	Sequence 23, Appl
44	35	76.1	383	17	US-10-899-771-23	Sequence 23, Appl
45	35	76.1	801	15	US-10-424-599-226123	Sequence 226123,

ALIGNMENTS

RESULT 1
US-10-476-570-20
; Sequence 20, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VIGLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 17-31

Query Match 100.0%; Score 46; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 LCTELQTTI 9
      |||||
Db      6 LCTELQTTI 14

RESULT 2
US-10-476-570-21
; Sequence 21, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 20-34
US-10-476-570-21

Query Match      100.0%; Score 46; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LCTELQTTI 9
      |||||
Db      3 LCTELQTTI 11

RESULT 3
US-10-476-570-8
; Sequence 8, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-34
US-10-476-570-8

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Query Match      100.0%; Score 46; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LCTELQTTI 9
      |||||
Db      9 LCTELQTTI 17

RESULT 4
US-10-476-570-53
; Sequence 53, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 30
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 15-44
US-10-476-570-53

Query Match      100.0%; Score 46; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LCTELQTTI 9
      |||||
Db      8 LCTELQTTI 16

RESULT 5
US-10-858-384-4
; Sequence 4, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E6 of HPV
US-10-858-384-4

Query Match 100.0%; Score 46; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.26; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 LCTELQTTI 9
| | | | | | | | | |
Db 8 LCTELQTTI 16

RESULT 6
US-10-476-570-9
; Sequence 9, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORAVILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 32
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-45
US-10-476-570-9

Query Match 100.0%; Score 46; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.28; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 LCTELQTTI 9
| | | | | | | | | |
Db 9 LCTELQTTI 17

RESULT 7
US-10-476-570-19
; Sequence 19, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORAVILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04

; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-46
US-10-476-570-19

Query Match 100.0%; Score 46; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.29; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 LCTELQTTI 9
| | | | | | | | | |
Db 9 LCTELQTTI 17

RESULT 8
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerps Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match 100.0%; Score 46; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.3; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 LCTELQTTI 9
| | | | | | | | | |
Db 15 LCTELQTTI 23

RESULT 9
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match 100.0%; Score 46; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9
Db 15 LCTELQTTI 23

RESULT 10
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR FILING DATE: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match 100.0%; Score 46; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9
Db 15 LCTELQTTI 23

RESULT 11
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGALT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: PARTICULARLY IN VACCINATION
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR FILING DATE: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 100.0%; Score 46; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9
Db 22 LCTELQTTI 30

RESULT 12
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 100.0%; Score 46; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9
Db 22 LCTELQTTI 30

RESULT 13
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Zur Hausen, Harald
; APPLICANT: Cid-Arregui, Angel
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 100.0%; Score 46; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9
Db 27 LCTELQTTI 35

RESULT 14
US-09-367-309A-1

```
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1
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Query Match 100.0%; Score 46; DB 9; Length 266;
Best Local Similarity 100.0%; Pred.No.2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy . 1 LCTELQTTI 9
Db 22 LCTELQTTI 30
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RESULT 15
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4
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Query Match 100.0%; Score 46; DB 13; Length 273;
Best Local Similarity 100.0%; Pred.No.2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9
Db 128 LCTELQTTI 136
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Search completed: June 29, 2005, 03:24:05
Job time : 57.55 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)
39.174 Million cell updates/sec

Title: US-08-170-344-4
Perfect score: 46
Sequence: 1 LCTELQTTI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	100.0	20	2	US-08-934-915-159
2	46	100.0	30	1	US-08-363-586-4
3	46	100.0	30	4	US-09-980-523A-4
4	46	100.0	158	4	US-09-980-523A-2
5	46	100.0	162	1	US-08-316-239B-3
6	46	100.0	162	1	US-08-316-239B-4
7	46	100.0	172	3	US-08-860-185-14
8	46	100.0	172	3	US-09-359-382-14
9	46	100.0	182	1	US-08-117-083-10
10	46	100.0	266	3	US-08-860-165-10
11	46	100.0	266	3	US-09-359-382-10
12	46	100.0	266	4	US-09-367-309A-1
13	46	100.0	273	3	US-09-485-885-4
14	46	100.0	292	3	US-09-485-885-10
15	46	100.0	371	3	US-09-485-885-6
16	46	100.0	390	3	US-09-485-885-14
17	35	76.1	32	1	US-08-466-285-2
18	35	76.1	32	3	US-08-164-768-2
19	35	76.1	158	2	US-08-247-904B-10
20	35	76.1	158	3	US-08-767-942A-19
21	35	76.1	271	1	US-08-117-083-14
22	35	76.1	278	3	US-09-485-885-21
23	35	76.1	383	3	US-09-485-885-23
24	34	73.9	637	4	US-09-187-906-7
25	33	71.7	14	1	US-07-509-122-3
26	33	71.7	141	4	US-09-270-767-33527
27	33	71.7	141	4	US-09-270-767-48744

Query Match 100.0%; Score 46; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.043;

28	33	71.7	346	4	US-09-543-681A-6716	Sequence 6716, Ap
29	32	69.6	236	4	US-09-634-137-32	Sequence 32, Appl
30	32	69.6	251	4	US-09-270-767-33015	Sequence 33015, A
31	31	67.4	14	3	US-08-271-539-3	Sequence 3, Appli
32	31	67.4	108	1	US-08-234-812-3	Sequence 3, Appli
33	31	67.4	108	2	US-08-663-809-3	Sequence 3, Appli
34	31	67.4	129	1	US-08-049-503-1	Sequence 1, Appli
35	31	67.4	129	1	US-08-225-224-2	Sequence 2, Appli
36	31	67.4	129	1	US-08-470-299-21	Sequence 21, Appli
37	31	67.4	129	2	US-08-874-697-1	Sequence 1, Appli
38	31	67.4	129	3	US-08-722-258-2	Sequence 2, Appli
39	31	67.4	129	3	US-08-897-020-1	Sequence 1, Appli
40	31	67.4	129	3	US-08-765-012A-16	Sequence 16, Appli
41	31	67.4	129	3	US-08-765-012A-17	Sequence 17, Appli
42	31	67.4	129	3	US-08-765-012A-18	Sequence 18, Appli
43	31	67.4	129	3	US-08-765-012A-19	Sequence 19, Appli
44	31	67.4	129	3	US-08-765-012A-20	Sequence 20, Appli
45	31	67.4	129	3	US-09-350-823-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-934-915-159
; Sequence 159, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-159

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9
| | | | |
Db 6 LCTELQTTI 14

RESULT 2

US-08-363-586-4
; Sequence 4, Application US/08363586
; Patent No. 5629161
; GENERAL INFORMATION:
; APPLICANT: Mueller, Martin
; APPLICANT: Gissmann, Lutz
; TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
; TITLE OF INVENTION: Peptides for the Diagnostic Purpose
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,586
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/909,296
; FILING DATE: 09-JUL-1992
; APPLICATION NUMBER: EP 91111720.8
; FILING DATE: 13-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wadler, Linda A.
; REGISTRATION NUMBER: 33,218
; REFERENCE/DOCKET NUMBER: 02481-1195-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-363-586-4

Query Match 100.0%; Score 46; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9
| | | | |
Db 15 LCTELQTTI 23

RESULT 3

US-09-980-523A-4
; Sequence 4, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE

; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION

; FILE REFERENCE: WO/01 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-4

Query Match 100.0%; Score 46; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9
| | | | |
Db 8 LCTELQTTI 16

RESULT 4

US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: WO/01 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 46; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.34; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTELQTTI 9
| | | | |
Db 22 LCTELQTTI 30

RESULT 5

US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an


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; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-316-239B-3

Query Match 100.0%; Score 46; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTELQTTI 9
DB 22 LCTELQTTI 30

RESULT 6
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
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; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-316-239B-4

Query Match 100.0%; Score 46; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTELQTTI 9
DB 22 LCTELQTTI 30

RESULT 7
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
; US-08-860-165-14

Query Match 100.0%; Score 46; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTELQTTI 9
DB 91 LCTELQTTI 99

RESULT 8
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
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; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match 100.0%; Score 46; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTELQTTI 9
Db 91 LCTELQTTI 99

RESULT 9
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Bournell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-10

Query Match 100.0%; Score 46; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTELQTTI 9
Db 23 LCTELQTTI 31

RESULT 10
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 46; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTELQTTI 9
Db 22 LCTELQTTI 30

RESULT 11
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

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Query Match      100.0%; Score 46; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTELQTTI 9
Db 22 LCTELQTTI 30

RESULT 12
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 46; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTELQTTI 9
Db 22 LCTELQTTI 30

RESULT 13
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match      100.0%; Score 46; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTELQTTI 9
Db 22 LCTELQTTI 30

RESULT 14
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match      100.0%; Score 46; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTELQTTI 9
Db 147 LCTELQTTI 155

RESULT 15
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match      100.0%; Score 46; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTELQTTI 9
Db 128 LCTELQTTI 136
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Search completed: June 28, 2005, 19:29:01
Job time : 17.15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-39
Perfect score: 47
Sequence: 1 EIDGPAGQA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	65	2 Q8B563	Q8B563 human papil
2	47	100.0	77	2 Q8B5P5	Q8B5P5 human papil
3	47	100.0	93	2 Q9QDH2	Q9QDH2 human papil
4	47	100.0	93	2 Q9QDH4	Q9QDH4 human papil
5	47	100.0	93	2 Q9QDH6	Q9QDH6 human papil
6	47	100.0	93	2 Q9QDH8	Q9QDH8 human papil
7	47	100.0	94	2 Q8B5P6	Q8B5P6 human papil
8	47	100.0	98	1 VE7 HPV16	P03129 human papil
9	47	100.0	98	2 Q8B5P6	O11650 human papil
10	47	100.0	98	2 O12337	O12337 human papil
11	47	100.0	98	2 O12338	O12338 human papil
12	47	100.0	98	2 Q8QRD2	Q8QRD2 human papil
13	47	100.0	98	2 Q8QRD4	Q8QRD4 human papil
14	47	100.0	98	2 Q8V1J0	Q8V1J0 human papil
15	47	100.0	98	2 Q778H3	Q778H3 human papil
16	47	100.0	98	2 Q778H5	Q778H5 human papil
17	42	89.4	98	2 Q8QRD3	Q8QRD3 human papil
18	42	89.4	99	1 VE7 HPV35	P27230 human papil
19	42	89.4	99	2 Q76WP2	Q76WP2 human papil
20	40	85.1	444	2 Q8P836	Q8P836 xanthomonas
21	38	80.9	43	2 Q91194	Q91194 human papil
22	38	80.9	275	2 Q732E2	Q732E2 mycobacteri
23	38	80.9	623	2 Q8PXC9	Q8PXC9 methanosarc
24	38	80.9	5990	2 Q9RLP6	Q9RLP6 mycobacteri
25	37	78.7	156	2 Q8X1C3	Q8X1C3 emericella
26	37	78.7	452	1 MTEC ENTCL	P14827 enterobacte
27	37	78.7	1485	1 Q841T5	Q841T5 streptomyce
28	36	76.6	98	1 VE7 HPV31	P17387 human papil
29	36	76.6	98	2 Q6T377	Q6T377 human papil
30	36	76.6	403	2 Q8WZG6	Q8WZG6 drosophila
31	36	76.6	403	2 Q9VCZ2	Q9VCZ2 drosophila

RESULT 1

Q8B563 ID Q8B563 PRELIMINARY; PRT; 65 AA.
AC Q8B563;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus.
OC Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteswootacharn K.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF548023; AAO16240.1; -;
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 65
SQ SEQUENCE 65 AA; 7373 MW; E9D74D7923700195 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIDGPAGQA 9
Db 37 EIDGPAGQA 45

RESULT 2

Q8B5P5 ID Q8B5P5 PRELIMINARY; PRT; 77 AA.
AC Q8B5P5;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus.
OC Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteswootacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469198; AAO15694.1; -;
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 77
SQ SEQUENCE 77 AA; 8782 MW; C5DE3A7E546AC31B CRC64;

Query Match 100.0%; Score 47; DB 2; Length 77;

Best Local Similarity 100.0%; Pred. No. 0.38; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIDGPAGQA 9
 |||||
 Db 37 EIDGPAGQA 45

RESULT 3

Q9QDH2 PRELIMINARY; PRT; 93 AA.
 AC Q9QDH2;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE E7 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF187869; AAF13399.1; -.
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 FT NON_TER 93 93
 SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 47; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 0.46;
 Mismatches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIDGPAGQA 9
 |||||
 Db 37 EIDGPAGQA 45

RESULT 4

Q9QDH4 PRELIMINARY; PRT; 93 AA.
 AC Q9QDH4;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE E7 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF187868; AAF13397.1; -.
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 FT NON_TER 93 93
 SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 47; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 0.46;
 Mismatches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIDGPAGQA 9
 |||||
 Db 37 EIDGPAGQA 45

RESULT 5

Q9QDH6 PRELIMINARY; PRT; 93 AA.

Q9QDH6;
 AC 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE E7 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF187867; AAF13395.1; -.
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 FT NON_TER 93 93
 SQ SEQUENCE 93 AA; 10513 MW; 92C7054341326A1F CRC64;

Query Match 100.0%; Score 47; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 0.46;
 Mismatches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIDGPAGQA 9
 |||||
 Db 37 EIDGPAGQA 45

RESULT 6

Q9QDH8 PRELIMINARY; PRT; 93 AA.
 AC Q9QDH8;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE E7 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF187866; AAF13393.1; -.
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 FT NON_TER 93 93
 SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 47; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 0.46;
 Mismatches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIDGPAGQA 9
 |||||
 Db 37 EIDGPAGQA 45

RESULT 7

Q8B5P6 PRELIMINARY; PRT; 94 AA.
 ID Q8B5P6
 AC Q8B5P6;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE E7 oncoprotein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Ponglikitmongkol M., Vaeteewoottacharn K.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF469197; AA015692.1; -.
 DR InterPro; IPR000148; Papvi_E7.
 DR EMBL; AF003023; AAB70740.1; -.
 DR EMBL; AF003024; AAB70741.1; -.
 DR EMBL; AF003025; AAB70742.1; -.
 DR EMBL; AF003026; AAB70743.1; -.
 DR PIR; A03688; W7WLS.
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
 Transcription regulation.
 FT SITE 58 61 C-XX-C motif-1.
 FT SITE 94 94 C-XX-C motif-2.
 SQ SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;

Query Match 100.0%; Score 47; DB 2; Length 94;
 Best Local Similarity 100.0%; Pred. No. 0.46;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIDGPAGQA 9
 |||||
 Db 37 EIDGPAGQA 45

RESULT 8

ID VE7_HPV16 STANDARD; PRT; 98 AA.

AC P03129;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE E7 protein.

GN Name=E7;

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10581;

(1)

RP SEQUENCE FROM N.A.

RX MEDLINE=85246220; PubMed=2990099;

RA Seedorf K., Krammer G., Durst M., Suhai S., Rowekamp W.G.;

RT "Human papillomavirus type 16 DNA sequence.";

RL Virology 145:181-185(1985).

RN (2)

RP SEQUENCE FROM N.A.

RX MEDLINE=90218027; PubMed=2157796;

RA Schneider-Maunoury S., Pehau-Arnauudet G., Breitburd F., Orth G.;

RT "Expression of the human papillomavirus type 16 genome in SK-v cells,

a line derived from a vulvar intraepithelial neoplasia.";

RL J. Gen. Virol. 71:809-817(1990).

RN (3)

RP SEQUENCE FROM N.A.

RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

RN (4)

RP SEQUENCE FROM N.A.

RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,

RA Beth-Giraldo E., Giraldo G.;

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

RN (5)

RP FUNCTION.

RX MEDLINE=88223347; PubMed=2836062;

RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;

RT "The human papillomavirus type 16 E7 gene encodes transactivation and

transformation functions similar to those of adenovirus E1A.";

RL Cell 53:539-547(1988).

CC -!- FUNCTION: E7 protein has both transforming and trans-activating

activities.

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 CC -----

DR EMBL; K02718; AAA46940.1; -.

DR EMBL; D00735; BRA00633.1; -.

DR EMBL; U76411; AAB18962.1; -.

DR EMBL; U76411; AAB18962.1; -.

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DR EMBL; U76411; AAB18962.1; -.

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DR EMBL; U76411; AAB18962.1; -.

DR EMBL; U76411; AAB18962.1; -.

DR EMBL; U76412; AAB18963.1; -.
 DR EMBL; U76413; AAB18964.1; -.
 DR EMBL; AF003020; AAB70737.1; -.
 DR EMBL; AF003023; AAB70740.1; -.
 DR EMBL; AF003024; AAB70741.1; -.
 DR EMBL; AF003025; AAB70742.1; -.
 DR EMBL; AF003026; AAB70743.1; -.
 DR PIR; A03688; W7WLS.
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
 Transcription regulation.
 FT SITE 58 61 C-XX-C motif-1.
 FT SITE 94 94 C-XX-C motif-2.
 SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 100.0%; Score 47; DB 1; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIDGPAGQA 9
 |||||
 Db 37 EIDGPAGQA 45

RESULT 9

O11650

ID O11650 PRELIMINARY; PRT; 98 AA.

AC O11650; (TrEMBLrel. 04, Created)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Putative transforming protein E7.

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10581;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;

RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,

RA Lee H.P.;

RT "Major sequence variants in E7 gene of human papillomavirus type 16

from cervical cancerous and noncancerous lesions of Korean women.";

RL Gynecol. Oncol. 66:275-281(1997).

RN (2)

RP SEQUENCE FROM N.A.

RA Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,

RA Lee H.-P.;

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

RN (3)

RP SEQUENCE FROM N.A.

RA Terai M., Ma Z., Burk R.D.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

RN (4)

RP SEQUENCE FROM N.A.

RX MEDLINE=22182962; PubMed=12195358;

RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,

RA Cheung J.L.K., Xu L.Y., Cheng A.F.;

RT "Human papillomavirus type 16 intratypic variant infection and risk

for cervical neoplasia in southern China.";

RL J. Infect. Dis. 186:696-700(2002).

RN (5)

RP SEQUENCE FROM N.A.

RA Terai M., Fu L., Ma Z., Burk R.D.;

RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; U76404; AAC58243.1; -.

DR EMBL; AF472509; AA015706.1; -.

DR EMBL; AF486326; AAL96631.1; -.

DR EMBL; AF486327; AAL96632.1; -.

DR EMBL; AF486330; AAL96635.1; -.

DR EMBL; AF486331; AAL96636.1; -.

DR EMBL; AF486332; AAL96637.1; -.

DR EMBL; AF486332; AAL96637.1; -.

DR EMBL; AF486332; AAL96637.1; -.

DR EMBL; AF486332; AAL96637.1; -.

DR EMBL; AF486332; AAL96637.1; -.

DR EMBL; AF486332; AAL96637.1; -.

DR EMBL; AF486333; AAL96638.1; -;
 DR EMBL; AF486334; AAL96639.1; -;
 DR EMBL; AF486336; AAL96641.1; -;
 DR EMBL; AF486338; AAL96643.1; -;
 DR EMBL; AF486346; AAL96651.1; -;
 DR EMBL; AF486350; AAL96655.1; -;
 DR EMBL; AF486351; AAL96656.1; -;
 DR EMBL; AF534061; AAO10404.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 10995 MW; 81B538534CC3281B CRC64;

Query Match 100.0%; Score 47; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIDGPAGQA 9
 |||||
 Db 37 EIDGPAGQA 45

RESULT 10

O12337 PRELIMINARY; PRT; 98 AA.

AC O12337;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Torneello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus
 type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 DR EMBL; AF003021; AAB70738.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIDGPAGQA 9
 |||||
 Db 37 EIDGPAGQA 45

RESULT 11

O12338 PRELIMINARY; PRT; 98 AA.

AC O12338;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Torneello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus

RT type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Jinhu X., Xinxing W., Yun T.;
 RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003022; AAB70739.1; -;
 DR EMBL; AF477385; AAM03025.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 10969 MW; 9BD612534CCEA59B CRC64;

Query Match 100.0%; Score 47; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIDGPAGQA 9
 |||||
 Db 37 EIDGPAGQA 45

RESULT 12

O8QRD2 PRELIMINARY; PRT; 98 AA.

AC O8QRD2;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22182962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RT "Human papillomavirus type 16 intratypic variant infection and risk
 for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700(2002).
 DR EMBL; AF486345; AAL96650.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 100.0%; Score 47; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIDGPAGQA 9
 |||||
 Db 37 EIDGPAGQA 45

RESULT 13

O8QRD4 PRELIMINARY; PRT; 98 AA.

AC O8QRD4;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22182962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RT "Human papillomavirus type 16 intratypic variant infection and risk

RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486329; AAL6634.1; -;
DR InterPro; IPR00148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11025 MW; 86E24B234CC3281B CRC64;

Query Match 100.0%; Score 47; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIDGPAGQA 9
Db |||||||||
37 EIDGPAGQA 45

RESULT 14

Q8VLJ0 PRELIMINARY; PRT; 98 AA.
AC Q8VLJ0;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Jinhu X., Xinxing W., Yun T.;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461264; AAL66736.1; -;
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10997 MW; 9BD610834CCEA59B CRC64;

Query Match 100.0%; Score 47; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIDGPAGQA 9
Db |||||||||
37 EIDGPAGQA 45

RESULT 15

Q778H3 PRELIMINARY; PRT; 98 AA.
AC Q778H3;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388063; CAB45119.1; -;
DR InterPro; IPR00148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 98
SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 47; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.48;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EIDGPAGQA 9
Db |||||||||
37 EIDGPAGQA 45

Search completed: June 28, 2005, 21:24:10
Job time : 56.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-39

Perfect score: 47

Sequence: 1 EIDGPACQA 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	98	1 W7LH35	E7 protein - human
2	42	89.4	99	1 W7LH35	E7 protein - human
3	37	78.7	452	2 S07886	site-specific DNA-
4	36	76.6	98	1 W7LH31	E7 protein - human
5	35	74.5	346	2 B70594	hypothetical prote
6	35	74.5	347	2 AG1706	lipases homolog li
7	35	74.5	347	2 A11335	lipases homolog lm
8	35	74.5	415	2 AE3522	Leu/11e/Val-bindin
9	35	74.5	417	2 G70033	maltose/maltodextr
10	35	74.5	630	2 T28700	hypothetical prote
11	35	74.5	1557	2 T18412	lipid-binding prot
12	34	72.3	98	1 W7LH58	E7 protein - human
13	34	72.3	152	2 E64842	probable monooxyge
14	34	72.3	152	2 E90785	probable 4-hydroxy
15	34	72.3	152	2 C85645	probable 4-hydroxy
16	34	72.3	279	2 T26125	hypothetical prote
17	34	72.3	294	2 D70525	probable beta-1 -
18	34	72.3	299	2 T20605	hypothetical prote
19	34	72.3	313	2 T26465	hypothetical prote
20	34	72.3	379	2 G87528	hypothetical prote
21	34	72.3	381	2 T27806	hypothetical prote
22	34	72.3	419	2 AE1340	maltose/maltodextr
23	34	72.3	419	2 AC1711	maltose/maltodextr
24	34	72.3	438	2 T35355	hypothetical prote
25	34	72.3	441	2 T07926	probable starch sy
26	34	72.3	449	2 D70726	probable gabt - My
27	34	72.3	501	1 JN0539	head protein gps -
28	34	72.3	501	2 C85743	probable head-tail
29	34	72.3	501	2 D90767	probable head-tail

30 34 72.3 501 2 D90970 probable head-tail
31 34 72.3 501 2 D85717 hypothetical prote
32 34 72.3 903 1 C64444 cell division cont
33 34 72.3 1394 2 A35626 transforming growt
34 34 72.3 1712 2 A38261 masking protein pr
35 34 72.3 4342 2 H83343 probable non-ribos
36 33 70.2 144 2 A29101 vasopressin / neur
37 33 70.2 146 2 S60748 phaseolotoxin synt
38 33 70.2 164 1 NVHU2 vasopressin / neur
39 33 70.2 197 2 JC2320 hypothetical 22K p
40 33 70.2 216 2 E81670 cytidylate kinase
41 33 70.2 217 2 A97128 cytidylate kinase
42 33 70.2 222 2 B83854 msaA homolog -. Myc
43 33 70.2 223 2 S72954 probable cmk prote
44 33 70.2 230 2 G70504 hypothetical prote
45 33 70.2 248 2 B96676

ALIGNMENTS

RESULT 1

W7LH35

E7 protein - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03688; S12367; T10428

R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virolgy 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03688

A:Molecule type: DNA

A:Residues: 1-98 <SEE>

A:Cross-references: UNIPROT:P03129; GB:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333033

R:Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vousden, K.H.

EMBO J. 9, 153-160, 1990

A:Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 large

A:Reference number: S12367; MUID:90107938; PMID:2153075

A:Accession: S12367

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-98 <BAR>

R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human papillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10428

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-98 <KEN>

A:Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333033

C:Genetics:

A:Gene: E7

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:58-94/Region: zinc finger CCCC motif

Query Match 100.0%; Score 47; DB 1; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.054;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIDGPACQA 9

Db 37 EIDGPACQA 45

RESULT 2

W7LH35

E7 protein - human papillomavirus type 35

C:Species: human papillomavirus type 35

A:Note: host Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Accession: F40824; S36522
R;Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A;Title: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 31
A;Reference number: A40824; MUID:92124753; PMID:1310198
A;Accession: F40824
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-99 <VAR>
A;Cross-references: UNIPROT:P27230; GB:M74117; NID:g333050; PIDN:AAA46967.1; PID:g333052
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36522
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99
A;Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52562.1; PID:g396999
A;Experimental source: strain 35H
C;Superfamily: Papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;58-95/Region: zinc finger CCCC motif

Query Match 89.4%; Score 42; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.5; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0

Qy 2 IDGPAGQA 9
|||
Db 39 IDGPAGQA 46
|||

RESULT 3
S07886
site-specific DNA-methyltransferase (adenine-specific) (EC 2.1.1.72) EcaI - Enterobacter
C;Species: Enterobacter cloacae
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S07886
R;Brenner, V.; Venetianer, P.; Kiss, A.
Nucleic Acids Res. 18, 355-359, 1990
A;Title: Cloning and nucleotide sequence of the gene encoding the EcaI DNA methyltransferase
A;Reference number: S07886; MUID:90221818; PMID:2183182
A;Accession: S07886
A;Molecule type: DNA
A;Residues: 1-452 <BRE>
A;Cross-references: UNIPROT:P14827; EMBL:X17111; NID:g41314; PIDN:CAA34968.1; PID:g41315
C;Genetics: ecaIM
A;Gene: ecaIM
C;Keywords: methyltransferase; S-adenosylmethionine

Query Match 78.7%; Score 37; DB 2; Length 452;
Best Local Similarity 87.5%; Pred. No. 23; Mismatches 0; Indels 1; Gaps 0;
Matches 7; Conservative 0

Qy 1 EIDGPAGQ 8
|||
Db 9 EIDGPAGQ 16
|||

RESULT 4
W7ML31
E7 protein - human papillomavirus type 31
C;Species: human papillomavirus type 31
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: B32444
R;Goldsborough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated virus
A;Reference number: A94398; MUID:89299478; PMID:2545036
A;Accession: B32444
A;Status: translation not shown

A;Molecule type: DNA
A;Residues: 1-98 <GOL>
A;Cross-references: UNIPROT:P17387; GB:J04353; NID:g333048; PIDN:AAA46951.1; PID:g459917
C;Comment: This protein may be involved in the oncogenic potential of this virus.
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;58-94/Region: zinc finger CCCC motif

Query Match 76.6%; Score 36; DB 1; Length 98;
Best Local Similarity 87.5%; Pred. No. 7.2; Mismatches 0; Indels 1; Gaps 0;
Matches 7; Conservative 0

Qy 2 IDGPAGQA 9
|||
Db 38 IDGPAGQA 45
|||

RESULT 5
B70594
hypothetical protein RV3256C - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: B70594
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70594
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-346 <COL>
A;Cross-references: UNIPROT:O05899; GB:Z95121; GB:AL123456; NID:g3261742; PIDN:CAB08352.1
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: RV3256C
C;Superfamily: Mycobacterium tuberculosis hypothetical protein RV3256C

Query Match 74.5%; Score 35; DB 2; Length 346;
Best Local Similarity 87.5%; Pred. No. 42; Mismatches 0; Indels 1; Gaps 0;
Matches 7; Conservative 0

Qy 1 EIDGPAGQ 8
|||
Db 274 EIDGPAGQ 281
|||

RESULT 6
AG1706
lipases homolog lin2194 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG1706
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1706
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-347 <GLA>
A;Cross-references: UNIPROT:Q929T0; GB:AL592022; PIDN:CAC97423.1; PID:gl6414707; GSPDB:G
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin2194

Query Match 74.5%; Score 35; DB 2; Length 347;
Matches 7; Conservative 0

Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BIDGPAGQ 8
:|||||:
Db 90 KIDGPAGK 97

RESULT 7
A11335
lipases homolog lmo2089 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: A11335
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mak, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: A11335
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <GLA>
A:Cross-references: UNIPROT:Q8YSH3; GB:NC_003210; PIDN:CAD00167.1; PID:g16411559; GSPDB:
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo2089

Query Match 74.5%; Score 35; DB 2; Length 347;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BIDGPAGQ 8
:|||||:
Db 90 KIDGPAGK 97

RESULT 8
AE3522
Leu/ile/Val-binding protein precursor [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AE3522
R:DelVecchio, V.G.; Kaparal, V.; Redkar, R.J.; Patra, G.; Mujier, C.; Los, T.; Ivanova, I.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AE3522
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-415 <KUR>
A:Cross-references: UNIPROT:Q8YDS2; GB:AE008918; PIDN:AAL53344.1; PID:g17984232; GSPDB:C
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI10103
A:Map position: 11

Query Match 74.5%; Score 35; DB 2; Length 415;
Best Local Similarity 87.5%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 BIDGPAGQ 8
:|||||:
Db 394 EIRGPAGQ 401

RESULT 9
G70033
maltose/maltodextrin-binding protein homolog yvdG - Bacillus subtilis

C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: G70033
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, A.; Ehrlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: G70033
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-417 <KUN>
A:Cross-references: UNIPROT:O06989; GB:Z99121; GB:AL009126; NID:g2635827; PIDN:CAB15466.1
A:Experimental source: strain 168
C:Genetics:
A:Gene: yvdG
C:Superfamily: maltose-binding protein

Query Match 74.5%; Score 35; DB 2; Length 417;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IDGPAGQA 9
:|||||:
Db 81 LDGPAGNA 88

RESULT 10
T28700
hypothetical protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28700
R:Parkhill, J.; Bentley, S.D.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1999
A:Reference number: Z20512
A:Accession: T28700
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-630 <PAR>
A:Cross-references: UNIPROT:O69824; EMBL:AL023496; NID:el292348; PID:el292367; PIDN:CAA11

Query Match 74.5%; Score 35; DB 2; Length 630;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IDGPAGQA 9
:|||||:
Db 562 VDGPAGTA 569

RESULT 11
T18412
lipid-binding protein precursor Dva-1 - Dictyocaulus viviparus
C:Species: Dictyocaulus viviparus
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C:Accession: T18412
R:Kennedy, M.W.; Britton, C.; Price, N.C.; Kelly, S.M.; Cooper, A.
J. Biol. Chem. 270, 19277-19281, 1995
A:Title: The Dva-1 polypeptide of the parasitic nematode Dictyocaulus viviparus. A small
A:Reference number: Z18932; MUID:95370256; PMID:7642601
A:Accession: T18412

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1557 <KEN>
A;Cross-references: UNIPROT:Q24702; EMBL:U02568; NID:g763531; PID:g763532; PIDN:AAC747403
A;Experimental source: specific host Bos taurus
C;Genetics:
A;Note: DVA
F:1-21/Domains: signal sequence #status predicted <SIG>
F:22-1557/Product: lipid-binding protein DVA-1 #status predicted <MAT>

Query Match 74.5%; Score 35; DB 2; Length 1557;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IDGPAGQA 9
|||||
Db 320 IDGPAGVA 327

RESULT 12
W7WL58
E7 protein - human papillomavirus type 58
C;Species: human papillomavirus type 58
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: F36779
R;Kirii, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
A;Title: Human papillomavirus type 58 DNA sequence.
A;Reference number: A36779; MUID:92024102; PMID:1656594
A;Accession: F36779
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-98 <KIR>
A;Cross-references: UNIPROT:P26557; GB:D90400; NID:g222386; PIDN:BAA31846.1; PID:g3333709
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:59-95/Region: zinc finger CCCC motif

Query Match 72.3%; Score 34; DB 1; Length 98;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IDGPAGQA 9
:|||||
Db 39 LDGPDGQA 46

RESULT 13
E64842
Probable monoxygenase b1007 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: E64842
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: E64842
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-152 <BLAT>
A;Cross-references: GB:A8000202; GB:U00096; NID:gl787233; PIDN:AAC74092.1; PID:gl787242;
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: 4-hydroxyphenylacetate 3-monoxygenase small chain

Query Match 72.3%; Score 34; DB 2; Length 152;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DGPAGQA 9
|||||
Db 14 DGPAGRA 20

Db 14 DGPAGRA 20

RESULT 14
E90785
Probable 4-hydroxyphenylacetate 3-monoxygenase ECs1253 [similarity] - Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 27-Nov-2001
C;Accession: E90785
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E90785
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAE34676.1; PID:gl3360713; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs1253
C;Superfamily: 4-hydroxyphenylacetate 3-monoxygenase small chain

Query Match 72.3%; Score 34; DB 2; Length 152;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DGPAGQA 9
|||||
Db 14 DGPAGRA 20

RESULT 15
C85645
Probable 4-hydroxyphenylacetate 3-monoxygenase Z1506 [imported] - Escherichia coli (stra
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: C85645
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: C85645
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <STO>
A;Cross-references: GB:AE005174; NID:gl2514364; PIDN:AAG55623.1; GSPDB:GN00145; UWGP:Z15
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z1506
C;Superfamily: 4-hydroxyphenylacetate 3-monoxygenase small chain

Query Match 72.3%; Score 34; DB 2; Length 152;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DGPAGQA 9
|||||
Db 14 DGPAGRA 20

Search completed: June 28, 2005, 21:27:54
Job time : 12.15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds
(without alignments)
59.826 Million cell updates/sec

Title: US-08-170-344-39
Perfect score: 47
Sequence: 1 EIDGPAGQA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10F_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	9	14	US-10-239-313A-689
2	47	100.0	9	16	Sequence 689, App
3	47	100.0	10	9	Sequence 20, Appl
4	47	100.0	10	14	Sequence 19, Appl
5	47	100.0	10	16	Sequence 19, Appl
6	47	100.0	10	16	Sequence 24, Appl
7	47	100.0	10	16	Sequence 29, Appl
8	47	100.0	10	16	Sequence 19, Appl
9	47	100.0	15	16	Sequence 39, Appl
10	47	100.0	15	16	Sequence 42, Appl
11	47	100.0	15	16	Sequence 73, Appl
					Sequence 82, Appl

12	47	100.0	20	15	US-10-432-465-47	Sequence 47, Appl
13	47	100.0	20	16	US-10-890-526-72	Sequence 72, Appl
14	47	100.0	21	16	US-10-612-818-6	Sequence 6, Appl
15	47	100.0	21	16	US-10-476-570-62	Sequence 62, Appl
16	47	100.0	21	16	US-10-306-541-106	Sequence 106, Appl
17	47	100.0	22	9	US-09-367-309A-6	Sequence 6, Appl
18	47	100.0	98	9	US-09-728-466-1	Sequence 1, Appl
19	47	100.0	98	9	US-09-820-765-4	Sequence 4, Appl
20	47	100.0	98	9	US-09-824-017-4	Sequence 4, Appl
21	47	100.0	98	10	US-09-986-118A-4	Sequence 4, Appl
22	47	100.0	98	14	US-10-267-311-8	Sequence 8, Appl
23	47	100.0	98	14	US-10-177-390-8	Sequence 8, Appl
24	47	100.0	98	14	US-10-201-764-19	Sequence 19, Appl
25	47	100.0	98	15	US-10-392-113-29	Sequence 29, Appl
26	47	100.0	98	15	US-10-654-129-4	Sequence 4, Appl
27	47	100.0	98	15	US-10-681-410-19	Sequence 19, Appl
28	47	100.0	98	16	US-10-772-988-3	Sequence 3, Appl
29	47	100.0	98	16	US-10-479-541-5	Sequence 5, Appl
30	47	100.0	98	17	US-10-042-526A-4	Sequence 4, Appl
31	47	100.0	98	17	US-10-657-399-1	Sequence 1, Appl
32	47	100.0	98	17	US-10-858-384-12	Sequence 12, Appl
33	47	100.0	98	17	US-10-484-063-26	Sequence 26, Appl
34	47	100.0	98	17	US-10-343-448-5	Sequence 5, Appl
35	47	100.0	98	17	US-10-679-956-8	Sequence 8, Appl
36	47	100.0	98	17	US-10-367-057-17	Sequence 17, Appl
37	47	100.0	99	15	US-10-115-440-7	Sequence 7, Appl
38	47	100.0	111	16	US-10-472-724-4	Sequence 4, Appl
39	47	100.0	121	14	US-10-267-311-12	Sequence 12, Appl
40	47	100.0	121	17	US-10-679-956-12	Sequence 12, Appl
41	47	100.0	198	14	US-10-267-311-35	Sequence 35, Appl
42	47	100.0	198	17	US-10-679-956-35	Sequence 35, Appl
43	47	100.0	220	13	US-10-000-903-1	Sequence 1, Appl
44	47	100.0	220	13	US-10-000-903-8	Sequence 8, Appl
45	47	100.0	220	17	US-10-899-771-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-239-313A-689
; Sequence 689, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAJA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 689
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-239-313A-689

Query Match 100.0%; Score 47; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EIDGPAGQA 9
Db 1 EIDGPAGQA 9

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RESULT 2
US-10-306-541-20
; Sequence 20, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-20

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```

Query Match          100.0%; Score 47; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EIDGPAGQA 9
Db 1 EIDGPAGQA 9

RESULT 3
US-09-891-823-19
; Sequence 19, Application US/09891823
; Publication No. US20020110566A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/09/891,823
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-891-823-19

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Query Match          100.0%; Score 47; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EIDGPAGQA 9
Db 2 EIDGPAGQA 10

RESULT 4
US-10-365-908-19
; Sequence 19, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.

```

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; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-19

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Query Match          100.0%; Score 47; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EIDGPAGQA 9
Db 2 EIDGPAGQA 10

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RESULT 5
US-10-306-541-24
; Sequence 24, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-24

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```

Query Match          100.0%; Score 47; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 EIDGPAGQA 9
Db 2 EIDGPAGQA 10

```

```

RESULT 6
US-10-306-541-29
; Sequence 29, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29

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; LENGTH: 10
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-29

Query Match      100.0%; Score 47; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.061; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 EIDGPAGQA 9
Db 1 EIDGPAGQA 9

RESULT 7
US-10-871-138-19
; Sequence 19, Application US/10871138
; Publication No. US20040235741A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/871,138
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-871-138-19

Query Match      100.0%; Score 47; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.061; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 EIDGPAGQA 9
Db 2 EIDGPAGQA 10

RESULT 8
US-10-306-541-39
; Sequence 39, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 39
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-39

Query Match      100.0%; Score 47; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.091; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 EIDGPAGQA 9
Db 5 EIDGPAGQA 13

RESULT 11
US-10-306-541-82
; Sequence 82, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
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; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-82

Query Match 100.0%; Score 47; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.091; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 EIDGPAGQA 9
| | | | | | | |
Db 3 EIDGPAGQA 11

RESULT 12
US-10-432-465-47
; Sequence 47, Application US/10432465
; Publication No. US20040091479A1
; GENERAL INFORMATION:
; APPLICANT: Nieland, John
; APPLICANT: Kaufmann, Andreas
; APPLICANT: Kather, Angela
; APPLICANT: Schinz, Manuela
; TITLE OF INVENTION: T-Cell Epitopes of the Papillomavirus L1
; TITLE OF INVENTION: Protein and E7 Protein and Their Use in Diagnosis and
; FILE REFERENCE: 50125/077001
; CURRENT APPLICATION NUMBER: US/10/432,465
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/14037
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 10059631.2
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-432-465-47

Query Match 100.0%; Score 47; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 EIDGPAGQA 9
| | | | | | | |
Db 4 EIDGPAGQA 12

RESULT 13
US-10-890-526-72
; Sequence 72, Application US/10890526
; Publication No. US20040258708A1
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/10/890,526
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: US/09/980,177

; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-890-526-72

Query Match 100.0%; Score 47; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 EIDGPAGQA 9
| | | | | | | |
Db 4 EIDGPAGQA 12

RESULT 14
US-10-612-818-6
; Sequence 6, Application US/10612818
; Publication No. US20040110925A1
; GENERAL INFORMATION:
; APPLICANT: Impact Diagnostics
; APPLICANT: Impact Diagnostics
; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus
; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papil
; TITLE OF INVENTION: Associated Cancers
; FILE REFERENCE: 3352-2-2
; CURRENT APPLICATION NUMBER: US/10/612,818
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/394,172
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/828,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E7 early coding region of HPV 16
US-10-612-818-6

Query Match 100.0%; Score 47; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 EIDGPAGQA 9
| | | | | | | |
Db 12 EIDGPAGQA 20

RESULT 15
US-10-476-570-62
; Sequence 62, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570

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; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 21
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E7 35-55
US-10-476-570-62
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Query Match      100.0%; Score 47; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EIDGPAGQA 9
      |||||
Db      3 EIDGPAGQA 11
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Search completed: June 29, 2005, 04:19:29
Job time : 57.85 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-39

Perfect score: 47

Sequence: 1 EIDGPAGQA 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	47	100.0	9	3	US-08-159-339A-214
2	47	100.0	10	4	Sequence 214, Appl
3	47	100.0	17	3	Sequence 19, Appl
4	47	100.0	18	3	Sequence 54, Appl
5	47	100.0	20	3	Sequence 9, Appl
6	47	100.0	20	3	Sequence 5, Appl
7	47	100.0	22	4	Sequence 72, Appl
8	47	100.0	22	4	Sequence 6, Appl
9	47	100.0	25	1	Sequence 2, Appl
10	47	100.0	30	4	Sequence 2, Appl
11	47	100.0	38	4	Sequence 6, Appl
12	47	100.0	98	1	Sequence 6, Appl
13	47	100.0	98	3	Sequence 42, Appl
14	47	100.0	98	3	Sequence 1, Appl
15	47	100.0	98	3	Sequence 4, Appl
16	47	100.0	98	3	Sequence 4, Appl
17	47	100.0	98	4	Sequence 8, Appl
18	47	100.0	98	4	Sequence 19, Appl
19	47	100.0	98	4	Sequence 4, Appl
20	47	100.0	98	4	Sequence 1, Appl
21	47	100.0	98	4	Sequence 4, Appl
22	47	100.0	98	4	Sequence 8, Appl
23	47	100.0	98	4	Sequence 19, Appl
24	47	100.0	98	4	Sequence 3, Appl
25	47	100.0	98	4	Sequence 7, Appl
26	47	100.0	98	4	Sequence 12, Appl
27	47	100.0	121	4	Sequence 12, Appl

28	47	100.0	172	3	US-08-860-165-12	Sequence 12, Appl
29	47	100.0	172	3	US-08-860-165-14	Sequence 14, Appl
30	47	100.0	172	3	US-09-359-382-12	Sequence 12, Appl
31	47	100.0	172	3	US-09-359-382-14	Sequence 14, Appl
32	47	100.0	198	4	US-09-613-303-35	Sequence 35, Appl
33	47	100.0	198	4	US-10-267-311-35	Sequence 35, Appl
34	47	100.0	220	3	US-09-485-885-1	Sequence 1, Appl
35	47	100.0	220	3	US-09-485-885-8	Sequence 8, Appl
36	47	100.0	239	3	US-09-485-885-12	Sequence 12, Appl
37	47	100.0	253	2	US-08-459-818-20	Sequence 20, Appl
38	47	100.0	253	2	US-08-889-666-20	Sequence 20, Appl
39	47	100.0	253	2	US-08-455-078-20	Sequence 20, Appl
40	47	100.0	253	2	US-08-725-776-20	Sequence 20, Appl
41	47	100.0	253	2	US-08-488-062-20	Sequence 20, Appl
42	47	100.0	263	1	US-08-117-083-9	Sequence 9, Appl
43	47	100.0	266	3	US-08-860-165-10	Sequence 10, Appl
44	47	100.0	266	3	US-09-359-382-10	Sequence 10, Appl
45	47	100.0	266	4	US-09-367-309A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-159-339A-214
; Sequence 214, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cellis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-214

Query Match 100.0%; Score 47; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIDGPAGQA 9
| | | | | | | | | |
Db 1 EIDGPAGQA 9

RESULT 2

US-10-365-908-19
; Sequence 19, Application US/10365908
; Patent No. 6797491
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-19

Query Match 100.0%; Score 47; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIDGPAGQA 9
| | | | | | | | | |
Db 2 EIDGPAGQA 10

RESULT 3

US-08-075-541D-54
; Sequence 54, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-54

Query Match 100.0%; Score 47; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIDGPAGQA 9
| | | | | | | | | |
Db 2 EIDGPAGQA 10

RESULT 4

US-08-075-541D-9
; Sequence 9, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-9

Query Match      100.0%; Score 47; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EIDGPAGQA 9
Db      1 EIDGPAGQA 9

RESULT 5
US-08-075-541D-5
; Sequence 5, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-5

Query Match      100.0%; Score 47; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EIDGPAGQA 9
Db      1 EIDGPAGQA 9

; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-9

Query Match      100.0%; Score 47; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EIDGPAGQA 9
Db      1 EIDGPAGQA 9

RESULT 6
US-09-980-177A-72
; Sequence 72, Application US/09980177A
; Patent No. 6838084
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/09/980,177A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-980-177A-72

Query Match      100.0%; Score 47; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EIDGPAGQA 9
Db      4 EIDGPAGQA 12

RESULT 7
US-09-367-309A-6
; Sequence 6, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-367-309A-6

Query Match      100.0%; Score 47; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EIDGPAGQA 9
Db      5 EIDGPAGQA 13

RESULT 8
US-08-363-586-2
; Sequence 2, Application US/08363586
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; Patent No. 5629161
; GENERAL INFORMATION:
; APPLICANT: Mueller, Martin
; APPLICANT: Gismann, Lutz
; TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
; TITLE OF INVENTION: Peptides for the Diagnostic Purpose
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363.586
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/909,296
; FILING DATE: 09-JUL-1992
; APPLICATION NUMBER: EP 91111720.8
; FILING DATE: 13-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wadler, Linda A.
; REGISTRATION NUMBER: 33,218
; REFERENCE/DOCKET NUMBER: 02481-1195-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-363-586-2

Query Match 100.0%; Score 47; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIDGPAGQA 9
| | | | |
Db 9 EIDGPAGQA 17

RESULT 9
US-09-486-394-2
; Sequence 2, Application US/09486394
; Patent No. 6478749
; GENERAL INFORMATION:
; APPLICANT: Hopfl, Reinhard
; TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
; FILE REFERENCE: 032929-001
; CURRENT APPLICATION NUMBER: US/09/486,394
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/04773
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: DE 197 37 409.3
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16

; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(30)
; OTHER INFORMATION: E7 peptide.
US-09-486-394-2

Query Match 100.0%; Score 47; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIDGPAGQA 9
| | | | |
Db 17 EIDGPAGQA 25

RESULT 10
US-09-501-097A-6
; Sequence 6, Application US/09501097A
; Patent No. 6734173
; GENERAL INFORMATION:
; APPLICANT: Tzyy-Choon Wu
; APPLICANT: Chien-Fu Hung
; TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
; FILE REFERENCE: 2240-169349
; CURRENT APPLICATION NUMBER: US/09/501,097A
; CURRENT FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 38
; TYPE: PRT
; ORGANISM: human papillomavirus
US-09-501-097A-6

Query Match 100.0%; Score 47; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIDGPAGQA 9
| | | | |
Db 8 EIDGPAGQA 16

RESULT 11
US-08-406-248-6
; Sequence 6, Application US/08406248
; Patent No. 5736318
; GENERAL INFORMATION:
; APPLICANT: Munger, Karl
; APPLICANT: Jones, D. Leanne
; TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
; TITLE OF INVENTION: TRANSFORMED CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Kusmer
; STREET: 200 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,248
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcdaniels, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: HAZ-011

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-406-248-6

Query Match 100.0%; Score 47; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 BIDGPAGQA 9
Db 37 BIDGPAGQA 45

RESULT 12
US-08-075-541D-42
Sequence 42, Application US/08075541D
Patent No. 6183745

GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
STATE: PENNSYLVANIA
COUNTRY: USA
ZIP: 19103-2398

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/au91/00575

FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S

REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020

TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-075-541D-42

Query Match 100.0%; Score 47; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 BIDGPAGQA 9
Db 37 BIDGPAGQA 45

RESULT 13
US-09-382-616A-1
Sequence 1, Application US/09382616A
Patent No. 6200746

GENERAL INFORMATION:
APPLICANT: Fisher, Christopher
APPLICANT: He, Wanxia
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
CURRENT APPLICATION NUMBER: US/09/382.616A
CURRENT FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/382,616
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 98
TYPE: PRT
ORGANISM: Papillomavirus sylvilagi
US-09-382-616A-1

Query Match 100.0%; Score 47; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 BIDGPAGQA 9
Db 37 BIDGPAGQA 45

RESULT 14
US-08-944-368A-4
Sequence 4, Application US/08944368A
Patent No. 6228368

GENERAL INFORMATION:
APPLICANT: Gissman, et al.
TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine
TITLE OF INVENTION: Formulations and Methods of Use
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/944,368A
FILING DATE:
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr, Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27013/34028
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-08-944-368A-4
Query Match      100.0%; Score 47; DB 3; Length 98;
Best Local Similarity 100.0%; Pred.No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EIDGPAGQA 9
      |||||
Db      37 EIDGPAGQA 45

RESULT 15
US-09-820-764-4
; Sequence 4, Application US/09820764
; Patent No. 6352696
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
;           HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
;           FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/820,764
; FILING DATE: 30-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-764-4

Query Match      100.0%; Score 47; DB 3; Length 98;
Best Local Similarity 100.0%; Pred.No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EIDGPAGQA 9
      |||||
Db      37 EIDGPAGQA 45

Search completed: June 28, 2005, 21:33:31
Job time : 17 secs
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Query Match 100.0%; Score 53; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9: Conservative 0; Mismatches 0; Indels

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Qy 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

RESULT 3
Q8B5P5 PRELIMINARY; PRT; 77 AA.
AC Q8B5P5;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC NCBI_TaxID=10561;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187868; AAF13397.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 77
SQ SEQUENCE 77 AA; 8782 MW; C5DE3A7E546AC31B CRC64;

Query Match 100.0%; Score 53; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

RESULT 4
Q9QDH2 PRELIMINARY; PRT; 93 AA.
AC Q9QDH2;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187869; AAF13399.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 53; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

RESULT 5
Q9QDH4 PRELIMINARY; PRT; 93 AA.
AC Q9QDH4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)

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DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187868; AAF13397.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 53; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

RESULT 6
Q9QDH6 PRELIMINARY; PRT; 93 AA.
AC Q9QDH6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187867; AAF13395.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10513 MW; 92C7054341326A1F CRC64;

Query Match 100.0%; Score 53; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

RESULT 7
Q9QDH8 PRELIMINARY; PRT; 93 AA.
AC Q9QDH8;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 53; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

RESULT 8
Q8B5P6 PRELIMINARY; PRT; 94 AA.
ID Q8B5P6
AC Q8B5P6
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E7 oncoprotein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaesteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF469197; AAO15692.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 94
SQ SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;

Query Match 100.0%; Score 53; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

RESULT 9
VE7_HPV16 STANDARD; PRT; 98 AA.
AC P03129;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85246220; PubMed=2990099;
RA Seedorf K., Kramer G., Duret M., Suhai S., Rowekamp W.G.;
RT "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90218027; PubMed=2157796;
RA Schneider-Maunoury S., Pehau-Arnauudet G., Breitburd F., Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-v cells,
a line derived from a vulvar intraepithelial neoplasia.";
RL J. Gen. Virol. 71:809-817(1990).
RN [3]

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RP SEQUENCE FROM N.A.
RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Girardo E., Giraldo G.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP FUNCTION.
RX MEDLINE=88223347; PubMed=2836062;
RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;
RT "The human papillomavirus type 16 E7 gene encodes transactivation and
transformation functions similar to those of adenovirus E1A.";
RL Cell 53:539-547(1988).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating
activities.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: K02718; AAA46940.1; -.
DR EMBL: D00735; BRA00633.1; -.
DR EMBL: U76411; AAB18962.1; -.
DR EMBL: U76412; AAB18963.1; -.
DR EMBL: U76413; AAB18964.1; -.
DR EMBL: AF003020; AAB70737.1; -.
DR EMBL: AF003023; AAB70740.1; -.
DR EMBL: AF003024; AAB70741.1; -.
DR EMBL: AF003025; AAB70742.1; -.
DR EMBL: AF003026; AAB70743.1; -.
DR F1R; A03688; W7WLHS.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW Transcription regulation.
FT SITE 58 61 C-XX-C motif-1.
FT SITE 91 94 C-XX-C motif-2.
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 100.0%; Score 53; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

RESULT 10
O11650 PRELIMINARY; PRT; 98 AA.
ID O11650
AC O11650;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transforming protein E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
RA Lee H.P.;
RT "Major sequence variants in E7 gene of human papillomavirus type 16
from cervical cancerous and noncancerous lesions of Korean women.";
RT

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RL Gynecol. Oncol. 66:275-281(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
RA Lee H.-P.; Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Terai M., Ma Z., Burk R.D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RN J. Infect. Dis. 186:696-700(2002).
RN [5]
RP SEQUENCE FROM N.A.
RA Terai M., Fu L., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U76404; AAC58243.1; -
DR EMBL; AF472509; AAO15706.1; -
DR EMBL; AF486326; AAL96631.1; -
DR EMBL; AF486327; AAL96632.1; -
DR EMBL; AF486330; AAL96635.1; -
DR EMBL; AF486331; AAL96636.1; -
DR EMBL; AF486332; AAL96637.1; -
DR EMBL; AF486333; AAL96638.1; -
DR EMBL; AF486334; AAL96639.1; -
DR EMBL; AF486336; AAL96641.1; -
DR EMBL; AF486338; AAL96643.1; -
DR EMBL; AF486346; AAL96651.1; -
DR EMBL; AF486350; AAL96655.1; -
DR EMBL; AF486351; AAL96656.1; -
DR EMBL; AF534061; AAO10404.1; -
DR InterPro; -PR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10995 MW; 81853B534CC3281B CRC64;

Query Match 100.0%; Score 53; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

RESULT 11
O12337 PRELIMINARY; PRT; 98 AA.
AC O12337;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX Toranesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RN J. Gen. Virol. 78:2199-2208(1997).
RL EMBL; AF003021; AAB70738.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.

Query Match 100.0%; Score 53; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

RESULT 12
O12338 PRELIMINARY; PRT; 98 AA.
ID O12338
AC O12338
DT 01-JUN-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX Toranesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RN J. Gen. Virol. 78:2199-2208(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Jinhu X., Xinxiang W., Yun T.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003022; AAB70739.1; -
DR EMBL; AF477385; AAM03025.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10969 MW; 9BD612534CCCEA59B CRC64;

Query Match 100.0%; Score 53; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

RESULT 13
O8QRD2 PRELIMINARY; PRT; 98 AA.
ID O8QRD2
AC O8QRD2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RN J. Infect. Dis. 186:696-700(2002).
RL EMBL; AF486345; AAL96650.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
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SQ SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

RESULT 12
O12338 PRELIMINARY; PRT; 98 AA.
ID O12338
AC O12338
DT 01-JUN-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX Toranesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RN J. Gen. Virol. 78:2199-2208(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Jinhu X., Xinxiang W., Yun T.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003022; AAB70739.1; -
DR EMBL; AF477385; AAM03025.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10969 MW; 9BD612534CCCEA59B CRC64;

Query Match 100.0%; Score 53; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

RESULT 13
O8QRD2 PRELIMINARY; PRT; 98 AA.
ID O8QRD2
AC O8QRD2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RN J. Infect. Dis. 186:696-700(2002).
RL EMBL; AF486345; AAL96650.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
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SQ SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 100.0%; Score 53; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLACYEQ 9
Db 19 TTDLACYEQ 27

RESULT 14

Q8QRD3 PRELIMINARY; PRT; 98 AA.

AC Q8QRD3;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486344; AAL96649.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLACYEQ 9
Db 19 TTDLACYEQ 27

RESULT 15

Q8QRD4 PRELIMINARY; PRT; 98 AA.

AC Q8QRD4;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486329; AAL96634.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11025 MW; 86E24B234CC3281B CRC64;

Query Match 100.0%; Score 53; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLACYEQ 9
Db 19 TTDLACYEQ 27

Search completed: June 28, 2005, 21:24:09
Job time : 56.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-38

Perfect score: 53

Sequence: 1 TTDLICYEQ 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	98	1 W7WLS3	E7 protein - human
2	48	90.6	97	1 W7WLS3	E7 protein - human
3	48	90.6	99	1 W7WLS3	E7 protein - human
4	48	90.6	99	2 S36574	E7 protein - human
5	44	83.0	98	1 W7WLS8	E7 protein - human
6	43	81.1	93	1 W7WLS4	E7 protein - human
7	43	81.1	98	1 W7WLS3	E7 protein - human
8	43	81.1	104	2 S36510	E7 protein - human
9	40	75.5	93	1 W7WLS	E7 protein - human
10	40	75.5	93	2 S36474	E7 protein - human
11	40	75.5	93	2 S36591	E7 protein - human
12	40	75.5	95	2 S36480	E7 protein - human
13	38	71.7	105	2 S36504	E7 protein - human
14	38	71.7	345	1 B46113	protein kinase (EC
15	38	71.7	393	1 TVBE66	protein kinase (EC
16	37	69.8	324	2 AF2160	glycosyltransferas
17	36	67.9	265	2 C96663	hypothetical prote
18	36	67.9	642	2 T11827	cyclomaltodextrin
19	36	67.9	777	1 TVVPCP	large T antigen -
20	36	67.9	782	2 S22560	large T antigen -
21	36	67.9	785	1 TVVPT	large T antigen -
22	36	67.9	803	2 S45916	hypothetical prote
23	36	67.9	1735	2 A57607	Munc13-1 - rat
24	36	67.9	1985	2 I61776	Munc13-2 - rat
25	36	67.9	2207	2 T42759	Munc13-3 protein -
26	35	66.0	101	1 W7WLS1	E7 protein - human
27	35	66.0	106	2 S36562	E7 protein - human
28	35	66.0	113	1 W7WLR1	E7 protein - rhesu
29	35	66.0	138	1 I51380	phospholipase A2 h

RESULT 1
W7WLS3
E7 protein - human papillomavirus type 16
C:Species: human papillomavirus type 16
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A03688; S12367; T10428
R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A:Title: Human papillomavirus type 16 DNA sequence.
A:Reference number: A22355; MUID:85246220; PMID:2990099
A:Accession: A03688
A:Molecule type: DNA
A:Residues: 1-98 <SEE>
A:Cross-references: UNIPROT:P03129; GB:K02718; MID:g333031; PIDN:AAA46940.1; PID:g333033
R:Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vousden, K.H.
EMBO J. 9, 153-160, 1990
A:Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 large
A:Reference number: S12367; MUID:90107938; PMID:2153075
A:Accession: S12367
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-98 <BAR>
R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A:Title: A negative element in the human papillomavirus type 16 genome acts at the level
A:Reference number: Z17014; MUID:91162763; PMID:1848319
A:Accession: T10428
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-98 <KEN>
A:Cross-references: EMBL:K02718; MID:g333031; PIDN:AAA46940.1; PID:g333033
C:Genetics:
A:Gene: E7
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:58-94/Region: zinc finger CCCC motif
Query Match 100.0%; Score 53; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLICYEQ 9

Db 19 TTDLICYEQ 27

RESULT 2

W7WLS3
E7 protein - human papillomavirus type 33
C:Species: human papillomavirus type 33
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A03689; S23831; S23827

R;Cole, S.T.; Streeck, R.E.
J. Virol. 58, 991-995, 1986
A;Title: Genome organization and nucleotide sequence of human papillomavirus type 33, which was submitted to the EMBL Data Library, August 1993
A;Reference number: A93020; MUID:86200464; PMID:3009902
A;Accession: A03689
A;Molecule type: DNA
A;Residues: 1-97 <COL>
A;Cross-references: UNIPROT:P06429; GB:M12732; NID:g333049; PIDN:AAA46959.1; PID:g463178
R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.W.C.; Meijer, C.J.; et al. submitted to the EMBL Data Library, January 1992
A;Description: HFV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via transcription of a DNA binding site
A;Reference number: S19906
A;Accession: S23831
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-97 <SNL>
A;Cross-references: EMBL:X64085; NID:g60278; PIDN:CAA5434.1; PID:g50281; EMBL:X64084; NID:g333052
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:58-94/Region: zinc finger CCCC motif

Query Match 90.6%; Score 48; DB 1; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0

Qy 2 TDLVCYEQ 9
|||||
Db 20 TDLVCYEQ 27

RESULT 3
W7WL35
E7 protein - human papillomavirus type 35
C;Species: human papillomavirus type 35
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: F40824; S36522
R;Marich, J.E.; Pontaler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A;Title: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35
A;Reference number: A40824; MUID:92124753; PMID:1310198
A;Accession: F40824
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-99 <MAR>
A;Cross-references: UNIPROT:P27230; GB:M74117; NID:g333050; PIDN:AAA46967.1; PID:g333052
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36522
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99
A;Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52562.1; PID:g396999
A;Experimental source: strain 35H
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:59-95/Region: zinc finger CCCC motif

Query Match 90.6%; Score 48; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0

Qy 2 TDLVCYEQ 9
|||||
Db 20 TDLVCYEQ 27

RESULT 4
S36574
E7 protein - human papillomavirus type 52
C;Species: human papillomavirus type 52

C;Date: 08-May-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S36574
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36574
A;Molecule type: DNA
A;Residues: 1-99
A;Cross-references: UNIPROT:P36831; EMBL:X74481; NID:g397038; PIDN:CAA52586.1; PID:g39704
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation

Query Match 90.6%; Score 48; DB 2; Length 99;
Best Local Similarity 88.9%; Pred. No. 0.12; Mismatches 1; Indels 0; Gaps 0;
Matches 8; Conservative 1

Qy 1 TDLVCYEQ 9
|||||
Db 19 TDLHCYEQ 27

RESULT 5
W7WL58
E7 protein - human papillomavirus type 58
C;Species: human papillomavirus type 58
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: F36779
R;Kiril, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
A;Title: Human papillomavirus type 58 DNA sequence.
A;Reference number: A36779; MUID:92024102; PMID:1656594
A;Accession: F36779
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-98 <KIR>
A;Cross-references: UNIPROT:P26557; GB:D90400; NID:g222386; PIDN:BAA31846.1; PID:g3337095
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:59-95/Region: zinc finger CCCC motif

Query Match 83.0%; Score 44; DB 1; Length 98;
Best Local Similarity 87.5%; Pred. No. 0.63; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1

Qy 2 TDLVCYEQ 9
|||||
Db 20 TDLFCYEQ 27

RESULT 6
W7WL42
E7 protein - human papillomavirus type 42
C;Species: human papillomavirus type 42
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: F39451
R;Philipp, W.; Honore, N.; Sapp, M.; Cole, S.T.; Streeck, R.E.
Virology 186, 331-334, 1992
A;Title: Human papillomavirus type 42: new sequence, conserved genome organization.
A;Reference number: A39451; MUID:92087479; PMID:1309278
A;Accession: F39451
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-93 <PHI>
A;Cross-references: UNIPROT:P27231; GB:M73236
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation

Query Match 81.1%; Score 43; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.91; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

Qy 3 DLYCYEQ 9
Db 24 DLYCYEQ 30

RESULT 7
WTWLS1
E7 protein - human papillomavirus type 31
C:Species: human papillomavirus type 31
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: B32444
R:Goldsbrough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virol. 171, 306-311, 1989
A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated virus
A:Reference number: A94398; MUID:89299478; PMID:2545036
A:Accession: B32444
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-98 <GOL>
A:Cross-references: UNIPROT:P17387; GB:J04353; NID:G333048; PIDN:AAA46951.1; PID:G459917
C:Comment: This protein may be involved in the oncogenic potential of this virus.
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:58-94/Region: zinc finger CCCC motif

Query Match 81.1%; Score 43; DB 1; Length 98;
Best Local Similarity 87.5%; Pred. No. 0.95; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TDLYCYEQ 9
Db 20 TDLHCYEQ 27

RESULT 8
S36510
E7 protein - human papillomavirus type 32
C:Species: human papillomavirus type 32
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36510
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36510
A:Molecule type: DNA
A:Residues: 1-104
A:Cross-references: UNIPROT:P36827; EMBL:X74475; NID:G396981; PIDN:CAA52550.1; PID:G3969
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 81.1%; Score 43; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DLYCYEQ 9
Db 30 DLYCYEQ 36

RESULT 9
WTWLS
E7 protein - human papillomavirus type 1a
C:Species: human papillomavirus type 1a
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: C17475
R:Danos, O.; Katinka, M.; Yaniv, M.
EMBO J. 1, 231-236, 1982
A:Title: Human papillomavirus 1a complete DNA sequence: a novel type of genome organization
A:Reference number: A90970; MUID:84182467; PMID:6325156
A:Accession: C17475

A:Molecule type: DNA
A:Residues: 1-93 <DAN>
A:Cross-references: UNIPROT:P06465; GB:V01116; GB:X03321; NID:G60966; PIDN:CAA24316.1; P1
R:Danos, O.; Engel, L.W.; Chen, E.Y.; Yaniv, M.; Howley, P.M.
J. Virol. 46, 557-566, 1983
A:Title: Comparative analysis of the human type 1a and bovine type 1 papillomavirus genome
A:Reference number: A92993; MUID:83189357; PMID:6302319
A:Contents: annotation
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 75.5%; Score 40; DB 1; Length 93;
Best Local Similarity 85.7%; Pred. No. 3.1; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DLYCYEQ 9
Db 23 DLYCYEQ 29

RESULT 10
S36474
E7 protein - human papillomavirus type 15
C:Species: human papillomavirus type 15
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36474
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36474
A:Molecule type: DNA
A:Residues: 1-93
A:Cross-references: UNIPROT:P36820; EMBL:X74468; NID:G396924; PIDN:CAA52507.1; PID:G3969
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 75.5%; Score 40; DB 2; Length 93;
Best Local Similarity 75.0%; Pred. No. 3.1; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TDLYCYEQ 9
Db 22 TDLHCYEQ 29

RESULT 11
S36591
E7 protein - human papillomavirus type 9
C:Species: human papillomavirus type 9
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36591
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36591
A:Molecule type: DNA
A:Residues: 1-93
A:Cross-references: UNIPROT:P36817; EMBL:X74464; NID:G397068; PIDN:CAA52484.1; PID:G3970
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 75.5%; Score 40; DB 2; Length 93;
Best Local Similarity 66.7%; Pred. No. 3.1; Mismatches 2; Indels 1; Gaps 0;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 22 TADLHCYEQ 30

RESULT 12

S36480
E7 protein - human papillomavirus type 17
C:Species: human papillomavirus type 17
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36480
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36480
A:Molecule type: DNA
A:Residues: 1-95
A:Cross-references: UNIPROT:P36821; EMBL:X74469; NID:g396932; PIDN:CAA52513.1; PID:g396932
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 75.5%; Score 40; DB 2; Length 95;
Best Local Similarity 75.0%; Pred. No. 3.2;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TDLYCYEQ 9
|||:||||
Db 22 TDLCYEE 29

RESULT 13
S36504
E7 protein - human papillomavirus type 30
C:Species: human papillomavirus type 30
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36504
R:Delius, H.; Hcfmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36504
A:Molecule type: DNA
A:Residues: 1-105
A:Cross-references: UNIPROT:P36826; EMBL:X74474; NID:g396973; PIDN:CAA52544.1; PID:g396932
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 71.7%; Score 38; DB 2; Length 105;
Best Local Similarity 85.7%; Pred. No. 7.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DLJCYEQ 9
|||:||||
Db 22 DLHCYEQ 28

RESULT 14
B46113
protein kinase (EC 2.7.1.37) - cercopithecine herpesvirus 9 (strain DHV)
N:Alternate names: kinase-related transforming protein; proto-oncogene protein-serine/threonine kinase
C:Species: cercopithecine herpesvirus 9
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C:Accession: B46113
R:Fletcher III, T.M.; Gray, W.L.
Virology 193, 762-773, 1993
A:Title: DNA sequence and genetic organization of the unique short (Us) region of the simian virus 40 genome
A:Reference number: B46113; MUID:93212509; PMID:8384754
A:Accession: B46113
A:Molecule type: DNA
A:Residues: 1-345 <FILE>
A:Cross-references: UNIPROT:Q04543; GB:L07067; NID:g310715; PIDN:AAA47887.1; PID:g310717
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase; transformant
F:47-310/Domain: protein kinase homology <KIN>
F:78/Active site: Lys #status predicted

Query Match 71.7%; Score 38; DB 1; Length 345;
Best Local S-milarity 100.0%; Pred. No. 23;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TDLYCY 7
|||||
Db 122 TDLYCY 127

RESULT 15
TVB866
protein kinase (EC 2.7.1.37) - human herpesvirus 3
N:Alternate names: kinase-related transforming protein; proto-oncogene protein-serine/threonine kinase
C:Species: human herpesvirus 3, varicella-zoster virus
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C:Accession: E27345
R:Davidson, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1816, 1986
A:Title: The complete DNA sequence of varicella-zoster virus.
A:Reference number: A27345; MUID:86306657; PMID:3018124
A:Accession: E27345
A:Molecule type: DNA
A:Residues: 1-393 <DAV>
A:Cross-references: UNIPROT:P09251; EMBL:X04370; NID:g59989; PIDN:CAA27949.1; PID:g60055
C:Genetics: 66
A:Gene: 66
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase; transformant
F:91-355/Domain: protein kinase homology <KIN>
F:122/Active site: Lys #status predicted

Query Match 71.7%; Score 38; DB 1; Length 393;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TDLYCY 7
|||||
Db 166 TDLYCY 171

Search completed: June 28, 2005, 21:27:53
Job time : 12.15 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds
(without alignments)
59.826 Million cell updates/sec

Title: US-08-170-344-38

Perfect score: 53

Sequence: 1 TTDLYCYBQ 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	15	16	US-10-476-570-47
2	53	100.0	15	16	US-10-306-541-65
3	53	100.0	15	16	US-10-306-541-81
4	53	100.0	20	16	US-10-432-465-45
5	53	100.0	20	16	US-10-890-526-70
6	53	100.0	21	16	US-10-612-818-7
7	53	100.0	21	16	US-10-476-570-15
8	53	100.0	30	10	US-09-828-845-3
9	53	100.0	30	17	US-10-827-007-3
10	53	100.0	30	17	US-10-827-083-3
11	53	100.0	98	9	US-09-728-466-1

12	53	100.0	98	9	US-09-820-765-4	Sequence 4, Appli
13	53	100.0	98	9	US-09-824-017-4	Sequence 4, Appli
14	53	100.0	98	10	US-09-986-118A-4	Sequence 4, Appli
15	53	100.0	98	14	US-10-267-311-8	Sequence 8, Appli
16	53	100.0	98	14	US-10-177-390-8	Sequence 8, Appli
17	53	100.0	98	14	US-10-201-764-19	Sequence 19, Appli
18	53	100.0	98	15	US-10-392-113-29	Sequence 29, Appli
19	53	100.0	98	15	US-10-654-129-4	Sequence 4, Appli
20	53	100.0	98	15	US-10-681-410-19	Sequence 19, Appli
21	53	100.0	98	16	US-10-772-988-3	Sequence 3, Appli
22	53	100.0	98	16	US-10-479-541-5	Sequence 5, Appli
23	53	100.0	98	17	US-10-042-526A-4	Sequence 4, Appli
24	53	100.0	98	17	US-10-657-399-1	Sequence 1, Appli
25	53	100.0	98	17	US-10-858-384-12	Sequence 12, Appli
26	53	100.0	98	17	US-10-484-063-26	Sequence 26, Appli
27	53	100.0	98	17	US-10-343-448-5	Sequence 5, Appli
28	53	100.0	98	17	US-10-679-956-8	Sequence 8, Appli
29	53	100.0	98	17	US-10-367-057-17	Sequence 17, Appli
30	53	100.0	99	15	US-10-115-440-7	Sequence 7, Appli
31	53	100.0	111	16	US-10-472-724-4	Sequence 4, Appli
32	53	100.0	121	14	US-10-267-311-12	Sequence 12, Appli
33	53	100.0	121	17	US-10-679-956-12	Sequence 12, Appli
34	53	100.0	198	14	US-10-267-311-35	Sequence 35, Appli
35	53	100.0	198	17	US-10-679-956-35	Sequence 35, Appli
36	53	100.0	220	13	US-10-000-903-1	Sequence 1, Appli
37	53	100.0	220	17	US-10-899-771-1	Sequence 1, Appli
38	53	100.0	239	13	US-10-000-903-12	Sequence 12, Appli
39	53	100.0	239	17	US-10-899-771-12	Sequence 12, Appli
40	53	100.0	266	9	US-09-367-309A-1	Sequence 1, Appli
41	53	100.0	289	15	US-10-115-440-5	Sequence 5, Appli
42	53	100.0	295	14	US-10-267-311-33	Sequence 33, Appli
43	53	100.0	295	17	US-10-679-956-33	Sequence 33, Appli
44	53	100.0	324	14	US-10-267-311-25	Sequence 25, Appli
45	53	100.0	324	17	US-10-679-956-25	Sequence 25, Appli

ALIGNMENTS

RESULT 1

US-10-476-570-47
; Sequence 47, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E7 13-27

Query Match 100.0%; Score 53; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 TTDLYCYEQ 9
      |||||
Db      7 TTDLYCYEQ 15

RESULT 2
US-10-306-541-65
; Sequence 65, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 65
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-65

Query Match      100.0%; Score 53; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTDLYCYEQ 9
      |||||
Db      2 TTDLYCYEQ 10

RESULT 3
US-10-306-541-81
; Sequence 81, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 81
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-81

Query Match      100.0%; Score 53; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTDLYCYEQ 9
      |||||
Db      1 TTDLYCYEQ 9

RESULT 4
US-10-432-465-45
; Sequence 45, Application US/10432465
; Publication No. US20040091479A1
; GENERAL INFORMATION:
; APPLICANT: Nieland, John
; APPLICANT: Kaufmann, Andreas
; APPLICANT: Kather, Angela
```

```
; APPLICANT: Schinz, Manuela
; TITLE OF INVENTION: T-Cell Epitopes of the Papillomavirus L1
; TITLE OF INVENTION: Protein and E7 Protein and Their Use in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/077001
; CURRENT APPLICATION NUMBER: US/10/432,465
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/14037
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 10059631.2
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-432-465-45

Query Match      100.0%; Score 53; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTDLYCYEQ 9
      |||||
Db      8 TTDLYCYEQ 16

RESULT 5
US-10-890-526-70
; Sequence 70, Application US/10890526
; Publication No. US20040258708A1
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/10/890,526
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: US/09/980,177
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-890-526-70

Query Match      100.0%; Score 53; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTDLYCYEQ 9
      |||||
Db      8 TTDLYCYEQ 16

RESULT 6
US-10-612-818-7
; Sequence 7, Application US/10612818
; Publication No. US20040110925A1
; GENERAL INFORMATION:
; APPLICANT: Impact Diagnostics
; APPLICANT: Impact Diagnostics
; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomaviruses
; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papil
```

US-09-980-177A-70

Query Match 100.0%; Score 53; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
 Db 8 TTDLYCYEQ 16

RESULT 5

US-08-075-541D-36
 ; Sequence 36, Application US/08075541D
 ; Patent No. 6183745
 ; GENERAL INFORMATION:
 ; APPLICANT: TINDLE, ROBERT
 ; APPLICANT: FERNANDO, GERMAIN
 ; APPLICANT: FRAZER, IAN
 ; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
 ; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PANITCH, SCHWARZE JACOBS & NADEL, P.C.
 ; STREET: 1601 MARKET STREET, 36TH FLOOR
 ; CITY: PHILADELPHIA
 ; STATE: PENNSYLVANIA
 ; COUNTRY: USA
 ; ZIP: 19103-2398

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/075.541D
 FILING DATE: 10-JUN-1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: AU pk 3876
 FILING DATE: 12-DEC-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: pct/au91/00575
 FILING DATE: 12-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: NADEL, ALAN S
 REGISTRATION NUMBER: 27,363
 REFERENCE/DOCKET NUMBER: 8795-4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-567-2020
 TELEFAX: 215-567-2991
 INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:
 LENGTH: 21 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-075-541D-36

Query Match 100.0%; Score 53; DB 3; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
 Db 3 TTDLYCYEQ 11

RESULT 6

US-08-363-586-1
 ; Sequence 1, Application US/08363586
 ; Patent No. 5629161

GENERAL INFORMATION:

APPLICANT: Mueller, Martin
 APPLICANT: Gissmann, Iutz
 TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
 TITLE OF INVENTION: Peptides for the Diagnostic Purpose
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ADDRESSEE: Dunner
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3315

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/363.586
 FILING DATE: 23-DEC-1994
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/909,296
 FILING DATE: 09-JUL-1992
 APPLICATION NUMBER: EP 9111720.8
 FILING DATE: 13-JUL-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Wadler, Linda A.
 REGISTRATION NUMBER: 33,218
 REFERENCE/DOCKET NUMBER: 02481-1195-00000

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-363-586-1

Query Match 100.0%; Score 53; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0067;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
 Db 14 TTDLYCYEQ 22

RESULT 7

US-08-934-915-51
 ; Sequence 51, Application US/08934915
 ; Patent No. 5932412

GENERAL INFORMATION:
 APPLICANT: DILLNER, JOAKIM
 APPLICANT: DILLNER, LENA
 APPLICANT: CHENG, HWEI-MING
 TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
 TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
 TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
 TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
 TITLE OF INVENTION: DIAGNOSTIC PURPOSES
 NUMBER OF SEQUENCES: 193
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MASON & ASSOCIATES, P.A.
 STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
 CITY: CLEARWATER
 STATE: FLORIDA
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-51

Query Match 100.0%; Score 53; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 18 TTDLYCYEQ 26

RESULT 8

US-09-486-394-1
Sequence 1, Application US/09486394
Patent No. 6478749
GENERAL INFORMATION:
APPLICANT: Hopfl, Reinhard
TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
FILE REFERENCE: 032929-001
CURRENT APPLICATION NUMBER: US/09/486,394
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/04773
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: DE 197 37 409.3
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent in version 3.1
SEQ ID NO 1
LENGTH: 30
TYPE: PRT
ORGANISM: Human papillomavirus type 16
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(30)
OTHER INFORMATION: E7 peptide.
US-09-486-394-1

Query Match 100.0%; Score 53; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

RESULT 9

US-09-828-645-3

Sequence 3, Application US/09828645
Patent No. 6743593
GENERAL INFORMATION:
APPLICANT: Hu, Yao Xiong
TITLE OF INVENTION: Immunological Methodology for Discerning Human Papillomavirus
FILE REFERENCE: 146-1-002
CURRENT APPLICATION NUMBER: US/09/828,645
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/194,796
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent in version 3.1
SEQ ID NO 3
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Derived from the E7 early region of HPV-16
US-09-828-645-3

Query Match 100.0%; Score 53; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 14 TTDLYCYEQ 22

RESULT 10

US-08-406-248-6
Sequence 6, Application US/08406248
Patent No. 5736318
GENERAL INFORMATION:
APPLICANT: Munger, Karl
APPLICANT: Jones, D. Leanne
TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
TITLE OF INVENTION: TRANSFORMED CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Kusmer
STREET: 200 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,248
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: HAZ-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-406-248-6

Query Match 100.0%; Score 53; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-38
Perfect score: 53
Sequence: 1 TTDLYCYEQ 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	18	3	US-08-075-541D-45
2	53	100.0	20	2	US-08-934-915-47
3	53	100.0	20	3	US-08-075-541D-46
4	53	100.0	20	4	US-09-980-177A-70
5	53	100.0	21	3	US-08-075-541D-36
6	53	100.0	30	1	US-08-363-586-1
7	53	100.0	30	2	US-08-934-915-51
8	53	100.0	30	4	US-09-486-394-1
9	53	100.0	30	4	US-08-828-645-3
10	53	100.0	98	1	US-08-406-248-6
11	53	100.0	98	3	US-08-075-541D-42
12	53	100.0	98	3	US-09-382-616A-1
13	53	100.0	98	3	US-08-944-368A-4
14	53	100.0	98	3	US-09-820-764-4
15	53	100.0	98	4	US-09-613-303-8
16	53	100.0	98	4	US-09-566-420-19
17	53	100.0	98	4	US-09-986-118A-4
18	53	100.0	98	4	US-09-728-466-1
19	53	100.0	98	4	US-09-824-017-4
20	53	100.0	98	4	US-10-267-311-8
21	53	100.0	98	4	US-10-201-764-19
22	53	100.0	98	4	US-09-637-746-3
23	53	100.0	98	4	US-09-501-097A-7
24	53	100.0	98	4	US-09-980-523A-12
25	53	100.0	121	4	US-09-613-303-12
26	53	100.0	121	4	US-10-267-311-12
27	53	100.0	172	3	US-08-860-165-12

28	53	100.0	172	3	US-09-359-382-12	Sequence 12, Appl
29	53	100.0	198	4	US-09-613-303-35	Sequence 35, Appl
30	53	100.0	198	4	US-10-267-311-35	Sequence 35, Appl
31	53	100.0	220	3	US-09-485-885-1	Sequence 1, Appl
32	53	100.0	239	3	US-09-485-885-12	Sequence 12, Appl
33	53	100.0	253	2	US-08-459-818-20	Sequence 20, Appl
34	53	100.0	253	2	US-08-889-666-20	Sequence 20, Appl
35	53	100.0	253	2	US-08-465-078-20	Sequence 20, Appl
36	53	100.0	253	2	US-08-725-776-20	Sequence 20, Appl
37	53	100.0	253	2	US-08-488-062-20	Sequence 20, Appl
38	53	100.0	263	1	US-08-117-083-9	Sequence 9, Appl
39	53	100.0	266	3	US-08-860-165-10	Sequence 10, Appl
40	53	100.0	266	4	US-09-359-382-10	Sequence 10, Appl
41	53	100.0	266	4	US-09-367-309A-1	Sequence 1, Appl
42	53	100.0	287	4	US-09-501-097A-25	Sequence 25, Appl
43	53	100.0	295	4	US-09-613-303-33	Sequence 33, Appl
44	53	100.0	295	4	US-10-267-311-33	Sequence 33, Appl
45	53	100.0	324	4	US-09-613-303-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-08-075-541D-45
; Sequence 45, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-45

Query Match 100.0%; Score 53; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
| | | | | | | |
Db 8 TTDLYCYEQ 16

RESULT 2

US-08-934-915-47
; Sequence 47, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-47

Query Match 100.0%; Score 53; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
| | | | | | | |
Db 3 TTDLYCYEQ 11

RESULT 3

US-08-075-541D-46
; Sequence 46, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN

; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-46

Query Match 100.0%; Score 53; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
| | | | | | | |
Db 2 TTDLYCYEQ 10

RESULT 4

US-09-980-177A-70
; Sequence 70, Application US/09980177A
; Patent No. 6838084
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/09/980,177A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16

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; TITLE OF INVENTION: Associated Cancers
; FILE REFERENCE: 3352-2-2
; CURRENT APPLICATION NUMBER: US/10/612,818
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/394,172
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/828,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E7 early coding region of HPV 16
US-10-612-818-7

Query Match      100.0%; Score 53; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTDLVCYEQ 9
Db      2 TTDLVCYEQ 10

RESULT 7
US-10-476-570-15
; Sequence 15, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLERE, Bernard
; APPLICANT: BOURGAULT-VIGLADA, Isabelle
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 15
; LENGTH: 21
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E7 7-27
US-10-476-570-15

Query Match      100.0%; Score 53; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTDLVCYEQ 9
Db      13 TTDLVCYEQ 21

RESULT 8
US-09-828-645-3
; Sequence 3, Application US/09828645
; Publication No. US20030027750A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yao Xiong
; TITLE OF INVENTION: Immunological Methodology for Discerning Human Papillomavirus
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; FILE REFERENCE: 146-1-002
; CURRENT APPLICATION NUMBER: US/09/828,645
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/194,796
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E7 early region of HPV-16
US-09-828-645-3

Query Match      100.0%; Score 53; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTDLVCYEQ 9
Db      14 TTDLVCYEQ 22

RESULT 9
US-10-827-007-3
; Sequence 3, Application US/10827007
; Publication No. US20050042599A1
; GENERAL INFORMATION:
; APPLICANT: Impact Diagnostics
; APPLICANT: Hu, Yao Xiong
; TITLE OF INVENTION: Immunological Methodology for Discerning Human Papillomavirus
; TITLE OF INVENTION: Contemplating Peptides From the E7 Early Coding Region of HPV 16
; FILE REFERENCE: 3352-2-1-3
; CURRENT APPLICATION NUMBER: US/10/827,007
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 09/828,645
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/194,796
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Derived from the E7-early coding region of HPV-16
US-10-827-007-3

Query Match      100.0%; Score 53; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTDLVCYEQ 9
Db      14 TTDLVCYEQ 22

RESULT 10
US-10-827-083-3
; Sequence 3, Application US/10827083
; Publication No. US20050042600A1
; GENERAL INFORMATION:
; APPLICANT: Impact Diagnostics
; APPLICANT: Hu, Yao Xiong
; TITLE OF INVENTION: Immunological Methodology for Discerning Human Papillomavirus
; TITLE OF INVENTION: Contemplating Peptides From the E7 Early Coding Region of HPV 16
; FILE REFERENCE: 3352-2-1-4
; CURRENT APPLICATION NUMBER: US/10/827,083
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 09/828,645
; PRIOR FILING DATE: 2001-04-05
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; PRIOR APPLICATION NUMBER: US 60/194,796
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Derived from the E7 early coding region of HPV-16
US-10-827-083-3

Query Match          100.0%; Score 53; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 14 TTDLYCYEQ 22

RESULT 11
US-09-728-466-1
; Sequence 1, Application US/09728466
; Patent No. US20010029022A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Christopher
; APPLICANT: He, Wanxia
; TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
; FILE REFERENCE: 28341/6216
; CURRENT APPLICATION NUMBER: US/09/728,466
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/382,616
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Papillomavirus sylvilagi
US-09-728-466-1

Query Match          100.0%; Score 53; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

RESULT 12
US-09-820-765-4
; Sequence 4, Application US/09820765
; Publication No. US20020039584A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; APPLICANT: HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/824,017
; FILING DATE: 03-Apr-2001
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/026,896
; FILING DATE: 1998-02-20
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/820,765
; FILING DATE: 30-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-765-4

Query Match          100.0%; Score 53; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

RESULT 13
US-09-824-017-4
; Sequence 4, Application US/09824017
; Publication No. US2002019768A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; APPLICANT: HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/824,017
; FILING DATE: 03-Apr-2001
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/026,896
; FILING DATE: 1998-02-20
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-824-017-4

Query Match      100.0%; Score 53; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

RESULT 14
US-09-986-118A-4
; Sequence 4, Application US/09986118A
; Publication No. US20030021806A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; HALEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/986,118A
; FILING DATE: 07-No. US20030021806A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-986-118A-4

Query Match      100.0%; Score 53; DB 10; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

RESULT 15
US-10-267-311-8
; Sequence 8, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
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; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-8

Query Match      100.0%; Score 53; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
Db 19 TTDLYCYEQ 27

Search completed: June 29, 2005, 04:19:29
Job time : 58.85 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-37
Perfect score: 50
Sequence: 1 MSCCRSRT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_eprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	103	2 Q919D6	Q919D6 human papil
2	50	100.0	130	2 Q919B4	Q919B4 human papil
3	50	100.0	130	2 Q919B8	Q919B8 human papil
4	50	100.0	130	2 Q919C0	Q919C0 human papil
5	50	100.0	130	2 Q919C2	Q919C2 human papil
6	50	100.0	130	2 Q919C8	Q919C8 human papil
7	50	100.0	130	2 Q919D0	Q919D0 human papil
8	50	100.0	138	2 Q919D2	Q919D2 human papil
9	50	100.0	143	2 Q919B6	Q919B6 human papil
10	50	100.0	143	2 Q919C4	Q919C4 human papil
11	50	100.0	151	2 Q12335	Q12335 human papil
12	50	100.0	151	2 Q12336	Q12336 human papil
13	50	100.0	151	2 Q76TS0	Q76TS0 human papil
14	50	100.0	151	2 Q77E16	Q77E16 human papil
15	50	100.0	151	2 Q77E16	Q77E16 human papil
16	50	100.0	151	2 Q77JC7	Q77JC7 human papil
17	50	100.0	151	2 Q77ZJ5	Q77ZJ5 human papil
18	50	100.0	151	2 Q80963	Q80963 human papil
19	50	100.0	151	2 Q80966	Q80966 human papil
20	50	100.0	151	2 Q89640	Q89640 human papil
21	50	100.0	151	2 Q89648	Q89648 human papil
22	50	100.0	151	2 Q89708	Q89708 human papil
23	50	100.0	151	2 Q89755	Q89755 human papil
24	50	100.0	151	2 Q89852	Q89852 human papil
25	50	100.0	151	2 Q89887	Q89887 human papil
26	50	100.0	151	2 Q8B564	Q8B564 human papil
27	50	100.0	151	2 Q8B564	Q8B564 human papil
28	50	100.0	151	2 Q8B20	Q8B20 human papil
29	50	100.0	151	2 Q8B21	Q8B21 human papil
30	50	100.0	151	2 Q9W8C3	Q9W8C3 human papil
31	50	100.0	151	2 Q9W931	Q9W931 human papil

32 50 100.0 151 2 Q9WME2 Q9wmp2 human papil
33 50 100.0 151 2 Q9WME3 Q9wmp3 human papil
34 50 100.0 151 2 Q9WME4 Q9wmp4 human papil
35 50 100.0 151 2 Q9WME5 Q9wmp5 human papil
36 50 100.0 151 1 VE6 HPV16 P03126 human papil
37 50 100.0 158 2 Q8JMU8 Q8jmu8 human papil
38 50 100.0 158 2 Q8QHNO Q8qhn0 human papil
39 50 100.0 158 2 Q8QHP5 Q8qhp5 human papil
40 50 100.0 158 2 Q8QHT0 Q8qht0 human papil
41 50 100.0 158 2 Q8QRD5 Q8qrd5 human papil
42 50 100.0 158 2 Q8QRD6 Q8qrd6 human papil
43 50 100.0 158 2 Q8QRD7 Q8qrd7 human papil
44 50 100.0 158 2 Q8QRD8 Q8qrd8 human papil
45 50 100.0 158 2 Q8QRD9 Q8qrd9 human papil

ALIGNMENTS

RESULT 1

Q919D6 PRELIMINARY; PRT; 103 AA.
ID Q919D6
AC Q919D6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE E6 protein (Fragment).
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040692; AAL01342.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;
Query Match Similarity 100.0%; Score 50; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.53; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
Qy 1 MSCCRSRT 9
Db 89 MSCCRSRT 97

RESULT 2

Q919B4 PRELIMINARY; PRT; 130 AA.
ID Q919B4
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE E6 protein (Fragment).
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).

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DR EMBL; AF404703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227BEDDC CRC64;

Query Match 100.0%; Score 50; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
Db 116 MSCCRSRT 124

RESULT 3
ID Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01359.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match 100.0%; Score 50; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
Db 116 MSCCRSRT 124

RESULT 4
ID Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;
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DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
Db 116 MSCCRSRT 124

RESULT 5
ID Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01355.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
Db 116 MSCCRSRT 124

RESULT 6
ID Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404696; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;
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Query Match 100.0%; Score 50; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
Db 116 MSCCRSRT 124

RESULT 7
Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0; (Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040695; AAL01347.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15735 MW; 98FB30EDCA21AF3 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
Db 116 MSCCRSRT 124

RESULT 8
Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2; (Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040694; AAL01345.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481ESA90895FC2 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.69;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSCCRSRT 9
Db 124 MSCCRSRT 132

RESULT 9
Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6; (Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040702; AAL01361.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match 100.0%; Score 50; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
Db 129 MSCCRSRT 137

RESULT 10
Q919C4 PRELIMINARY; PRT; 143 AA.
AC Q919C4; (Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040698; AAL01353.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9

Db 129 MSCCRSRT 137
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RESULT 11
O12335 PRELIMINARY; PRT; 151 AA.
ID O12335
AC O12335;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Torneello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Girardo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208 (1997).
DR EMBL; AF003015; AAB70732.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18238 MW; BFF32A8B016CC88B CRC64;

Query Match 100.0%; Score 50; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.75; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MSCCRSRT 9
|||||
Db 137 MSCCRSRT 145

RESULT 12
O12336 PRELIMINARY; PRT; 151 AA.
ID O12336
AC O12336;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Torneello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Girardo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208 (1997).
DR EMBL; AF003016; AAB70733.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match 100.0%; Score 50; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.75; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MSCCRSRT 9
|||||

Db 137 MSCCRSRT 145

RESULT 13
Q76TSO PRELIMINARY; PRT; 151 AA.
ID Q76TSO
AC Q76TSO;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34114; AAA91661.1; -;
DR EMBL; U34125; AAA91672.1; -;
DR EMBL; U34130; AAA91677.1; -;
DR EMBL; U34131; AAA91678.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.75; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MSCCRSRT 9
|||||
Db 137 MSCCRSRT 145

RESULT 14
Q778I6 PRELIMINARY; PRT; 151 AA.
ID Q778I6
AC Q778I6;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vosseu M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325 (2000).
DR EMBL; AJ388056; CAB45104.1; -;
DR EMBL; AJ388061; CAB45114.1; -;
DR EMBL; AJ388066; CAB45124.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.

DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
| | | | |
Db 137 MSCCRSRT 145

RESULT 15

Q77E16 PRELIMINARY; PRT; 151 AA.
AC Q77E16;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 oncoprotein (E6 protein).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M.; Vaeteswoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AF469197; AAO15691.1; -.
DR EMBL; AJ388063; CAB45118.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;

Query Match 100.0%; Score 50; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
| | | | |
Db 137 MSCCRSRT 145

Search completed: June 28, 2005, 21:24:08
Job time : 55.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-37

Perfect score: 50

Sequence: 1 MSCCRSRT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	158	1	WSWLS
2	40	80.0	371	2	G97530
3	37	74.0	837	2	A2112
4	37	74.0	870	2	T35338
5	36	72.0	152	2	T34649
6	36	72.0	303	2	AB3504
7	36	72.0	670	2	T10666
8	36	72.0	1905	2	I51553
9	35	70.0	98	2	I54366
10	35	70.0	141	2	C70575
11	35	70.0	151	2	S60314
12	35	70.0	166	2	S69692
13	35	70.0	229	2	S60454
14	35	70.0	414	2	T45639
15	34	68.0	716	2	T47449
16	34	68.0	757	2	C32052
17	34	68.0	757	2	C95344
18	34	68.0	1698	2	S51869
19	33.5	67.0	271	2	T01767
20	33	66.0	78	2	E70891
21	33	66.0	83	2	E95291
22	33	66.0	212	2	T47947
23	33	66.0	224	2	T28136
24	33	66.0	591	2	I48141
25	33	66.0	747	2	T33488
26	32	64.0	61	1	A59136
27	32	64.0	61	1	NINJ16
28	32	64.0	61	1	NINJ1R
29	32	64.0	61	1	NINJ1S

30 32 64.0 61 2 S42858
31 32 64.0 87 2 AD3436
32 32 64.0 125 1 VSWTA2
33 32 64.0 133 1 VSBH2
34 32 64.0 136 2 S22977
35 32 64.0 152 1 KRSHHC
36 32 64.0 152 2 T47111
37 32 64.0 152 2 T47109
38 32 64.0 152 2 T47108
39 32 64.0 152 2 T47112
40 32 64.0 214 2 D84899
41 32 64.0 279 2 T23663
42 32 64.0 297 2 A23543
43 32 64.0 299 2 C97102
44 32 64.0 337 2 T27660
45 32 64.0 339 2 T46713

ALIGNMENTS

RESULT 1

WSWLS

Protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human papillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10427

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C:Genetics:

A:Gene: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 50; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.4;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9

Db 144 MSCCRSRT 152

RESULT 2

G97530

Probable zinc-binding alcohol dehydrogenase [imported] - Agrobacterium tumefaciens (strain

C:Species: Agrobacterium tumefaciens

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C:Accession: G97530

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,

A.: Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A:Reference number: A97359; MUID:21608551; PMID:11743194

A:Accession: G97530

A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-371 <KUR>
A:Cross-references: UNIPROT:Q8UF19; GB:AE007869; PIDN:NAK87200.1; PID:gl5156478; GSPDB:C
C:Genetics:
A:Gene: AGR_C_2601
A:Map position: circular chromosome
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

Query Match 80.0%; Score 40; DB 2; Length 371;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
| | | | |
Db 1 MECCRSRT 9
| | | | |

RESULT 3
A42112
mucin-like peptide MLP 2677 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Mar-2004
C:Accession: A42112
R:Yu, G.; Huan, L.J.; Khatri, I.A.; Wang, D.; Bennick, A.; Fahim, R.E.; Forstner, G.G.;
J. Biol. Chem. 267, 5401-5407, 1992
A:Title: cDNA for the carboxyl-terminal region of a rat intestinal mucin-like peptide.
A:Reference number: A42112; MUID:92184794; PMID:1371999
A:Accession: A42112
A:Status: preliminary
A:Molecule type: nucleic acid; protein
A:Residues: 1-837 <XUI>
A:Experimental source: intestine
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIP:87420)
F:582-650/Domain: von Willebrand factor type C repeat homology <VWC>

Query Match 74.0%; Score 37; DB 2; Length 837;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SCCRST 9
| | | | |
Db 777 SCREERT 784
| | | | |

RESULT 4
T25338
hypothetical protein ZK1037.11 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25338; T27667
R:Mortimore, B.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20018
A:Accession: T25338
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-870 <WIL>
A:Cross-references: UNIPROT:Q9XTQ4; EMBL:Z82057; PIDN:CAB04861.1; GSPDB:GN00023; CESP:ZK
A:Experimental source: clone T26H8
R:Baaham, V.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z20401
A:Accession: T27667
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-870 <W12>
A:Cross-references: EMBL:Z81142; PIDN:CAB03512.1; GSPDB:GN00023; CESP:ZK1037.11
A:Experimental source: clone ZK1037
C:Genetics:
A:Gene: CESP:ZK1037.11
A:Map position: 5
A:Introns: 161/1; 162/3; 212/3; 233/3; 301/3; 517/2; 562/3; 578/1; 825/2

Query Match 74.0%; Score 37; DB 2; Length 870;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SCCRSSR 8
| | | | |
Db 279 SCKSSR 285
| | | | |

RESULT 5
T34649
hypothetical protein SC1A11.02c SC1A11.02c - Streptomyces coelicolor (fragment)
C:Species: Streptomyces coelicolor
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T34649
R:Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1999
A:Reference number: Z21551
A:Accession: T34649
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-152 <SEE>
A:Cross-references: EMBL:AL035205; PIDN:CAA22742.1; GSPDB:GN00070; SCOEDB:SC1A11.02c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC1A11.02c

Query Match 72.0%; Score 36; DB 2; Length 152;
Best Local Similarity 75.0%; Pred. No. 58;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SCCRST 9
| | | | |
Db 18 ACCSSRT 25
| | | | |

RESULT 6
AE3504
tryptophan synthase (EC 4.2.1.20) [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
C:Accession: AE3504
R:DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I.
; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesc
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi
A:Reference number: AD3252; PMID:11756688
A:Accession: AE3504
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-303 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL53200.1; PID:gl7984074; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI2019
A:Map position: I

Query Match 72.0%; Score 36; DB 2; Length 303;
Best Local Similarity 75.0%; Pred. No. 87;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SCCRST 9
| | | | |
Db 10 ACCRLST 17
| | | | |

RESULT 7
T10666
hypothetical protein F6E21.40 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10666
R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16533
A;Accession: T10666
A;Molecule type: DNA
A;Residues: 1-670 <BEV>
A;Cross-references: UNIPROT:Q9M090; EMBL:AL049914; GSPDB:GN00062; ATSP:F6E21.40
A;Experimental source: cultivar Columbia; BAC clone F6E21
C;Genetics:
A;Gene: ATSP:F6E21.40
A;Map position: 4
A;Introns: 47/3; 87/1; 123/3; 203/3; 230/2; 255/3; 284/3; 305/1; 335/3; 347/3; 370/3; 39
C;Superfamily: Schizosaccharomyces pombe negative regulator of mitosis skbl

Query Match 72.0%; Score 36; DB 2; Length 670;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSS 7
Db 141 VSCCRSS 147

RESULT 8
I51553
Plexin - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51553
R;Ohka, K.; Mitutani, A.; Kawakami, A.; Murakami, Y.; Kasuya, Y.; Takagi, S.; Tanaka, H.
Neuron 14, 1189-1199, 1995
A;Title: Plexin: a novel neuronal cell surface molecule that mediates cell adhesion via
A;Reference number: I51553; MUID:95329274; PMID:7605632
A;Accession: I51553
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1905 <OHT>
A;Cross-references: UNIPROT:Q91823; GB:D38175; NID:961514; PIDN:BAA07374.1; PID:g961515
C;Keywords: duplication

Query Match 72.0%; Score 36; DB 2; Length 1905;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SCCRSRT 9
Db 1506 SCCRSPT 1513

RESULT 9
I54366
dopamine D4 receptor - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I54366
R;Nothen, M.M.; Cichon, S.; Hemmer, S.; Hebebrand, J.; Remschmidt, H.; Lehmkuhl, G.; Pou
Hum. Mol. Genet. 3, 2207-2212, 1994
A;Title: Human dopamine D4 receptor gene: frequent occurrence of a null allele and obser
A;Reference number: I54366; MUID:95187162; PMID:7881421
A;Accession: I54366
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-98 <RES>
A;Cross-references: UNIPROT:Q16303; GB:S76942; NID:9913280; PIDN:AAB33728.1; PID:g913281
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor

Query Match 70.0%; Score 35; DB 2; Length 98;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCRSSRT 9
Db 83 CCRSSST 89

RESULT 10
C70575
probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: C70575
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
Comor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome s
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70575
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-141 <COL>
A;Cross-references: GB:Z95324; GB:AL123456; NID:93261760; PIDN:CAB08586.1; PID:e315469; I
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: PPE

Query Match 70.0%; Score 35; DB 2; Length 141;
Best Local Similarity 62.5%; Pred. No. 80;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SCCRSRT 9
Db 134 TCCBRAGT 141

RESULT 11
S60314
hair keratin cysteine rich protein - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S60314
R;Fratini, A.; Powell, B.C.; Hynd, P.I.; Keough, R.A.; Rogers, G.E.
J. Invest. Dermatol. 102, 178-185, 1994
A;Title: Dietary cysteine regulates the levels of mRNAs encoding a family of cysteine-ric
A;Reference number: S60314; MUID:94149288; PMID:7508963
A;Accession: S60314
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-151 <FRA>
A;Cross-references: UNIPROT:Q28576; EMBL:X73462; NID:9512030; PIDN:CAA51841.1; PID:g51203
C;Superfamily: ultra-high-sulfur keratin

Query Match 70.0%; Score 35; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SCCRSS 7
Db 73 SCCRSS 78

RESULT 12
S69692
hypotheical protein YDR396w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: S69692
R;Dietrich, F.S.
submitted to the EMBL Data Library, July 1995
A;Description: The sequence of S. cerevisiae cosmid 9481, 9509, 9926, 9461, and lambda d
A;Reference number: S69665
A;Accession: S69692

A;Molecule type: DNA
A;Residues: 1-166 <DIE>
A;Cross-references: UNIPROT:O13522; EMBL:U32274; NID:g2194162; GSPDB:GN0000
C;Genetics:
A;Gene: MIPS:YDR396W
A;Cross-references: SGD:S0002804
A;Map position: 4R
C;Superfamily: Saccharomyces hypothetical protein YDR396W

Query Match 70.0%; Score 35; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SCCRST 7
Db 51 SCCRST 56

RESULT 13
S60454
Glucose starvation-induced protein (clone pZS3) - maize (fragment)
C;Species: Zea mays (maize)
C;Date: 27-Apr-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S60454; S49585
R;Chevalier, C.; Bourgeois, B.; Pradet, A.; Raymond, P.
Plant Mol. Biol. 28, 473-485, 1995
A;Title: Molecular cloning and characterization of six cDNAs expressed during glucose starvation
A;Reference number: S60453; MUID:95359405; PMID:7632917
A;Accession: S60454
A;Molecule type: mRNA
A;Residues: 1-229 <CHE>
A;Cross-references: UNIPROT:Q41855; EMBL:X82617; NID:g575425; PIDN:CAAS7939.1; PID:g5754

Query Match 70.0%; Score 35; DB 2; Length 229;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SCCRST 9
Db 59 ACCRAS 66

RESULT 14
T45639
Hypothetical protein F13I12.80 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
R;Accession: T45639
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, November 1999
A;Reference number: Z23010
A;Accession: T45639
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-414 <CHO>
A;Cross-references: UNIPROT:Q9SD70; EMBL:AL133292
A;Experimental source: cultivar Columbia; BAC clone F13I12
C;Genetics:
A;Map position: 3
A;Note: F13I12.80
C;Superfamily: Arabidopsis thaliana hypothetical protein At2g23160

Query Match 70.0%; Score 35; DB 2; Length 414;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCRSRT 9
Db 143 CCKSKT 155

RESULT 15
T47449
Hypothetical protein T14D3.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47449
R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K.;
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24467
A;Accession: T47449
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-716 <JOR>
A;Cross-references: UNIPROT:Q9M1V0; EMBL:AL138649
A;Experimental source: cultivar Columbia; BAC clone T14D3
C;Genetics:
A;Map position: 3
A;Introns: 50/3; 150/2; 177/3; 308/3; 548/3; 589/3
A;Note: T14D3.30

Query Match 68.0%; Score 34; DB 2; Length 716;
Best Local Similarity 75.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SCCRST 9
Db 534 SCCRST 541

Search completed: June 28, 2005, 21:27:52
Job time : 12.15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds
(without alignments)
59,826 Million cell updates/sec

Title: US-08-170-344-37

Perfect score: 50

Sequence: 1 MSCCRSRT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	50	100.0	20	17	US-10-938-249-513
3	50	100.0	24	16	US-10-476-570-44
4	50	100.0	151	14	US-10-177-390-6
5	50	100.0	151	17	US-10-484-063-20
6	50	100.0	151	17	US-10-484-063-27
7	50	100.0	158	17	US-10-858-384-2
8	50	100.0	158	17	US-10-367-057-16
9	50	100.0	171	16	US-10-472-724-2
10	50	100.0	266	9	US-09-367-309A-1
11	50	100.0	273	13	US-10-000-903-4
					Sequence 9, Appli
					Sequence 513, Appl
					Sequence 44, Appl
					Sequence 6, Appli
					Sequence 20, Appl
					Sequence 27, Appl
					Sequence 2, Appli
					Sequence 16, Appl
					Sequence 2, Appli
					Sequence 1, Appli
					Sequence 4, Appli

12	50	100.0	273	17	US-10-899-771-4	Sequence 4, Appli
13	50	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
14	50	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
15	50	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
16	50	100.0	371	17	US-10-899-771-6	Sequence 6, Appli
17	50	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
18	50	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
19	42	84.0	125	15	US-10-425-114-67214	Sequence 67214, A
20	41	82.0	35	15	US-10-424-599-245237	Sequence 245237, A
21	40	80.0	10	17	US-10-484-063-10	Sequence 10, Appl
22	40	80.0	43	10	US-09-397-945-213	Sequence 213, App
23	40	80.0	43	15	US-10-653-595-213	Sequence 213, App
24	40	80.0	137	10	US-09-397-945-211	Sequence 211, App
25	40	80.0	137	15	US-10-653-595-211	Sequence 211, App
26	38	76.0	82	15	US-10-424-599-233659	Sequence 233659, A
27	37	74.0	51	16	US-10-437-963-160782	Sequence 160782, A
28	37	74.0	67	15	US-10-424-599-204363	Sequence 204363, A
29	37	74.0	69	16	US-10-425-115-244446	Sequence 244446, A
30	37	74.0	132	16	US-10-767-701-47475	Sequence 47475, A
31	37	74.0	188	15	US-10-425-114-44271	Sequence 44271, A
32	37	74.0	245	15	US-10-425-114-65786	Sequence 65786, A
33	37	74.0	686	16	US-10-437-963-196497	Sequence 196497, A
34	36	72.0	61	9	US-09-864-761-36259	Sequence 36259, A
35	36	72.0	71	16	US-10-437-963-173711	Sequence 173711, A
36	36	72.0	100	16	US-10-437-963-135435	Sequence 135435, A
37	36	72.0	101	16	US-10-425-115-310834	Sequence 310834, A
38	36	72.0	131	16	US-10-425-115-310833	Sequence 310833, A
39	36	72.0	138	16	US-10-425-115-186241	Sequence 186241, A
40	36	72.0	148	16	US-10-408-765A-2274	Sequence 2274, Ap
41	36	72.0	212	16	US-10-425-115-207769	Sequence 207769, A
42	36	72.0	224	15	US-10-425-114-57284	Sequence 57284, A
43	36	72.0	248	15	US-10-424-599-270059	Sequence 270059, A
44	36	72.0	254	15	US-10-425-114-47308	Sequence 47308, A
45	36	72.0	347	16	US-10-437-963-111831	Sequence 111831, A

ALIGNMENTS

RESULT 1
US-10-484-063-9
; Sequence 9, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-9

Query Match 100.0%; Score 50; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches: 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSCCRSRT 9
Db 7 MSCCRSRT 15

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RESULT 2
US-10-938-249-513
; Sequence 513, Application US/10938249
; Publication No. US20050037969A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Hematopoietic
; TITLE OF INVENTION: Cells
; FILE REFERENCE: 020054-001130US
; CURRENT APPLICATION NUMBER: US/10/938,249
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US/09/724,553
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/134,114
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,117
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,118
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/162,498
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/170,453
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 60/176,195
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/182,296
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 60/196,267
; PRIOR FILING DATE: 2000-04-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 543
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 513
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HPV16 E6 C-terminal
US-10-938-249-513

Query Match 100.0%; Score 50; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
Db 6 MSCCRSRT 14

RESULT 3
US-10-476-570-44
; Sequence 44, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980

PRIORITY FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 24
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 135-158
US-10-476-570-44

Query Match 100.0%; Score 50; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
Db 10 MSCCRSRT 18

RESULT 4
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match 100.0%; Score 50; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
Db 137 MSCCRSRT 145

RESULT 5
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20
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Query Match 100.0%; Score 50; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
| | | | | | | | | |
Db 137 MSCCRSRT 145

RESULT 6
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match 100.0%; Score 50; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
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Db 137 MSCCRSRT 145

RESULT 7
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 100.0%; Score 50; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
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Db 144 MSCCRSRT 152

RESULT 8
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 100.0%; Score 50; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
| | | | | | | | | |
Db 144 MSCCRSRT 152

RESULT 9
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 100.0%; Score 50; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
| | | | | | | | | |
Db 149 MSCCRSRT 157

RESULT 10

APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine

;; APPLICANT: Gerard, Catherine Marie Ghislaine
;; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
;; FILE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
;; FILE REFERENCE: B45124
;; CURRENT APPLICATION NUMBER: US/10/899,771
;; CURRENT FILING DATE: 2004-07-27
;; PRIOR APPLICATION NUMBER: US/09/581,976
;; PRIOR FILING DATE: 2000-06-20
;; PRIOR APPLICATION NUMBER: PCT/EP98/08563
;; PRIOR FILING DATE: 1998-12-18
;; PRIOR APPLICATION NUMBER: GB 9727262.9
;; PRIOR FILING DATE: 1997-12-24
;; NUMBER OF SEQ ID NOS: 28
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 10
;; LENGTH: 292
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus
;; OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
;; OTHER INFORMATION: 16)
US-10-899-771-10

Query Match 100.0%; Score 50; DB 17; Length 292;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
Db 269 MSCCRSRT 277

RESULT 15

US-10-000-903-6
;; Sequence 6, Application US/10000903
;; Publication No. US20020182221A1
;; GENERAL INFORMATION:
;; APPLICANT: Bruck, Claudine
;; APPLICANT: Cabezón Silva, Teresa
;; APPLICANT: Delisse, Anne-Marie Eva. Fernande
;; APPLICANT: Gerard, Catherine Marie Ghislaine
;; APPLICANT: Lombardo-Bencheikh, Angela
;; TITLE OF INVENTION: Vaccine
;; FILE REFERENCE: B45107
;; CURRENT APPLICATION NUMBER: US/10/000,903
;; CURRENT FILING DATE: 2001-10-01
;; PRIOR APPLICATION NUMBER: PCT/EP98/05285
;; PRIOR FILING DATE: 1998-08-17
;; PRIOR APPLICATION NUMBER: GB 9717953.5
;; PRIOR FILING DATE: 1997-08-22
;; NUMBER OF SEQ ID NOS: 23
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 6
;; LENGTH: 371
;; TYPE: PRT
;; ORGANISM: Homo sapien
US-10-000-903-6

Query Match 100.0%; Score 50; DB 13; Length 371;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
Db 250 MSCCRSRT 258

Search completed: June 29, 2005, 04:19:28
Job time : 58.85 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-37

Perfect score: 50

Sequence: 1 MSCCRSRT 9

Scoring table: BLOSUM62

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- Issued Patents_AA.*
- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	50	100.0	21	US-08-934-915-167	Sequence 167, App
2	50	100.0	158	US-09-980-523A-2	Sequence 2, Appl
3	50	100.0	162	US-08-316-239B-3	Sequence 3, Appl
4	50	100.0	162	US-08-316-239B-4	Sequence 4, Appl
5	50	100.0	172	US-08-860-165-12	Sequence 12, Appl
6	50	100.0	172	US-09-359-382-12	Sequence 12, Appl
7	50	100.0	266	US-08-860-165-10	Sequence 10, Appl
8	50	100.0	266	US-09-359-382-10	Sequence 10, Appl
9	50	100.0	266	US-09-367-309A-1	Sequence 1, Appl
10	50	100.0	273	US-09-485-885-4	Sequence 4, Appl
11	50	100.0	292	US-09-485-885-10	Sequence 10, Appl
12	50	100.0	371	US-09-485-885-6	Sequence 6, Appl
13	50	100.0	390	US-09-485-885-14	Sequence 14, Appl
14	38	76.0	113	US-09-252-991A-29076	Sequence 29076, A
15	37	74.0	207	US-09-270-767-32689	Sequence 32689, A
16	37	74.0	207	US-09-270-767-47906	Sequence 47906, A
17	36	72.0	136	US-09-252-991A-21156	Sequence 21156, A
18	36	72.0	230	US-09-252-991A-33122	Sequence 33122, A
19	36	72.0	953	US-09-252-991A-30039	Sequence 30039, A
20	35	70.0	44	US-09-270-767-58297	Sequence 58297, A
21	35	70.0	47	US-08-660-789-6	Sequence 6, Appl
22	35	70.0	47	US-09-074-114-6	Sequence 6, Appl
23	35	70.0	87	US-09-252-991A-25071	Sequence 25071, A
24	35	70.0	109	US-09-252-991A-29444	Sequence 29444, A
25	35	70.0	140	US-09-270-767-35721	Sequence 35721, A
26	35	70.0	140	US-09-270-767-50938	Sequence 50938, A
27	35	70.0	147	US-09-252-991A-17724	Sequence 17724, A

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Best Local Similarity 100.0%; Pred. No. 0.32;

28	35	70.0	168	4	US-09-252-991A-32502	Sequence 32502, A
29	35	70.0	214	4	US-09-270-767-42972	Sequence 42972, A
30	35	70.0	654	4	US-09-252-991A-20916	Sequence 20916, A
31	34	68.0	23	4	US-09-860-793-8	Sequence 8, Appl
32	34	68.0	31	4	US-09-894-882-360	Sequence 360, App
33	34	68.0	31	4	US-09-894-882-363	Sequence 363, App
34	34	68.0	31	4	US-09-894-882-479	Sequence 479, App
35	34	68.0	31	4	US-09-894-882-480	Sequence 480, App
36	34	68.0	70	4	US-09-894-882-359	Sequence 359, App
37	34	68.0	70	4	US-09-894-882-362	Sequence 362, App
38	34	68.0	101	4	US-09-270-767-35252	Sequence 35252, A
39	34	68.0	101	4	US-09-270-767-50469	Sequence 50469, A
40	34	68.0	120	4	US-09-252-991A-22015	Sequence 22015, A
41	34	68.0	138	4	US-09-489-039A-12930	Sequence 12930, A
42	34	68.0	146	4	US-09-252-991A-20461	Sequence 20461, A
43	34	68.0	154	4	US-09-252-991A-25612	Sequence 25612, A
44	34	68.0	171	4	US-08-311-731A-381	Sequence 381, App
45	34	68.0	179	4	US-09-252-991A-18885	Sequence 18885, A

ALIGNMENTS

RESULT 1
US-08-934-915-167
; Sequence 167, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 167:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-167

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
Db 7 MSCCRSRT 15

RESULT 2
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO91 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 50; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
Db 144 MSCCRSRT 152

RESULT 3
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 50; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
Db 144 MSCCRSRT 152

RESULT 4
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 50; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MSCCRSRT 9
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 Db 144 MSCCRSRT 152

RESULT 5

US-08-860-165-12
 ; Sequence 12, Application US/08860165A
 ; Patent No. 6004557
 ; GENERAL INFORMATION:
 ; APPLICANT: EDWARDS, Stirling John
 ; APPLICANT: COX, John Cooper
 ; APPLICANT: WEBB, Elizabeth Ann
 ; APPLICANT: FRAZER, Ian
 ; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
 ; FILE REFERENCE: 17227/130
 ; CURRENT APPLICATION NUMBER: US/08/860,165A
 ; CURRENT FILING DATE: 1997-09-22
 ; EARLIER APPLICATION NUMBER: PCT/AU95/00868
 ; EARLIER FILING DATE: 1995-12-20
 ; EARLIER APPLICATION NUMBER: AU PN0157
 ; EARLIER FILING DATE: 1994-12-20
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 172
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
 US-08-860-165-12

Query Match 100.0%; Score 50; DB 3; Length 172;
 Best Local Similarity 100.0%; Pred. No. 1.8; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
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 Db 82 MSCCRSRT 90

RESULT 6

US-09-359-382-12
 ; Sequence 12, Application US/09359382
 ; Patent No. 6306397
 ; GENERAL INFORMATION:
 ; APPLICANT: EDWARDS, Stirling John
 ; APPLICANT: COX, John Cooper
 ; APPLICANT: WEBB, Elizabeth Ann
 ; APPLICANT: FRAZER, Ian
 ; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
 ; FILE REFERENCE: 017227/0148
 ; CURRENT APPLICATION NUMBER: US/09/359,382
 ; CURRENT FILING DATE: 1999-07-23
 ; EARLIER APPLICATION NUMBER: US 08/860,165
 ; EARLIER FILING DATE: 1997-09-22
 ; EARLIER APPLICATION NUMBER: PCT/AU95/00868
 ; EARLIER FILING DATE: 1995-12-20
 ; EARLIER APPLICATION NUMBER: AU PN0157/94
 ; EARLIER FILING DATE: 1994-12-20
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 172
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus type 16
 US-09-359-382-12

Query Match 100.0%; Score 50; DB 3; Length 172;
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 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
 |||||
 Db 82 MSCCRSRT 90

RESULT 7

US-08-860-165-10
 ; Sequence 10, Application US/08860165A
 ; Patent No. 6004557
 ; GENERAL INFORMATION:
 ; APPLICANT: EDWARDS, Stirling John
 ; APPLICANT: COX, John Cooper
 ; APPLICANT: WEBB, Elizabeth Ann
 ; APPLICANT: FRAZER, Ian
 ; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
 ; FILE REFERENCE: 17227/130
 ; CURRENT APPLICATION NUMBER: US/08/860,165A
 ; CURRENT FILING DATE: 1997-09-22
 ; EARLIER APPLICATION NUMBER: PCT/AU95/00868
 ; EARLIER FILING DATE: 1995-12-20
 ; EARLIER APPLICATION NUMBER: AU PN0157
 ; EARLIER FILING DATE: 1994-12-20
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 266
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
 US-08-860-165-10

Query Match 100.0%; Score 50; DB 3; Length 266;
 Best Local Similarity 100.0%; Pred. No. 2.5; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9
 |||||
 Db 144 MSCCRSRT 152

RESULT 8

US-09-359-382-10
 ; Sequence 10, Application US/09359382
 ; Patent No. 6306397
 ; GENERAL INFORMATION:
 ; APPLICANT: EDWARDS, Stirling John
 ; APPLICANT: COX, John Cooper
 ; APPLICANT: WEBB, Elizabeth Ann
 ; APPLICANT: FRAZER, Ian
 ; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
 ; FILE REFERENCE: 017227/0148
 ; CURRENT APPLICATION NUMBER: US/09/359,382
 ; CURRENT FILING DATE: 1999-07-23
 ; EARLIER APPLICATION NUMBER: US 08/860,165
 ; EARLIER FILING DATE: 1997-09-22
 ; EARLIER APPLICATION NUMBER: PCT/AU95/00868
 ; EARLIER FILING DATE: 1995-12-20
 ; EARLIER APPLICATION NUMBER: AU PN0157/94
 ; EARLIER FILING DATE: 1994-12-20
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 266
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus type 16
 US-09-359-382-10

Query Match 100.0%; Score 50; DB 3; Length 266;
 Best Local Similarity 100.0%; Pred. No. 2.5; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCCRSRT 9

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Db      144 MSCCRSRT 152
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RESULT 9
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JTM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1
Query Match      100.0%; Score 50; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MSCCRSRT 9
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Db      144 MSCCRSRT 152

RESULT 10
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4
Query Match      100.0%; Score 50; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      250 MSCCRSRT 258

RESULT 11
US-09-485-885-10
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; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10
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Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MSCCRSRT 9
|||||
Db      269 MSCCRSRT 277

RESULT 12
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6
Query Match      100.0%; Score 50; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MSCCRSRT 9
|||||
Db      250 MSCCRSRT 258

RESULT 13
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
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; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/495,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match      100.0%; Score 50; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 3.4; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy      1 MSCCRSRT 9
      |||||
Db      269 MSCCRSRT 277

RESULT 14
US-09-252-991A-29076
; Sequence 29076, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29076
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29076

Query Match      76.0%; Score 38; DB 4; Length 113;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SCCRSRT 9
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Db      49 ACCRSRS 56

RESULT 15
US-09-270-767-32689
; Sequence 32689, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 32689
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32689

Query Match      74.0%; Score 37; DB 4; Length 207;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 CCRSRT 9
      |||
Db      106 CCRDSRT 112

Search completed: June 28, 2005, 21:33:31
Job time : 18 secs
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-36
Perfect score: 63
Sequence: 1 WTGRMSCC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	103	2 Q919D6	Q919D6 human papil
2	63	100.0	130	2 Q919B4	Q919B4 human papil
3	63	100.0	130	2 Q919B8	Q919B8 human papil
4	63	100.0	130	2 Q919C0	Q919C0 human papil
5	63	100.0	130	2 Q919C2	Q919C2 human papil
6	63	100.0	130	2 Q919C8	Q919C8 human papil
7	63	100.0	130	2 Q919D0	Q919D0 human papil
8	63	100.0	138	2 Q919D2	Q919D2 human papil
9	63	100.0	143	2 Q919B6	Q919B6 human papil
10	63	100.0	143	2 Q919C4	Q919C4 human papil
11	63	100.0	151	2 Q12335	Q12335 human papil
12	63	100.0	151	2 Q12336	Q12336 human papil
13	63	100.0	151	2 Q76TS0	Q76TS0 human papil
14	63	100.0	151	2 Q778I6	Q778I6 human papil
15	63	100.0	151	2 Q77E16	Q77E16 human papil
16	63	100.0	151	2 Q77JC7	Q77JC7 human papil
17	63	100.0	151	2 Q77ZJ5	Q77ZJ5 human papil
18	63	100.0	151	2 Q80963	Q80963 human papil
19	63	100.0	151	2 Q80966	Q80966 human papil
20	63	100.0	151	2 Q89640	Q89640 human papil
21	63	100.0	151	2 Q89648	Q89648 human papil
22	63	100.0	151	2 Q89708	Q89708 human papil
23	63	100.0	151	2 Q89755	Q89755 human papil
24	63	100.0	151	2 Q89852	Q89852 human papil
25	63	100.0	151	2 Q89887	Q89887 human papil
26	63	100.0	151	2 Q8B564	Q8B564 human papil
27	63	100.0	151	2 Q8BB19	Q8BB19 human papil
28	63	100.0	151	2 Q8BB20	Q8BB20 human papil
29	63	100.0	151	2 Q8BB21	Q8BB21 human papil
30	63	100.0	151	2 Q9W8C3	Q9W8C3 human papil
31	63	100.0	151	2 Q9W931	Q9W931 human papil

32 63 100.0 151 2 Q9WMP2 human papil
33 63 100.0 151 2 Q9WMP3 human papil
34 63 100.0 151 2 Q9WMP4 human papil
35 63 100.0 151 2 Q9WMP5 human papil
36 63 100.0 151 2 VEE HPV16
37 63 100.0 158 2 Q8JMU8 human papil
38 63 100.0 158 2 Q8QHN0 human papil
39 63 100.0 158 2 Q8QHP5 human papil
40 63 100.0 158 2 Q8QHT0 human papil
41 63 100.0 158 2 Q8QRD5 human papil
42 63 100.0 158 2 Q8QRD6 human papil
43 63 100.0 158 2 Q8QRD7 human papil
44 63 100.0 158 2 Q8QRD8 human papil
45 63 100.0 158 2 Q8QRD9 human papil

ALIGNMENTS

RESULT 1

Q919D6 PRELIMINARY; PRT; 103 AA.
ID Q919D6
AC Q919D6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404692; AAL01342.1; .
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; S6; 1.
FT NON TER 1 1
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;

Query Match 100.0%; Score 63; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WTGRMSCC 9
Db 84 WTGRMSCC 92

RESULT 2

Q919B4 PRELIMINARY; PRT; 130 AA.
ID Q919B4
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).

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DR EMBL; AF404703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227BEDDC CRC64;
Query Match 100.0%; Score 63; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRCSGCC 9
Db 111 WTGRCSGCC 119

RESULT 3
Q919B8 ID Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01359.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;
Query Match 100.0%; Score 63; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRCSGCC 9
Db 111 WTGRCSGCC 119

RESULT 4
Q919C0 ID Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
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DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
Query Match 100.0%; Score 63; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRCSGCC 9
Db 111 WTGRCSGCC 119

RESULT 5
Q919C2 ID Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01355.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
Query Match 100.0%; Score 63; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRCSGCC 9
Db 111 WTGRCSGCC 119

RESULT 6
Q919C8 ID Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404696; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;
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Query Match      100.0%; Score 63; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRCSGCC 9
Db 111 WTGRCSGCC 119

RESULT 7
Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04695; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15735 MW; 9FB30EEDCA21AF3 CRC64;

Query Match      100.0%; Score 63; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRCSGCC 9
Db 111 WTGRCSGCC 119

RESULT 8
Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04694; AAL01345.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA9089FC2 CRC64;

Query Match      100.0%; Score 63; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.044;

Qy 1 WTGRCSGCC 9
Db 111 WTGRCSGCC 119

RESULT 9
Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04702; AAL01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match      100.0%; Score 63; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRCSGCC 9
Db 124 WTGRCSGCC 132

RESULT 10
Q919C4 PRELIMINARY; PRT; 143 AA.
AC Q919C4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04698; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match      100.0%; Score 63; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRCSGCC 9
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Db 124 WTGRMSCC 132
|||||
RESULT 11
ID O12335 PRELIMINARY; PRT; 151 AA.
AC O12335
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Torneello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Girardo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003015; AAB70732.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18238 MW; BFF32A8B016CC88B CRC64;

Query Match 100.0%; Score 63; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9
|||||
Db 132 WTGRMSCC 140

RESULT 12
ID O12336 PRELIMINARY; PRT; 151 AA.
AC O12336
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Torneello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Girardo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003016; AAB70733.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match 100.0%; Score 63; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9
|||||
Db 132 WTGRMSCC 140

RESULT 13
ID O12335 PRELIMINARY; PRT; 151 AA.
AC O12335
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34114; AAA91661.1; -.
DR EMBL; U34125; AAA91672.1; -.
DR EMBL; U34130; AAA91677.1; -.
DR EMBL; U34131; AAA91678.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 100.0%; Score 63; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9
|||||
Db 132 WTGRMSCC 140

RESULT 14
ID O77816 PRELIMINARY; PRT; 151 AA.
AC O77816
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388056; CAB45104.1; -.
DR EMBL; AJ388061; CAB45114.1; -.
DR EMBL; AJ388066; CAB45124.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
```

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Db 132 WTGRMSCC 140
|||||
RESULT 13
ID O76TSO PRELIMINARY; PRT; 151 AA.
AC O76TSO
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34114; AAA91661.1; -.
DR EMBL; U34125; AAA91672.1; -.
DR EMBL; U34130; AAA91677.1; -.
DR EMBL; U34131; AAA91678.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 100.0%; Score 63; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9
|||||
Db 132 WTGRMSCC 140

RESULT 14
ID O77816 PRELIMINARY; PRT; 151 AA.
AC O77816
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388056; CAB45104.1; -.
DR EMBL; AJ388061; CAB45114.1; -.
DR EMBL; AJ388066; CAB45124.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
```



```

DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;

Query Match      100.0%; Score 63; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRCMSCC 9
Db 132 WTGRCMSCC 140

RESULT 15
Q77E16
ID Q77E16 PRELIMINARY; PRT; 151 AA.
AC Q77E16;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE E6 oncoprotein (E6 protein).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M.; Vaeteswoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AF469197; AAO15691.1; -.
DR EMBL; AJ388063; CAB45118.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;

Query Match      100.0%; Score 63; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRCMSCC 9
Db 132 WTGRCMSCC 140

```

Search completed: June 28, 2005, 21:24:08
 Job time : 55.1 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-36

Perfect score: 63

Sequence: 1 WTGRMSCC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	158	1 W6WLS3	protein E6 - human
2	54	85.7	149	1 W6WLS3	E6 protein - human
3	47	74.6	149	1 W6WLS3	E6 protein - human
4	46	73.0	153	1 S15621	E6 protein - human
5	46	73.0	159	1 S15614	E6 protein - human
6	46	73.0	191	1 W6WLR1	E6 protein - rhesu
7	45	71.4	159	2 S36497	E6 protein - human
8	45	71.4	280	2 G84839	late embryogenesis
9	44	69.8	136	2 C71018	probable NADH-plas
10	44	69.8	138	2 H75114	co-induced hydroge
11	44	69.8	142	2 S36509	E6 protein - human
12	44	69.8	148	2 A61237	E6 protein - human
13	44	69.8	148	2 S36515	E6 protein - human
14	44	69.8	148	2 S36573	E6 protein - human
15	43	68.3	150	1 W6WLS2	E6 protein - human
16	43	68.3	296	2 E70432	conserved hypothet
17	42	66.7	149	1 W6WLS8	E6 protein - human
18	42	66.7	154	2 S36527	E6 protein - human
19	42	66.7	480	1 B70804	DNA repair protein
20	41	65.1	107	2 H84839	late embryogenesis
21	41	65.1	151	1 W6WLS1	E6 protein - human
22	41	65.1	155	1 W6WLS6	E6 protein - human
23	41	65.1	155	2 A44890	E6 protein - human
24	41	65.1	292	2 H84285	succinate dehydrog
25	40	63.5	149	1 W6WLS3	E6 protein - human
26	40	63.5	150	1 W6WLS1	E6 protein - human
27	40	63.5	150	1 W6WLS6	E6 protein - human
28	40	63.5	153	2 S36503	E6 protein - human
29	40	63.5	369	2 E84542	hypothetical prote

30 40 63.5 400 2 JCS657 LIM domain-contain
31 40 63.5 426 1 A47179 homeotic protein L
32 40 63.5 565 2 H86477 protein F1504.19 l
33 40 63.5 580 2 T18439 hypothetical prote
34 40 63.5 600 2 T18446 hypothetical prote
35 40 63.5 6420 2 T30283 polyketide synthas
36 39 61.9 154 2 S36555 E6 protein - human
37 39 61.9 154 2 S36584 E6 protein - human
38 39 61.9 378 2 JCS658 LIM domain-contain
39 38 60.3 101 2 JQ0877 cyc02 protein prec
40 38 60.3 136 1 MMEHB cell fusion protei
41 38 60.3 150 1 W6WLS1 E6 protein - pygmy
42 38 60.3 150 1 W6WLS3 E6 protein - human
43 38 60.3 150 1 W6WLS4 E6 protein - human
44 38 60.3 222 2 E84560 hypothetical prote
45 38 60.3 310 2 T17980 hypothetical prote

ALIGNMENTS

RESULT 1

W6WLS3

protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SBE>

A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G3330302

J.Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: 217014; MUID:91162763; PMID:1848319

A:Accession: T10427

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G3330302

C:Genetics:

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 63; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.033; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0;

Oy 1 WTGRMSCC 9

Db 139 WTGRMSCC 147

RESULT 2

W6WLS3

E6 protein - human papillomavirus type 35

C:Species: human papillomavirus type 35

A>Note: host Homo sapiens (nan)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: E40824; S36521

R:Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.

Virology 186, 770-776, 1992

A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillon

A:Reference number: A40824; MUID:92124753; PMID:1310198

A:Accession: E40824

A>Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-149 <MAP>
A:Cross-references: UNIPROT:P27228; GB:M74117; NID:G333050; PIDN:AAA46966.1; PID:G333051
R:Delius, H.; Hofmann, B.
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36521
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149
A:Cross-references: EMBL:X74477; NID:G396997; PIDN:CAA52561.1; PID:G396998
A:Experimental source: strain 35H
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 85.7%; Score 54; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 0.59; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0

Qy 1 WTGRCMSC 8
Db 132 WTGRCMSC 139
|||||

RESULT 3
W6WL31
E6 protein - human papillomavirus type 31
C:Species: human papillomavirus type 31
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
R:Goldsbrough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.
A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated virus
A:Reference number: A34398; MUID:89299478; PMID:2545036
A:Accession: A32444
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-149 <GOL>
A:Cross-references: UNIPROT:P17386; GB:J04353; NID:G333048; PIDN:AAA46950.1; PID:G459916
C:Comment: This protein may be involved in the oncogenic potential of this virus.
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 74.6%; Score 47; DB 1; Length 149;
Best Local Similarity 75.0%; Pred. No. 5.7; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 2

Qy 1 WTGRCMSC 8
Db 132 WTGRCIAC 139
|||||

RESULT 4
E6 protein - human papillomavirus type 57
C:Species: human papillomavirus type 57
A:Note: host Homo sapiens (man)
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C:Accession: S15621
R:Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
A:Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and 57
A:Reference number: S15614; MUID:91188699; PMID:1964523
A:Accession: S15621
A:Molecule type: DNA
A:Residues: 1-153 <HIR>
A:Cross-references: UNIPROT:P22158; EMBL:X55965; NID:G60882; PIDN:CAA39430.1; PID:G60883

C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:29-65/Region: zinc finger CCCC motif
F:102-138/Region: zinc finger CCCC motif

Query Match 73.0%; Score 46; DB 1; Length 153;
Best Local Similarity 75.0%; Pred. No. 7.9; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1

Qy 1 WTGRCMSC 8
Db 131 WTGHCMNC 138
|||||

RESULT 5
S15614
E6 protein - human papillomavirus type 2a
C:Species: human papillomavirus type 2a
A:Note: host Homo sapiens (man)
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C:Accession: S15614
R:Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
A:Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and 57
A:Reference number: S15614; MUID:91188699; PMID:1964523
A:Accession: S15614
A:Molecule type: DNA
A:Residues: 1-159 <HIR>
A:Cross-references: UNIPROT:P25484; EMBL:X55964
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:35-71/Region: zinc finger CCCC motif
F:108-144/Region: zinc finger CCCC motif

Query Match 73.0%; Score 46; DB 1; Length 159;
Best Local Similarity 75.0%; Pred. No. 8.1; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1

Qy 1 WTGRCMSC 8
Db 137 WTGHCMNC 144
|||||

RESULT 6
W6WL31
E6 protein - rhesus papillomavirus (type 1)
C:Species: rhesus papillomavirus
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: A38503
R:Ostrow, R.S.; LaBresh, K.V.; Faras, A.J.
Virology 181, 424-429, 1991
A:Title: Characterization of the complete RHPV 1 genomic sequence and an integration loci
A:Reference number: A38503; MUID:91135018; PMID:1847267
A:Accession: A38503
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-191 <OST>
A:Cross-references: UNIPROT:P22159; EMBL:M37717
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:60-96/Region: zinc finger CCCC motif
F:133-169/Region: zinc finger CCCC motif

Query Match 73.0%; Score 46; DB 1; Length 191;
Best Local Similarity 75.0%; Pred. No. 9.2; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1

Qy 1 WTGRCMSC 8
Db 162 WTGRCLMC 169
|||||

RESULT 7

S36497
E6 protein - human papillomavirus type 27
C:Species: human papillomavirus type 27
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36497
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36497
A:Molecule type: DNA
A:Residues: 1-159
A:Cross-references: UNIPROT:P36808; EMBL:X74473; NID:G396964; PIDN:CAAS2536.1; PID:G39696
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 71.4%; Score 45; DB 2; Length 159;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WTGRCMSC 8
||| |||
Db 137 WTGHCQC 144

RESULT 8
G84839
late embryogenesis abundant M17 protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: G84839
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; PMID:20083487; PMID:10617197
A:Accession: G84839
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-280 <STO>
A:Cross-references: UNIPROT:Q9S7S3; GB:AE002093; NID:G3894196; PIDN:AAC78545.1; GSPDB:GN
C:Genetics:
A:Gene: At2g41260
A:Map position: 2

Query Match 71.4%; Score 45; DB 2; Length 280;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WTGRCMSC 9
||| |||
Db 87 WTGRCRYCC 95

RESULT 9
C71018
probable NADH-plastoquinone oxidoreductase subunit - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 16-Aug-2004
C:Accession: C71018
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; PMID:98344137; PMID:9679194
A:Accession: C71018
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-136 <KAW>
A:Cross-references: UNIPROT:O59110; GB:AP000006; NID:G3236133; PIDN:BAA30547.1; PID:d103
A:Experimental source: strain OT3
A>Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:
A:Gene: PH1440
F:39-95/Domain: ferredoxin 2[4Fe-4S] homology <FER2>

Query Match 69.8%; Score 44; DB 2; Length 136;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WTGRCMSC 8
||| |||
Db 73 WTGRCVFC 80

RESULT 10
H75114
co-induced hydrogenase related, chain X PAB1894 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 16-Aug-2004
C:Accession: H75114
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A:Reference number: A75001
A:Accession: H75114
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-138 <KAW>
A:Cross-references: UNIPROT:Q9V0S0; GB:AJ248285; GB:AL096836; NID:G5458067; PIDN:CAB4963;
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB1894
C:Superfamily: ferredoxin 2[4Fe-4S] homology

Query Match 69.8%; Score 44; DB 2; Length 138;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WTGRCMSC 8
||| |||
Db 73 WTGRCVFC 80

RESULT 11
S36509
E6 protein - human papillomavirus type 32
C:Species: human papillomavirus type 32
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36509
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36509
A:Molecule type: DNA
A:Residues: 1-142
A:Cross-references: UNIPROT:P36810; EMBL:X74475; NID:G396981; PIDN:CAAS2549.1; PID:G39698
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 69.8%; Score 44; DB 2; Length 142;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WTGRCMSC 8
||| |||
Db 133 WTGRCVFC 140

RESULT 12
A61237
E6 protein - human papillomavirus type 52
C:Species: human papillomavirus type 52
C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996

C;Accession: A61237
R;Takami, Y.; Kondoh, G.; Saito, J.; Noda, K.; Sudiro, T.M.; Sjahrurachman, A.; Warsa, U
Int. J. Cancer 48, 516-522, 1991
A;Title: Cloning and characterization of human papillomavirus type 52 from cervical carcinoma
A;Reference number: A61237; MUID:91258022; PMID:1646174
C;Accession: A61237
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-148 <TAK>
C;Superfamily: papillomavirus E6 protein

Query Match 69.8%; Score 44; DB 2; Length 148;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTGRCMSC 8
|||||

Db 132 WTGRCTQC 139

RESULT 13

S36515
E6 protein - human papillomavirus type 34
C;Species: human papillomavirus type 34
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36515

R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36515
A;Molecule type: DNA

A;Residues: 1-148
A;Cross-references: UNIPROT:P36911; EMBL:X74476; NID:G396989; PIDN:CAAS2555.1; PID:G3969
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 69.8%; Score 44; DB 2; Length 148;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTGRCMSC 8
|||||

Db 133 WTGRCTQC 140

RESULT 14

S36573
E6 protein - human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36573

R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36573
A;Molecule type: DNA

A;Residues: 1-148
A;Cross-references: UNIPROT:P36914; EMBL:X74481; NID:G397038; PIDN:CAAS2585.1; PID:G3970
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 69.8%; Score 44; DB 2; Length 148;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTGRCMSC 8
|||||

Db 132 WTGRCTQC 139

RESULT 15

W6WL42
E6 protein - human papillomavirus type 42
C;Species: human papillomavirus type 42
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: E39451
R;Philipp, W.; Honore, N.; Sapp, M.; Cole, S.T.; Streeck, R.E.
Virology 186, 331-334, 1992

A;Title: Human papillomavirus type 42: new sequence, conserved genome organization.
A;Reference number: A39451; MUID:92087479; PMID:1309278

A;Accession: E39451

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-150 <PHI>

A;Cross-references: UNIPROT:P27229; GB:M73236

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

Query Match 68.3%; Score 43; DB 1; Length 150;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTGRCMSC 8

|||||

Db 133 WTGRCTHC 140

Search completed: June 28, 2005, 21:27:51

Job time : 11.15 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds
(without alignments)
59.826 Million cell updates/sec

Title: US-08-170-344-36

Perfect score: 63

Sequence: 1 WTGRMSSCC 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/FCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/FCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	16	17	US-10-484-063-9
2	63	100.0	20	17	US-10-938-249-513
3	63	100.0	24	16	US-10-476-570-44
4	63	100.0	151	14	US-10-177-390-6
5	63	100.0	151	17	US-10-484-063-20
6	63	100.0	151	17	US-10-484-063-27
7	63	100.0	158	17	US-10-858-384-2
8	63	100.0	158	17	US-10-367-057-16
9	63	100.0	171	16	US-10-472-724-2
10	63	100.0	266	9	US-09-367-309A-1
11	63	100.0	273	13	US-10-000-903-4
					Sequence 9, Appli
					Sequence 513, App
					Sequence 44, Appli
					Sequence 6, Appli
					Sequence 20, Appl
					Sequence 27, Appl
					Sequence 2, Appli
					Sequence 16, Appl
					Sequence 2, Appli
					Sequence 1, Appli
					Sequence 4, Appli

Sequence 4, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 14, Appl
Sequence 14, Appl
Sequence 515, App
Sequence 441, App
Sequence 41, App
Sequence 437, App
Sequence 437, App
Sequence 284860,
Sequence 144303,
Sequence 220633,
Sequence 341074,
Sequence 1669, Ap
Sequence 1669, Ap
Sequence 254541,
Sequence 55128, A
Sequence 2521, Ap
Sequence 67824, A
Sequence 61887, A
Sequence 64902, A
Sequence 43, Appl
Sequence 214017,
Sequence 18618, A
Sequence 67918, A
Sequence 3195, Ap
Sequence 525, App
Sequence 534, App
Sequence 266658,
Sequence 36259, A

ALIGNMENTS

RESULT 1

US-10-484-063-9
; Sequence 9, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-9

Query Match 100.0%; Score 63; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSSCC 9
Db 2 WTGRMSSCC 10

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RESULT 2
US-10-938-249-513
; Sequence 513, Application US/10938249
; Publication No. US20050037969A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Hematopoietic
; FILE REFERENCE: 020054-001130US
; CURRENT APPLICATION NUMBER: US/10/938,249
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US/09/724,553
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/134,114
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,117
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,118
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/162,498
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/170,453
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 60/176,195
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/182,296
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 60/196,267
; PRIOR FILING DATE: 2000-04-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 543
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 513
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HPV16 E6 C-terminal
US-10-938-249-513

Query Match      100.0%; Score 63; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WTGRCMSCC 9
      |||||
Db      1 WTGRCMSCC 9

RESULT 3
US-10-476-570-44
; Sequence 44, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980

Query Match      100.0%; Score 63; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WTGRCMSCC 9
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Db      1 WTGRCMSCC 9

RESULT 4
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match      100.0%; Score 63; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WTGRCMSCC 9
      |||||
Db      132 WTGRCMSCC 140

RESULT 5
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20
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Query Match 100.0%; Score 63; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9
Db 132 WTGRMSCC 140

RESULT 6
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match 100.0%; Score 63; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9
Db 132 WTGRMSCC 140

RESULT 7
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 100.0%; Score 63; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9
Db 139 WTGRMSCC 147

RESULT 8
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 100.0%; Score 63; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9
Db 139 WTGRMSCC 147

RESULT 9
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 100.0%; Score 63; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9
Db 144 WTGRMSCC 152

RESULT 10

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US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, ROBERICK I.
; APPLICANT: MALLIAROS, JTM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 63; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. NO. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WTGRCSGCC 9
Db      139 WTGRCSGCC 147

RESULT 11
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match      100.0%; Score 63; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. NO. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WTGRCSGCC 9
Db      245 WTGRCSGCC 253

RESULT 12
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine

```

```

; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a Cpg Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

Query Match      100.0%; Score 63; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. NO. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WTGRCSGCC 9
Db      245 WTGRCSGCC 253

RESULT 13
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match      100.0%; Score 63; DB 13; Length 292;
Best Local Similarity 100.0%; Pred. NO. 0.46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WTGRCSGCC 9
Db      264 WTGRCSGCC 272

RESULT 14
US-10-899-771-10
; Sequence 10, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.

```

; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (Clyta from Streptococcus
; OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-10

Query Match 100.0%; Score 63; DB 17; Length 292;
Best Local Similarity 100.0%; Pred.No. 0.46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9
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Db 264 WTGRMSCC 272

RESULT 15

US-10-000-903-6
; Sequence 6, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-6

Query Match 100.0%; Score 63; DB 13; Length 371;
Best Local Similarity 100.0%; Pred.No. 0.55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9
|||
Db 245 WTGRMSCC 253

Search completed: June 29, 2005, 04:19:27
Job time : 58.85 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-36

Perfect score: 63

Sequence: 1 WTGRMCCC 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	100.0	21	US-08-934-915-167	Sequence 167, Appl
2	63	100.0	158	US-09-980-523A-2	Sequence 2, Appl
3	63	100.0	162	US-08-316-239B-3	Sequence 3, Appl
4	63	100.0	162	US-08-316-239B-4	Sequence 4, Appl
5	63	100.0	172	US-08-860-165-12	Sequence 12, Appl
6	63	100.0	172	US-09-359-382-12	Sequence 12, Appl
7	63	100.0	266	US-08-860-165-10	Sequence 10, Appl
8	63	100.0	266	US-09-359-382-10	Sequence 10, Appl
9	63	100.0	266	US-09-367-309A-1	Sequence 1, Appl
10	63	100.0	273	US-09-485-885-4	Sequence 4, Appl
11	63	100.0	292	US-09-485-885-10	Sequence 10, Appl
12	63	100.0	371	US-09-485-885-6	Sequence 6, Appl
13	63	100.0	390	US-09-485-885-14	Sequence 14, Appl
14	46	73.0	144	US-09-252-991A-16576	Sequence 16576, A
15	43	68.3	158	US-09-270-767-36255	Sequence 36255, A
16	43	68.3	158	US-09-270-767-51472	Sequence 51472, A
17	43	68.3	220	US-09-311-021-150	Sequence 150, App
18	42	66.7	217	US-09-252-991A-27361	Sequence 27361, A
19	42	66.7	261	US-09-949-016-9721	Sequence 9721, Ap
20	40	63.5	55	US-08-852-666-10	Sequence 10, Appl
21	40	63.5	200	US-09-252-991A-22034	Sequence 22034, A
22	40	63.5	226	US-09-252-991A-23893	Sequence 23893, A
23	40	63.5	368	US-09-000-094-20	Sequence 20, Appl
24	40	63.5	368	US-10-011-749-20	Sequence 20, Appl
25	40	63.5	375	US-09-000-094-22	Sequence 22, Appl
26	40	63.5	375	US-10-011-749-22	Sequence 22, Appl
27	40	63.5	399	US-09-252-991A-25098	Sequence 25098, A

28	40	63.5	405	4	US-09-949-016-9433	Sequence 9433, Ap
29	40	63.5	465	3	US-09-000-094-24	Sequence 24, Appl
30	40	63.5	465	4	US-10-011-749-24	Sequence 24, Appl
31	40	63.5	1587	3	US-09-000-094-46	Sequence 46, Appl
32	40	63.5	1587	4	US-10-011-749-46	Sequence 46, Appl
33	39	61.9	34	4	US-09-270-767-60688	Sequence 60688, A
34	39	61.9	243	4	US-09-270-767-45191	Sequence 45191, A
35	39	61.9	266	4	US-09-252-991A-18776	Sequence 18776, A
36	38.5	61.1	73	4	US-09-270-767-35372	Sequence 35372, A
37	38.5	61.1	73	4	US-09-270-767-50589	Sequence 50589, A
38	38.5	61.1	84	4	US-09-198-452A-1276	Sequence 1276, Ap
39	38.5	61.1	139	4	US-09-270-767-59799	Sequence 59799, A
40	38.5	61.1	586	4	US-09-270-767-44373	Sequence 44373, A
41	38	60.3	16	2	US-08-986-234-33	Sequence 33, Appl
42	38	60.3	66	4	US-09-673-395A-147	Sequence 147, App
43	38	60.3	87	4	US-09-252-991A-27237	Sequence 27237, A
44	38	60.3	384	4	US-09-289-198-304	Sequence 304, App
45	38	60.3	384	4	US-09-429-755-304	Sequence 304, App

ALIGNMENTS

RESULT 1

US-08-934-915-167
; Sequence 167, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 167:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-167

Query Match 100.0%; Score 63; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0086;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9
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Db 2 WTGRMSCC 10

RESULT 2

US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGALT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCES
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 63; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9
| | | | | | | |
Db 139 WTGRMSCC 147

RESULT 3

US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 63; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 63; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9
| | | | | | | |
Db 139 WTGRMSCC 147

RESULT 4

US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 63; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9
| | | | |
Db 139 WTGRMSCC 147

RESULT 5

US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match 100.0%; Score 63; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9
| | | | |
Db 77 WTGRMSCC 85

RESULT 6

US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match 100.0%; Score 63; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9
| | | | |
Db 77 WTGRMSCC 85

RESULT 7

US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 63; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9
| | | | |
Db 139 WTGRMSCC 147

RESULT 8

US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 63; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTGRMSCC 9

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; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-10

Query Match      100.0%; Score 63; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WTGRCSGCC 9
Db      264 WTGRCSGCC 272

RESULT 12
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-6

Query Match      100.0%; Score 63; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WTGRCSGCC 9
Db      245 WTGRCSGCC 253

RESULT 13
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:

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; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-10

Query Match      100.0%; Score 63; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WTGRCSGCC 9
Db      139 WTGRCSGCC 147

RESULT 10
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-4

Query Match      100.0%; Score 63; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WTGRCSGCC 9
Db      245 WTGRCSGCC 253

RESULT 11
US-09-485-885-10

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```
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match      100.0%; Score 63; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WTGRCMSCC 9
Db      264 WTGRCMSCC 272

RESULT 14
US-09-252-991A-16576
; Sequence 16576, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16576
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16576

Query Match      73.0%; Score 46; DB 4; Length 144;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 WTGRCMSCC 9
Db      63 WPGSCFSCC 71

RESULT 15
US-09-270-767-36255
; Sequence 36255, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
```

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; SEQ ID NO 36255
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-36255

Query Match      68.3%; Score 43; DB 4; Length 158;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 WTGRCMSCC 9
Db      86 WCWRCWSCC 94

Search completed: June 28, 2005, 21:33:30
Job time : 18 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-35
Perfect score: 52
Sequence: 1 YRDGNPYAV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	81	2 Q80886	Q80886 human papil
2	52	100.0	84	2 Q80882	Q80882 human papil
3	52	100.0	90	2 Q80883	Q80883 human papil
4	52	100.0	90	2 Q80884	Q80884 human papil
5	52	100.0	90	2 Q80885	Q80885 human papil
6	52	100.0	91	2 Q80887	Q80887 human papil
7	52	100.0	99	2 Q919B2	Q919B2 human papil
8	52	100.0	103	2 Q919D6	Q919D6 human papil
9	52	100.0	130	2 Q919B4	Q919B4 human papil
10	52	100.0	130	2 Q919B8	Q919B8 human papil
11	52	100.0	130	2 Q919C0	Q919C0 human papil
12	52	100.0	130	2 Q919C2	Q919C2 human papil
13	52	100.0	130	2 Q919C8	Q919C8 human papil
14	52	100.0	130	2 Q919D0	Q919D0 human papil
15	52	100.0	138	2 Q919D2	Q919D2 human papil
16	52	100.0	143	2 Q919B6	Q919B6 human papil
17	52	100.0	143	2 Q919C4	Q919C4 human papil
18	52	100.0	151	2 Q12335	Q12335 human papil
19	52	100.0	151	2 Q12336	Q12336 human papil
20	52	100.0	151	2 Q76TS0	Q76TS0 human papil
21	52	100.0	151	2 Q778I6	Q778I6 human papil
22	52	100.0	151	2 Q77E16	Q77E16 human papil
23	52	100.0	151	2 Q77JC7	Q77JC7 human papil
24	52	100.0	151	2 Q77ZJ5	Q77ZJ5 human papil
25	52	100.0	151	2 Q80966	Q80966 human papil
26	52	100.0	151	2 Q89640	Q89640 human papil
27	52	100.0	151	2 Q89648	Q89648 human papil
28	52	100.0	151	2 Q89708	Q89708 human papil
29	52	100.0	151	2 Q89755	Q89755 human papil
30	52	100.0	151	2 Q89852	Q89852 human papil
31	52	100.0	151	2 Q89887	Q89887 human papil

32	52	100.0	151	2	Q8B564	Q8B564 human papil
33	52	100.0	151	2	Q8BB19	Q8BB19 human papil
34	52	100.0	151	2	Q8BB20	Q8BB20 human papil
35	52	100.0	151	2	Q8BB21	Q8BB21 human papil
36	52	100.0	151	2	Q8W8C3	Q8W8C3 human papil
37	52	100.0	151	2	Q9W931	Q9W931 human papil
38	52	100.0	151	2	Q9WMP2	Q9WMP2 human papil
39	52	100.0	151	2	Q9WMP3	Q9WMP3 human papil
40	52	100.0	151	2	Q9WMP4	Q9WMP4 human papil
41	52	100.0	151	2	Q9WMP5	Q9WMP5 human papil
42	52	100.0	158	1	VE6 HPV16	P03126 human papil
43	52	100.0	158	2	Q8JMU8	Q8JMU8 human papil
44	52	100.0	158	2	Q8QHN0	Q8QHN0 human papil
45	52	100.0	158	2	Q8QHT0	Q8QHT0 human papil

ALIGNMENTS

RESULT 1
Q80886 PRELIMINARY; PRT; 81 AA.
AC Q80886;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galuira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14515; AAB60569.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9784 MW; DD5PEDBC9F845B97 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
| | | | |
Db 13 YRDGNPYAV 21

RESULT 2
Q80882 PRELIMINARY; PRT; 84 AA.
AC Q80882;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical;
RA Haegert D.G., Galuira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14511; AAB60565.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

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DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 84
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;
Query Match 100.0%; Score 52; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
Db 10 YRDGNPYAV 18

RESULT 3
Q80883 PRELIMINARY; PRT; 90 AA.
AC Q80883;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14512; AAB60566.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10904 MW; 5D3ADF843AD6060B CRC64;
Query Match 100.0%; Score 52; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
Db 13 YRDGNPYAV 21

RESULT 4
Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.

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FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFACCCC01 CRC64;
Query Match 100.0%; Score 52; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
Db 13 YRDGNPYAV 21

RESULT 5
Q80885 PRELIMINARY; PRT; 90 AA.
AC Q80885;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14514; AAB60568.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10964 MW; BC2531643ACBA76C CRC64;
Query Match 100.0%; Score 52; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
Db 13 YRDGNPYAV 21

RESULT 6
Q80887 PRELIMINARY; PRT; 91 AA.
AC Q80887;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14516; AAB60570.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 11136 MW; 22PDF3EA185ACBA7 CRC64;

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Query Match      100.0%; Score 52; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRDGNPYAV 9
DB 13 YRDGNPYAV 21

RESULT 7
QY19B2 PRELIMINARY; PRT; 99 AA.
AC QY19B2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040704; AAL01342.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR PFam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;

Query Match      100.0%; Score 52; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRDGNPYAV 9
DB 30 YRDGNPYAV 38

RESULT 8
QY19D6 PRELIMINARY; PRT; 103 AA.
AC QY19D6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040692; AAL01342.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR PFam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 103
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;

Query Match      100.0%; Score 52; DB 2; Length 103;

QY 1 YRDGNPYAV 9
DB 13 YRDGNPYAV 21

Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRDGNPYAV 9
DB 6 YRDGNPYAV 14

RESULT 9
QY19B4 PRELIMINARY; PRT; 130 AA.
AC QY19B4;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR PFam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;

Query Match      100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRDGNPYAV 9
DB 33 YRDGNPYAV 41

RESULT 10
QY19B8 PRELIMINARY; PRT; 130 AA.
AC QY19B8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040701; AAL01359.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR PFam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match      100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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7

LE
C
E
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C

1 YRDGNPYAV 9

1 VPDGNDVAV 9

Query match 100.0%; Score 32; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.21;

7

Q919D2
 ID Q919D2 PRELIMINARY; PRT; 138 AA.
 AC Q919D2;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE E6 protein (fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404694; AAL01345.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;
 Query Match 100.0%; Score 52; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 0.23;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YRDGNPYAV 9
 Db 41 YRDGNPYAV 49

Search completed: June 28, 2005, 21:24:08
 Job time : 56.1 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-35

Perfect score: 52

Sequence: 1 YRDGNPYAV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	52	100.0	158	1	W6WLS8	protein E6 - human
2	48	92.3	149	1	W6WLS8	E6 protein - human
3	46	88.5	151	1	W6WLS1	E6 protein - human
4	42	80.8	148	2	A61237	E6 protein - human
5	42	80.8	148	2	S36573	E6 protein - human
6	40	76.9	154	2	S36527	E6 protein - human
7	39	75.0	149	1	W6WLS3	E6 protein - human
8	38	73.1	149	1	W6WLS3	E6 protein - human
9	38	73.1	521	2	S76556	hypothetical prote
10	38	73.1	1204	2	C75015	probable pyrolysin
11	38	73.1	2499	1	A30788	mannose 6-phosphat
12	37	71.2	216	2	T12727	hypothetical prote
13	37	71.2	704	2	A45985	microsome endopep
14	37	71.2	719	2	S51739	transcription repr
15	37	71.2	845	2	JC5256	adipocyte transcri
16	37	71.2	857	2	JC4169	phosphoenolpyruvat
17	37	71.2	1227	2	T23004	hypothetical prote
18	36	69.2	153	2	S36503	E6 protein - human
19	36	69.2	155	1	W6WLS6	E6 protein - human
20	36	69.2	264	2	C72770	probable DNA-(apur
21	36	69.2	435	2	S22268	malate dehydrogena
22	36	69.2	441	2	S33066	malate dehydrogena
23	36	69.2	441	2	S24231	malate dehydrogena
24	36	69.2	529	2	S24231	listeriolysin prec
25	36	69.2	529	2	A43505	listeriolysin O pr
26	36	69.2	529	2	AC1100	listeriolysin O pr
27	36	69.2	530	2	AH3194	glycogen synthase
28	35	67.3	150	2	S36544	E6 protein - human
29	35	67.3	224	2	A95394	hypothetical prote

ALIGNMENTS

RESULT 1

W6WLS8

protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Kramer, G.; Duret, M.; Suhai, S.; Rowekamp, W.G.

Virolgy 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

J.Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

R. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human papillomavirus type 16 genome acts at the level

A:Reference number: 217014; MUID:91162763; PMID:1848319

A:Accession: T10427

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C:Genetics:

A:Gene: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 52; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.032;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9

|||||||

Db 61 YRDGNPYAV 69

RESULT 2

W6WLS8

E6 protein - human papillomavirus type 58

C:Species: human papillomavirus type 58

A:Note: host Homo sapiens (nan)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C:Accession: E36779

R:Kiril, Y.; Iwamoto, S.; Matsukura, T.

Virolgy 185, 424-427, 1991

A:Title: Human papillomavirus type 58 DNA sequence.

A:Reference number: A36779; MUID:92024102; PMID:1656594

A:Accession: E36779

A>Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-149 <KIR>
A:Cross-references: UNIPROT:P26555; GB:D90400; NID:g222386; PIDN:BAR31845.1; PID:g333709
C:Species: human papillomavirus type 51
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 92.3%; Score 48; DB 1; Length 149;
Best Local Similarity 88.9%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 8; Conservative 1; Mismatches 0;

Qy 1 YRDGNPYAV 9
||| ||| |||
Db 54 YRDGNPYAV 62

RESULT 3
W6WL51
E6 protein - human papillomavirus type 51
C:Species: human papillomavirus type 51
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: E40415
R:Lungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991
A:Title: Biologic properties and nucleotide sequence analysis of human papillomavirus type 51
A:Reference number: A40415; MUID:91303675; PMID:1649326
A:Accession: E40415
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-151 <LUN>
A:Cross-references: UNIPROT:P26554; GB:M62877
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 88.5%; Score 46; DB 1; Length 151;
Best Local Similarity 88.9%; Pred. No. 0.38; Indels 1; Gaps 0;
Matches 8; Conservative 0; Mismatches 1;

Qy 1 YRDGNPYAV 9
||| ||| |||
Db 54 YRDGNPYAV 62

RESULT 4
A61237
E6 protein - human papillomavirus type 52
C:Species: human papillomavirus type 52
C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996
C:Accession: A61237
R:Takami, Y.; Kondoh, G.; Saito, J.; Noda, K.; Sudiro, T.M.; Sjahrurachman, A.; Warsa, U.
Int. J. Cancer 48, 516-522, 1991
A:Title: Cloning and characterization of human papillomavirus type 52 from cervical carcinoma
A:Reference number: A61237; MUID:91258022; PMID:1646174
A:Accession: A61237
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <TAK>
C:Superfamily: papillomavirus E6 protein

Query Match 80.8%; Score 42; DB 2; Length 148;
Best Local Similarity 77.8%; Pred. No. 2; Indels 2; Gaps 0;
Matches 7; Conservative 0; Mismatches 2;

Qy 1 YRDGNPYAV 9
||| ||| |||
Db 54 YRDGNPYAV 62

RESULT 5

S36573
E6 protein - human papillomavirus type 52
C:Species: human papillomavirus type 52
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36573
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36573
A:Molecule type: DNA
A:Residues: 1-148
A:Cross-references: UNIPROT:P36814; EMBL:X74481; NID:g397038; PIDN:CAA52585.1; PID:g397038
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 80.8%; Score 42; DB 2; Length 148;
Best Local Similarity 77.8%; Pred. No. 2; Indels 2; Gaps 0;
Matches 7; Conservative 0; Mismatches 2;

Qy 1 YRDGNPYAV 9
||| ||| |||
Db 54 YRDGNPYAV 62

RESULT 6
S36527
E6 protein - human papillomavirus type 53
C:Species: human papillomavirus type 53
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36527
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36527
A:Molecule type: DNA
A:Residues: 1-154
A:Cross-references: UNIPROT:P36815; EMBL:X74482; NID:g397046; PIDN:CAA52591.1; PID:g397046
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 76.9%; Score 40; DB 2; Length 154;
Best Local Similarity 77.8%; Pred. No. 4.8; Indels 2; Gaps 0;
Matches 7; Conservative 0; Mismatches 2;

Qy 1 YRDGNPYAV 9
||| ||| |||
Db 58 YRDGNPYAV 66

RESULT 7
W6WL33
E6 protein - human papillomavirus type 33
C:Species: human papillomavirus type 33
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A03683
R:Cole, S.T.; Strecek, R.E.
J. Virol. 58, 991-995, 1986
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 33, which
A:Reference number: A93020; MUID:86200464; PMID:3009902
A:Accession: A03683
A:Molecule type: DNA
A:Residues: 1-149 <COL>
A:Cross-references: UNIPROT:P06427; GB:M12732; NID:g333049; PIDN:AAA46958.1; PID:g463177
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 75.0%; Score 39; DB 1; Length 149;
Best Local Similarity 55.6%; Pred. No. 7.1; Indels 1; Gaps 0;
Matches 5; Conservative 3; Mismatches 3;

Qy 1 YRDGNPYAV 9
Db 54 YREGNPGI 62

RESULT 8
W6WL35
E6 protein - human papillomavirus type 35
C:Species: human papillomavirus type 35
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: E40824; S36521
R:Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35
A:Reference number: A40824; MUID:92124753; PMID:1310198
A:Accession: E40824
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-149 <MAR>
A:Cross-references: UNIPROT:P27228; GB:M74117; NID:g333050; PIDN:AAA46966.1; PID:g333051
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36521
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149
A:Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52561.1; PID:g396998
A:Experimental source: strain 35H
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 73.1%; Score 38; DB 1; Length 149;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
Db 54 YREGQPYGV 62

RESULT 9
S76556
hypothetical protein all0371 - Synecocystis sp. (strain PCC 6803)
C:Species: Synecocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76556
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76556
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-521 <KAN>
A:Cross-references: UNIPROT:Q55755; EMBL:D64002; GB:AB001339; NID:g1001612; PIDN:BAAL040
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 73.1%; Score 38; DB 2; Length 521;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YRDGNPY 7
Db 297 YSDGNPY 303

RESULT 10

C75015
probable pyrolysin (EC 3.4.-.-) homolog PAB1252 [similarity] - Pyrococcus abyssi (strain
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: C75015
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A:Reference number: A75001
A:Accession: C75015
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1204 <KAW>
A:Cross-references: UNIPROT:Q9UY51; GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB50563
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB1252
C:Keywords: hydrolase

Query Match 73.1%; Score 38; DB 2; Length 1204;
Best Local Similarity 66.7%; Pred. No. 93;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9

Db 536 YRYGNPVI 544

RESULT 11

A30788
mannose 6-phosphate receptor protein, cation-independent - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A25908; A30788; S09404
R:Lobel, P.; Dahms, N.M.; Kornfeld, S.
J. Biol. Chem. 263, 2563-2570, 1988
A:Title: Cloning and sequence analysis of the cation-independent mannose 6-phosphate rec
A:Reference number: A92706; MUID:88115411; PMID:2963004
A:Accession: A25908
A:Molecule type: mRNA
A:Residues: 1-2499 <LOB>
A:Cross-references: UNIPROT:P08169; GB:J03527; NID:g162873; PIDN:AAA30455.1; PID:g162874;
R:Glickman, J.N.; Conibear, E.; Pearce, B.M.F.
EMBO J. 8, 1041-1047, 1989

A:Title: Specificity of binding of clathrin adaptors to signals on the mannose-6-phosphat
A:Reference number: S09404; MUID:89305502; PMID:2545438
A:Contents: annotation; HA-II adaptor binding
C:Comment: This protein binds phosphorylated lysosomal enzymes and insulin-like growth fa
C:Superfamily: mannose 6-phosphate receptor, cation-independent; fibronectin type II repe
C:Keywords: Golgi apparatus; membrane protein
F:1912-1951/Domain: fibronectin type II repeat homology <2F1>
F:2360-2363/Region: HA-II adaptor binding

Query Match 73.1%; Score 38; DB 1; Length 2499;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YRDGNPY 7

Db 717 YRDGTPY 723

RESULT 12

T12727
hypothetical protein 11 - Methanobacterium phage psiM2
C:Species: Methanobacterium phage psiM2
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T12727
R:Pfister, P.; Wasserfallen, A.; Stettler, R.; Leisinger, T.
submitted to the EMBL Data Library, May 1998

A;Description: Archaeophaga psiM2 complete genomic DNA.

A;Reference number: Z17578

A;Accession: T12727

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-216 <PFI>

A;Cross-references: UNIPROT:O80201; EMBL:AF065411; NID:g3249585; PID:g3249596; PIDN:AAC2

A;Experimental source: host Methanobacterium thermoautotrophicum strain Marburg

C;Superfamily: Methanobacterium phage psiM2 hypothetical protein 11

Query Match 71.2%; Score 37; DB 2; Length 216;

Best Local Similarity 66.7%; Pred. No. 24;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRDGNPYAV 9

Db 143 YEDGSPYRV 151

RESULT 13

A45985

microsomal endopeptidase MEP - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A45985

R;Kawabata, S.; Nakagawa, K.; Muta, T.; Iwanaga, S.; Davie, E.W.

J. Biol. Chem. 268, 12498-12503, 1993

A;Title: Rabbit liver microsomal endopeptidase with substrate specificity for processing

A;Reference number: A45985; MUID:93286083; PMID:8509389

A;Accession: A45985

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Residues: 1-704 <KAW>

A;Cross-references: UNIPROT:P42675; GB:D13310; NID:g391848; PIDN:BAA02570.1; PID:g391849

A;Experimental source: liver

A;Note: sequence extracted from NCBI backbone (NCBIN:133580, NCBIP:133581)

C;Superfamily: thimet oligopeptidase

Query Match

Best Local Similarity 71.2%; Score 37; DB 2; Length 704;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRDGNPYA 8

Db 549 YDGNPIA 556

RESULT 14

S51739

transcription repressor AEBP1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C;Accession: S60227; S51739

R;He, G.P.; Muise, A.; Li, A.W.; Ro, H.S.

Nature 378, 92-96, 1995

A;Title: A eukaryotic transcriptional repressor with carboxypeptidase activity.

A;Reference number: S60227; MUID:96061010; PMID:7477299

A;Accession: S60227

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-719 <HE2>

A;Cross-references: UNIPROT:Q61281; EMBL:X80478; NID:g607131; PIDN:CAA56648.1; PID:g6071

Query Match

Best Local Similarity 71.2%; Score 37; DB 2; Length 719;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRDGNP 6

Db 228 YRDGNP 233

RESULT 15

JC5256

adipocyte transcription factor, AEBP1 - human

C;Species: Homo sapiens (man)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: JC5256

R;Ohno, I.; Hashimoto, J.; Shimizu, K.; Takaoka, K.; Ochi, T.; Matsubara, K.; Okubo, K.

Biochem. Biophys. Res. Commun. 228, 411-414, 1996

A;Title: A cDNA cloning of human AEBP1 from primary cultured osteoblasts and its expressi

A;Reference number: JC5256; MUID:97079196; PMID:8920928

A;Accession: JC5256

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-845 <OHN>

A;Cross-references: UNIPROT:Q14113; DDBJ:D86479; NID:gl468942; PIDN:BAA13094.1; PID:gl468

Query Match

Best Local Similarity 71.2%; Score 37; DB 2; Length 845;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRDGNP 6

Db 333 YRDGNP 338

Search completed: June 28, 2005, 21:27:51

Job time : 12.15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds
(without alignments)

59.826 Million cell updates/sec

Title: US-08-170-344-35

Perfect score: 52

Sequence: 1 YRDGNPRAV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US05_PUBCOMB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US04_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US03_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	15	16	US-10-476-570-30
2	52	100.0	20	16	US-10-476-570-11
3	52	100.0	151	14	US-10-177-390-6
4	52	100.0	151	17	US-10-484-063-20
5	52	100.0	151	17	US-10-484-063-27
6	52	100.0	158	17	US-10-858-384-2
7	52	100.0	158	17	US-10-367-057-16
8	52	100.0	171	16	US-10-472-724-2
9	52	100.0	266	9	US-09-367-309A-1
10	52	100.0	273	13	US-10-000-903-4
11	52	100.0	273	17	US-10-899-771-4
					Sequence 30, Appl
					Sequence 11, Appl
					Sequence 6, Appl
					Sequence 20, Appl
					Sequence 27, Appl
					Sequence 2, Appl
					Sequence 16, Appl
					Sequence 2, Appl
					Sequence 1, Appl
					Sequence 4, Appl

52 100.0 292 13 US-10-000-903-10 Sequence 10, Appl
52 100.0 292 17 US-10-899-771-10 Sequence 10, Appl
52 100.0 371 13 US-10-000-903-6 Sequence 6, Appl
52 100.0 371 17 US-10-899-771-6 Sequence 6, Appl
52 100.0 390 13 US-10-000-903-14 Sequence 14, Appl
52 100.0 390 17 US-10-899-771-14 Sequence 14, Appl
48 82.3 9 11 US-09-739-466C-11 Sequence 11, Appl
46 88.5 117 17 US-10-751-845-126 Sequence 126, App
20 46 88.5 236 17 US-10-751-845-157 Sequence 157, App
21 46 88.5 237 17 US-10-751-845-158 Sequence 158, App
22 46 88.5 261 17 US-10-751-845-160 Sequence 160, App
23 45 86.5 22 16 US-10-612-818-4 Sequence 4, Appl
24 44 84.6 9 17 US-10-751-845-83 Sequence 83, Appl
25 44 84.6 21 16 US-10-476-570-54 Sequence 54, Appl
26 44 84.6 22 16 US-10-476-570-26 Sequence 26, Appl
27 44 84.6 22 17 US-10-858-384-6 Sequence 27, Appl
28 44 84.6 23 16 US-10-476-570-27 Sequence 27, Appl
29 44 84.6 24 17 US-10-751-845-65 Sequence 65, Appl
30 41 78.8 9 14 US-10-161-097-42 Sequence 42, Appl
31 41 78.8 436 15 US-10-424-599-270568 Sequence 270568,
32 41 78.8 443 15 US-10-425-114-45886 Sequence 45886, A
33 41 78.8 443 15 US-10-425-114-46250 Sequence 46250, A
34 41 78.8 443 15 US-10-425-114-51704 Sequence 51704, A
35 39 75.0 374 16 US-10-437-963-195496 Sequence 195496,
36 39 75.0 415 16 US-10-437-963-195493 Sequence 195493,
37 39 75.0 453 16 US-10-437-963-170490 Sequence 170490,
38 39 75.0 582 16 US-10-437-963-180853 Sequence 180853,
39 38 73.1 349 15 US-10-424-599-186197 Sequence 186197,
40 37 71.2 70 16 US-10-425-115-287834 Sequence 287834,
41 37 71.2 153 9 US-09-925-301-856 Sequence 856, App
42 37 71.2 536 15 US-10-367-095-10 Sequence 10, Appl
43 37 71.2 536 15 US-10-368-046-10 Sequence 10, Appl
44 37 71.2 536 16 US-10-367-367-10 Sequence 10, Appl
45 37 71.2 536 17 US-10-918-337-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-10-476-570-30
; Sequence 30, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide B6 55-69
US-10-476-570-30

Query Match 100.0%; Score 52; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
|
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Db 7 YRDGNPYAV 15

RESULT 2

US-10-476-570-11
; Sequence 11, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 61-80
US-10-476-570-11

Query Match 100.0%; Score 52; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
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Db 1 YRDGNPYAV 9

RESULT 3

US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerps Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match 100.0%; Score 52; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
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Db 54 YRDGNPYAV 62

RESULT 4

US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match 100.0%; Score 52; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
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Db 54 YRDGNPYAV 62

RESULT 5

US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match 100.0%; Score 52; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
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Db 54 YRDGNPYAV 62

RESULT 6

US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US2005003025A1
; GENERAL INFORMATION:

```

; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
; US-10-858-384-2

Query Match          100.0%; Score 52; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
Db 61 YRDGNPYAV 69

RESULT 7
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Cui, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-367-057-16

Query Match          100.0%; Score 52; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
Db 61 YRDGNPYAV 69

RESULT 8
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17

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; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; US-10-472-724-2

Query Match          100.0%; Score 52; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
Db 66 YRDGNPYAV 74

RESULT 9
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; US-09-367-309A-1

Query Match          100.0%; Score 52; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
Db 61 YRDGNPYAV 69

RESULT 10
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22

```

; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match 100.0%; Score 52; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
Db 167 YRDGNPYAV 175

RESULT 11

US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

Query Match 100.0%; Score 52; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
Db 167 YRDGNPYAV 175

RESULT 12

US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernandez
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5

; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match 100.0%; Score 52; DB 13; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
Db 186 YRDGNPYAV 194

RESULT 13

US-10-899-771-10
; Sequence 10, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (Clyta from Streptococcus
; OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-10

Query Match 100.0%; Score 52; DB 17; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
Db 186 YRDGNPYAV 194

RESULT 14

US-10-000-903-6
; Sequence 6, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernandez
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17


```
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-6

Query Match      100.0%; Score 52; DB 13; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.36; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRDGNPYAV 9
Db 167 YRDGNPYAV 175

RESULT 15
US-10-899-771-6
; Sequence 6, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 16)
US-10-899-771-6

Query Match      100.0%; Score 52; DB 17; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.36; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRDGNPYAV 9
Db 167 YRDGNPYAV 175
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Search completed: June 29, 2005, 04:19:26
Job time : 58.85 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-35

Perfect score: 52

Sequence: 1 YRDGNPYAV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PTCUTS_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	9	3	US-08-159-339A-219
2	52	100.0	158	4	US-09-980-523A-2
3	52	100.0	162	1	US-08-316-239B-3
4	52	100.0	162	1	US-08-316-239B-4
5	52	100.0	172	3	US-08-860-165-14
6	52	100.0	172	3	US-09-359-382-14
7	52	100.0	266	3	US-08-860-165-10
8	52	100.0	266	3	US-09-359-382-10
9	52	100.0	266	4	US-09-367-309A-1
10	52	100.0	273	3	US-09-485-885-4
11	52	100.0	292	3	US-09-485-885-10
12	52	100.0	371	3	US-09-485-885-6
13	52	100.0	390	3	US-09-485-885-14
14	44	84.6	9	3	US-08-159-339A-133
15	44	84.6	22	4	US-09-980-523A-6
16	44	84.6	23	4	US-09-601-729-276
17	41	78.8	9	4	US-09-574-749B-42
18	40	76.9	20	2	US-08-934-915-162
19	37	71.2	253	4	US-09-710-279-2428
20	37	71.2	281	3	US-09-134-001C-3445
21	37	71.2	484	1	US-08-111-939-12
22	37	71.2	578	3	US-09-503-172A-2
23	37	71.2	719	4	US-09-641-741-28
24	37	71.2	845	4	US-09-641-741-29
25	37	71.2	1128	1	US-08-111-939-2
26	37	71.2	1128	4	US-09-641-741-30
27	37	71.2	1128	4	US-09-060-482-8

28	37	71.2	1158	4	US-09-060-482-2	Sequence 2, Appli
29	37	71.2	1172	4	US-09-949-016-8593	Sequence 8593, Ap
30	37	71.2	1391	4	US-10-080-505-11	Sequence 11, Appl
31	37	71.2	1391	4	US-10-080-505-15	Sequence 15, Appl
32	36	69.2	197	4	US-09-902-540-12611	Sequence 12611, A
33	36	69.2	626	4	US-09-485-717-2	Sequence 2, Appli
34	36	69.2	626	4	US-09-948-722-2	Sequence 2, Appli
35	34	65.4	172	3	US-08-860-165-12	Sequence 12, Appl
36	34	65.4	172	3	US-09-359-382-12	Sequence 12, Appl
37	34	65.4	188	4	US-09-704-321-2	Sequence 2, Appli
38	34	65.4	194	4	US-09-489-039A-8510	Sequence 8510, Ap
39	34	65.4	275	4	US-09-828-523A-4	Sequence 4, Appli
40	34	65.4	284	4	US-09-828-523A-54	Sequence 54, Appli
41	34	65.4	320	4	US-09-252-991A-29355	Sequence 29355, A
42	34	65.4	348	4	US-09-902-540-15695	Sequence 15695, A
43	34	65.4	390	4	US-09-328-352-4913	Sequence 4913, Ap
44	34	65.4	461	1	US-08-186-222-2	Sequence 2, Appli
45	33	63.5	9	4	US-09-593-870A-30	Sequence 30, Appli

ALIGNMENTS

RESULT 1
US-08-159-339A-219
; Sequence 219, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cellis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 219:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-219

Query Match 100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
| | | | | | | | | |
Db 1 YRDGNPYAV 9

RESULT 2

US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCES
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 52; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
| | | | | | | | | |
Db 61 YRDGNPYAV 69

RESULT 3

US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 52; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
| | | | | | | | | |
Db 61 YRDGNPYAV 69

RESULT 4

US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 52; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
| | | | | | | | | |
Db 61 YRDGNPYAV 69

RESULT 5
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860.165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match 100.0%; Score 52; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
| | | | | | | | | |
Db 130 YRDGNPYAV 138

RESULT 6
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359.382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860.165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match 100.0%; Score 52; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
| | | | | | | | | |
Db 130 YRDGNPYAV 138

RESULT 7
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860.165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 52; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRDGNPYAV 9
| | | | | | | | | |
Db 61 YRDGNPYAV 69

RESULT 8
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359.382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860.165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 52; DB 3; Length 266;

REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-34

Perfect score: 58

Sequence: 1 LSFVCPWCA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	105	1	VE7 HPV18
2	58	100.0	105	2	Q6PGP1
3	58	100.0	105	2	Q8V9K9
4	58	100.0	105	2	Q9QNP5
5	58	100.0	105	2	Q9QNP6
6	58	100.0	105	2	Q9QNP7
7	58	100.0	106	1	VE7 HPV45
8	58	100.0	106	2	Q9Y4Y3
9	58	100.0	106	2	O10609
10	58	100.0	109	1	VE7 HPV70
11	55	94.8	110	1	VE7 HPV68
12	55	94.8	110	1	VE7 HPVME
13	55	94.8	110	2	O73452
14	54	93.1	109	1	VE7 HPV39
15	52	89.7	100	2	Q9IR58
16	46	79.3	232	2	Q87XC2
17	46	79.3	240	2	Q63HK1
18	46	79.3	261	2	Q6X3N0
19	45	77.6	107	2	Q81965
20	45	77.6	215	2	Q7YV98
21	45	77.6	222	2	Q8XRE5
22	43	74.1	490	1	MOT3_YEAST
23	43	74.1	647	2	Q6FN39
24	42	72.4	108	2	Q9WHG1
25	42	72.4	283	2	Q75L43
26	41	70.7	69	2	Q8ECP8
27	41	70.7	99	2	Q49204
28	41	70.7	205	2	Q6AFY6
29	41	70.7	211	2	Q6H016
30	41	70.7	292	1	PFLC_ECOLI
31	41	70.7	292	2	Q7UB90

32 41 70.7 292 2 Q8FBA2
33 41 70.7 292 2 Q8X748
34 41 70.7 308 2 Q83I89
35 41 70.7 338 2 Q6AIV6
36 41 70.7 677 2 Q746S9
37 41 70.7 686 2 Q9UYM9
38 40 69.0 116 2 Q8J828
39 40 69.0 134 2 Q28897
40 40 69.0 144 2 Q9YHR3
41 40 69.0 166 2 Q74H04
42 40 69.0 204 1 D5BA_LEGPN
43 40 69.0 214 2 Q9A783
44 40 69.0 216 2 Q88911
45 40 69.0 217 2 Q9FMB1

ALIGNMENTS

RESULT 1
VE7 HPV18
ID VE7 HPV18 STANDARD; PRT; 105 AA.
AC P06788;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87283882; PubMed=3039146;
RA Cole S.T., Danos O.;
RT "Nucleotide sequence and comparative analysis of the human papillomavirus type 18 genome. Phylogeny of papillomaviruses and repeated structure of the E6 and E7 gene products.";
RT J. Mol. Biol. 193:599-608(1987).
RL [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88188247; PubMed=2833614;
RA Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M., Sugimura T.;
RT "Nucleotide sequences of cDNAs for human papillomavirus type 18 transcripts in HeLa cells.";
RT J. Virol. 62:1640-1646(1988).
RL [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87053870; PubMed=3023067;
RA Schneider-Gaedcke A., Schwarz E.;
RT "Different human cervical carcinoma cell lines show similar transcription patterns of human papillomavirus type 18 early genes.";
RL EMO J. 5:2285-2292(1986).
RL [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=87218459; PubMed=3034571;
RA Seedorf K., Oltersdorf T., Kraemer G., Roewekamp W.;
RT "Identification of early proteins of the human papilloma viruses type 16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells.";
RL EMO J. 6:139-144(1987).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating activities.

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DR EMBL; X05015; CRA28665.1; -;
DR EMBL; M20324; AAA99513.1; -;
DR EMBL; M20325; AAA99515.1; -;
DR EMBL; M26798; AAA6947.1; -;
DR EMBL; X04773; CRA28467.1; -;
DR EMBL; A06324; CRA00540.1; -;
DR EMBL; A06328; CRA00543.1; -;
DR PIR; B26165; W7WL18
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW Transcription regulation.
FT SITE 63 66 C-XX-C motif-1.
FT SITE 98 101 C-XX-C motif-2.
FT CONFLICT 73 73 K -> E (in Ref. 1 and 4).
SQ SEQUENCE 105 AA; 11995 MW; 2CDB119534D0186A CRC64;

Query Match 100.0%; Score 58; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 94 LSFVCPWCA 102

RESULT 2
Q6PGP1 PRELIMINARY; PRT; 105 AA.
ID Q6PGP1
AC Q6PGP1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Straube R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC056907; AAH56907.1; -;
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW Hypothetical protein.
SQ SEQUENCE 105 AA; 11995 MW; 2CDB119534D0186A CRC64;

Query Match 100.0%; Score 58; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 94 LSFVCPWCA 102

RESULT 3
Q8V9K9 PRELIMINARY; PRT; 105 AA.
ID Q8V9K9
AC Q8V9K9
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21568387; PubMed=11711624;
RX DOI=10.1128/JVI.75.24.12339-12346.2001;
RA Shera K.A., Shera C.A., McDougall J.K.;
RT "Small Tumor Virus Genomes Are Integrated near Nuclear Matrix
RT Attachment Regions in Transformed Cells.";
RL J. Virol. 75:12339-12346 (2001).
DR EMBL; AF339137; AAL34455.1; -;
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 105 AA; 12036 MW; 2528DEA165850C71 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 94 LSFVCPWCA 102

RESULT 4
Q9QNP5 PRELIMINARY; PRT; 105 AA.
ID Q9QNP5
AC Q9QNP5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RA Laassri M., Gul'ko L., Vinokurova S., Kisseljova N., Veiko V.,
RA Kisseljev F.;
RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
RT Transformation Potential of E7 Gene and its Mutants.";
RL Virus Genes 182:139-149 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RL Submitted (DEC-1998) to the EMBL/GenBank/DBSJ databases.
DR EMBL; Y18493; CAB53099.1; -;
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 105 AA; 11952 MW; 247BF448A6BBB4FA CRC64;

Query Match 100.0%; Score 58; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.043;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 0.043; Mismatches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
 |||||
 Db 94 LSFVCPWCA 102

RESULT 5

Q9QNP6 PRELIMINARY; PRT; 105 AA.
 AC Q9QNP6; (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 18.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10582;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Laasari M., Gul'ko L., Vinokurova S., Kisseljova N., Veiko V.,
 RA Kisseljev F.;
 RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
 RT Transformation Potential of E7 Gene and its Mutants.";
 RL Virus Genes 182:139-149(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Veiko V.P.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y18492; CAB53097.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 105 AA; 12009 MW; C4979555DAD4A960 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 105;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
 |||||
 Db 94 LSFVCPWCA 102

RESULT 6

Q9QNP7 PRELIMINARY; PRT; 105 AA.
 AC Q9QNP7; (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 18.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10582;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Laasari M., Gul'ko L., Vinokurova S., Kisseljova N., Veiko V.,
 RA Kisseljev F.;
 RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
 RT Transformation Potential of E7 Gene and its Mutants.";
 RL Virus Genes 182:139-149(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Veiko V.P.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y18491; CAB53097.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 105 AA; 12010 MW; 24799BB534D4496A CRC64;

Query Match 100.0%; Score 58; DB 2; Length 105;

RESULT 7

VE7 HPV45 STANDARD; PRT; 106 AA.
 AC P21736;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE E7 protein.
 GN Name=E7;
 OS Human papillomavirus type 45.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94265501; PubMed=8205838;
 RA Delius H., Hofmann B.;
 RT "Primer-directed sequencing of human papillomavirus types.";
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kaplan J.B., Burk R.D.;
 RL Submitted (AUG-1990) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: E7 protein has both transforming and trans-activating activities.
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 CC

DR EMBL; X74479; CAA52574.1; -;
 DR EMBL; M38198; AAA46974.1; -;
 DR PIR; S36562; S36562.
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
 KW Transcription regulation.
 FT SITE 64 67 C-XX-C motif-1.
 FT SITE 99 102 C-XX-C motif-2.
 FT CONFLICT 3 3 G -> E (in Ref. 2).
 FT CONFLICT 5 5 R -> Q (in Ref. 2).
 SQ SEQUENCE 106 AA; 12049 MW; 4C53808A7285AD41 CRC64;

Query Match 100.0%; Score 58; DB 1; Length 106;
 Best Local Similarity 100.0%; Pred. No. 0.044;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
 |||||
 Db 95 LSFVCPWCA 103

RESULT 8

Q9Y4Y3 PRELIMINARY; PRT; 106 AA.
 AC Q9Y4Y3;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE E7 protein.
 GN Name=HPV45 E7;

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sastre-Garau X., Favre M., Couturier J., Orth G.;
RT "Distinct patterns of alteration of myc genes associated with
RT integration of human papillomavirus type 16 oe type 45 in two genital
RT tumours.";
RL J. Gen. Virol. 81:198-199(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Favre M.G.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ242956; CAB44707.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 106 AA; 11977 MW; 1912D1DE742F6BED CRC64;

Query Match 100.0%; Score 58; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 95 LSFVCPWCA 103

RESULT 9
ID O10609 PRELIMINARY; PRT; 106 AA.
AC O10609;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Oncoprotein E7.
OS Human papillomavirus type 45.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10593;
RN [1]
RP SEQUENCE FROM N.A.
RA Sastre-Garau X., Favre M., Couturier J., Orth G.;
RT "Distinct patterns of alteration of myc genes associated with
RT integration of HPV16 or HPV45 DNA in two genital tumors.";
RL J. Gen. Virol. 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RA Favre M.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y13218; CAA73661.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 106 AA; 11977 MW; 1912D1DE742F6BED CRC64;

Query Match 100.0%; Score 58; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 95 LSFVCPWCA 103

RESULT 10
ID VE7 HPV70 STANDARD; PRT; 109 AA.
AC P50785;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E7 protein.

```

```

GN Name=E7;
OS Human papillomavirus type 70.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=39457;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96249586; PubMed=8815087;
RA Forslund O., Hansson B.G.;
RT "Human papillomavirus type 70 genome cloned from overlapping PCR
RT products: complete nucleotide sequence and genomic organization.";
RL J. Clin. Microbiol. 34:802-809(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=97060129; PubMed=8904450;
RA Longuet M., Beaudenon S., Orth G.;
RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70,
RT related to the potentially oncogenic HPV39.";
RL J. Clin. Microbiol. 34:738-744(1996).
CC -I- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC
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CC
CC EMBL; U21941; AAC54851.1; -.
CC EMBL; U22461; AAC54881.1; -.
CC InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW Transcription regulation.
FT SITE 66 69 C-XX-C motif-1.
FT SITE 101 104 C-XX-C motif-2.
FT SEQUENCE 109 AA; 12657 MW; 2FD3C643DPAFF891 CRC64;

Query Match 100.0%; Score 58; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 97 LSFVCPWCA 105

RESULT 11
VE7 HPV68
ID VE7 HPV68 STANDARD; PRT; 110 AA.
AC P54668;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E7 protein.
DE Name=E7;
OS Human papillomavirus type 68.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=45240;
RN [1]
RP SEQUENCE FROM N.A.
RA Longuet M., Beaudenon S., Orth G.;
RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70,
RT related to the potentially oncogenic HPV39.";
RL J. Clin. Microbiol. 34:738-744(1996).
CC
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DR EMBL; X67160; CAA47633.1; -.
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
 KW Transcription regulation.
 FT SITE 67 70 C-XX-C motif-1.
 FT SITE 102 105 C-XX-C motif-2.
 SQ SEQUENCE 110 AA; 12756 MW; B52459199048093D CRC64;

Query Match 94.8%; Score 55; DB 1; Length 110;
 Best Local Similarity 88.9%; Pred. No. 0.14;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSFVCPWCA 9
 |:|||||
 DB 98 LNFVCPWCA 106

RESULT 12

VE7_HPVME STANDARD; PRT; 110 AA.
 AC P27963;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE E7 protein.
 GN Name=E7;

OS Human papillomavirus type ME180.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91374616; PubMed=1716694;
 RA Reuter S., Delius H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.;
 RT "Characterization of a novel human papillomavirus DNA in the cervical
 RT carcinoma cell line ME180";
 RL J. Virol. 65:5564-5568(1991).

CC -!- FUNCTION: E7 protein has both transforming and trans-activating
 CC activities.

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DR EMBL; M73258; AAF14012.1; -.
 DR PIR; D40509; W7WLPF.
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
 KW Transcription regulation.
 FT SITE 69 72 C-XX-C motif-1.
 FT SITE 102 105 C-XX-C motif-2.
 SQ SEQUENCE 110 AA; 12672 MW; 90ECC0E004AA66B CRC64;

Query Match 94.8%; Score 55; DB 1; Length 110;
 Best Local Similarity 88.9%; Pred. No. 0.14;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSFVCPWCA 9
 |:|||||
 DB 98 LNFVCPWCA 106

RESULT 13

073452 PRELIMINARY; PRT; 110 AA.
 AC O73452;
 DT 01-AUG-1998 (TRENBLrel. 07, Created)
 DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 68.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=45240;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91374616; PubMed=1716694;
 RA Reuter S., Delius H., Kahn T., Hofmann B., zur Hausen H., Schwarz E.;
 RT "Characterization of a novel human papillomavirus DNA in the cervical
 RT carcinoma cell line ME180";
 RL J. Virol. 65:5564-5568(1991).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98090464; PubMed=9427755; DOI=10.1093/emboj/17.1.215;
 RA Reuter S., Bartelmann M., Vogt M., Geisen C., Napieriski I., Kahn T.,
 RA Delius H., Lichter P., Weitz S., Korn B., Schwarz E.;
 RT "APM-1, a novel human gene, identified by aberrant cotranscription
 RT with papillomavirus oncogenes in aa cervical carcinoma cell line,
 RT encodes a BTB/POZ-zinc finger protein with growth inhibitory
 RT activity";
 RL EMO J. 17:215-222(1998).
 DR EMBL; Y14591; CAA74932.1; -.
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 110 AA; 12700 MW; 90ECC0E01476B0DB CRC64;

Query Match 94.8%; Score 55; DB 2; Length 110;
 Best Local Similarity 88.9%; Pred. No. 0.14;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSFVCPWCA 9
 |:|||||
 DB 98 LNFVCPWCA 106

RESULT 14

VE7_HPV39 STANDARD; PRT; 109 AA.
 AC P24837;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE E7 protein.
 GN Name=E7;
 OS Human papillomavirus type 39.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10588;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91135017; PubMed=1847266;
 RA Volpers C., Strebeck R.B.;
 RT "Genome organization and nucleotide sequence of human papillomavirus
 RT type 39";
 RL Virology 181:419-423(1991).
 CC -!- FUNCTION: E7 protein has both transforming and trans-activating
 CC activities.

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CC EMBL; M62849; AAA47051.1; -.
DR PIR; B38502; W7WL39.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW Transcription regulation.
FT SITE 66 C-XX-C motif-1.
FT SITE 101 104 C-XX-C motif-2.
SQ SEQUENCE 109 AA; 12497 MW; E4743EASAE6798C2B CRC64;

Query Match 93.1%; Score 54; DB 1; Length 109;
Best Local Similarity 88.9%; Pred. No. 0.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LSFVCPWCA 9
Db 97 LGFVCPWCA 105

RESULT 15
Q9IR58 PRELIMINARY; PRT; 100 AA.
AC Q9IR58;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 82.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=129724;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087389; PubMed=10618284;
RA Kino N., Sata T., Sato Y., Sugase M., Matsukura T.;
RT "Molecular cloning and nucleotide sequence analysis of a novel human
RT papillomavirus (Type 82) associated with vaginal intraepithelial
RT neoplasia."
RL Clin. Diagn. Lab. Immunol. 7:91-95 (2000).
DR EMBL; AB027021; BAA90736.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 100 AA; 11325 MW; 47E8C0D0FD67A81D CRC64;

Query Match 89.7%; Score 52; DB 2; Length 100;
Best Local Similarity 88.9%; Pred. No. 0.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LSFVCPWCA 9
Db 90 LSLVCPWCA 98

Search completed: June 28, 2005, 21:24:07
Job time : 56.1 secs
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-34
Perfect score: 58
Sequence: 1 LSFVCPWCA 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	105	1 W7WL18	E7 protein - human
2	58	100.0	106	2 S36562	E7 protein - human
3	55	94.8	110	1 W7WLPK	E7 protein - human
4	54	93.1	109	1 W7WL39	HMS1 protein - human
5	43	74.1	490	2 S52830	probable formate a
6	41	70.7	292	1 C65202	hypothetical prote
7	41	70.7	292	2 P86086	hypothetical prote
8	41	70.7	292	2 A91239	alpha chain of for
9	41	70.7	686	2 B75061	methyviologen-red
10	40	69.0	134	2 E69421	hypothetical prote
11	40	69.0	170	2 S01449	conserved hypothet
12	40	69.0	214	2 F87477	frnE protein VCA01
13	40	69.0	217	2 A82491	frnE protein [impo
14	40	69.0	224	2 A13595	frnE protein VCA01
15	40	69.0	242	2 G37573	frnE protein VCA01
16	40	69.0	242	2 A82794	polyketide biosynt
17	40	69.0	287	2 T19917	hypothetical prote
18	40	69.0	322	2 AD3607	homoserine o-succi
19	40	69.0	330	1 F69534	pyruvate formate-1
20	40	69.0	591	2 G30988	probable chaperoni
21	40	69.0	646	2 A85834	probable chaperoni
22	40	69.0	648	2 E64973	hypothetical prote
23	40	69.0	946	2 T31488	hypothetical prote
24	39	67.2	101	1 W7WL51	E7 protein - human
25	39	67.2	212	2 C70733	hypothetical prote
26	39	67.2	256	2 A82595	polyketide synthas
27	39	67.2	311	2 C71247	hypothetical prote
28	39	67.2	1735	1 S22812	DNA-directed RNA p
29	38	65.5	118	2 T11891	NADH2 dehydrogenas

30 38 65.5 305 2 T44300 probable pyridine
31 38 65.5 330 2 AD2854 conserved hypothet
32 38 65.5 386 2 A97631 hypothetical 37.4K
33 38 65.5 580 2 S44908 ZK652.5 protein -
34 38 65.5 812 2 S64929 hypothetical prote
35 37.5 64.7 583 2 S36781 esterase D - Pseud
36 37 63.8 76 2 JE0003 hypothetical 8.6K
37 37 63.8 90 2 S66276 hypothetical metalloca
38 37 63.8 96 2 T07136 probable metalloca
39 37 63.8 179 2 G83452 conserved hypothet
40 37 63.8 195 2 F65174 hypothetical 22.5
41 37 63.8 207 2 F87034 conserved hypothet
42 37 63.8 207 2 A70866 hypothetical prote
43 37 63.8 220 2 T46524 probable disulfide
44 37 63.8 258 2 B97900 formate acetyltran
45 37 63.8 258 2 G95028 hypothetical prote

ALIGNMENTS

RESULT 1

W7WL18
E7 protein - human papillomavirus type 18
C:Species: human papillomavirus type 18
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: B26165; H26251
R:Seedorf, K.; Olteradorf, T.; Kraemmer, G.; Roewekamp, W.

EMBO J. 6, 139-144, 1987

A:Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)

A:Reference number: A91068; MUID:87218459; PMID:3034571

A:Accession: B26165

A:Molecule type: DNA

A:Residues: 1-105 <SEE>

A:Cross-references: UNIPROT:P06788; GB:X04773; NID:G60876; PIDN:CAA28467.1; PID:G60878

R:Cole, S.T.; Danos, O.

J. Mol. Biol. 193, 599-608, 1987

A:Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 1

A:Reference number: A92937; MUID:87283882; PMID:3039146

A:Accession: H26251

A:Molecule type: DNA

A:Residues: 1-105 <COL>

A:Cross-references: GB:X05015; NID:G60975; PIDN:CAA28665.1; PID:G60977

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 100.0%; Score 58; DB 1; Length 105;

Best Local Similarity 100.0%; Pred. No. 0.063;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 LSFVCPWCA 9

Db

94 LSFVCPWCA 102

RESULT 2

S36562

E7 protein - human papillomavirus type 45

C:Species: human papillomavirus type 45

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S36562

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36562

A:Molecule type: DNA

A:Residues: 1-106

A:Cross-references: UNIPROT:P21736; EMBL:X74479; NID:G397022; PIDN:CAA52574.1; PID:G39702

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 100.0%; Score 58; DB 2; Length 106;

Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
| | | | | | | | | |
Db 95 LSFVCPWCA 103

RESULT 3
W7MLPR
E7 protein - human papillomavirus type ME180 (provirus)
C:Species: human papillomavirus type ME180
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: D40509
R:Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5568, 1991
A:Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma
A:Reference number: A40509; MUID:91374616; PMID:1716694
A:Accession: D40509
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-110 <REU>
A:Cross-references: UNIPROT:P27963; GB:M73258; NID:g184383; PIDN:AAF14012.1; PID:g647887
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 94.8%; Score 55; DB 1; Length 110;
Best Local Similarity 88.9%; Pred. No. 0.18;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
| | | | | | | | | |
Db 98 LNFVCPWCA 106

RESULT 4
W7MLJ9
E7 protein - human papillomavirus type 39
C:Species: human papillomavirus type 39
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: B38502
R:Volpers, C.; Strebeck, R.E.
Virology 181, 419-423, 1991
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
A:Reference number: A38502; MUID:91135017; PMID:1847266
A:Accession: B38502
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-109 <VOL>
A:Cross-references: UNIPROT:P24837; GB:M62849; EMBL:M38185; NID:g333245; PIDN:AAA47051.1
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 93.1%; Score 54; DB 1; Length 109;
Best Local Similarity 88.9%; Pred. No. 0.25;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
| | | | | | | | | |
Db 97 LGFVCPWCA 105

RESULT 5
S52830
HMS1 protein - Yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YM9916.09; protein YMR070w
C:Species: Saccharomyces cerevisiae
C:Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S52830; S59820
R:Pearson, D.; Bowman, S.
submitted to the EMBL Data Library, April 1995

A:Reference number: S52814
A:Accession: S52830
A:Molecule type: DNA
A:Residues: 1-490 <PEA>
A:Cross-references: UNIPROT:P54785; EMBL:Z48952; NID:g763008; PIDN:CAA88795.1; PID:g76301
A:Experimental source: strain AB972
R:Madison, J.; Winston, F.
submitted to the EMBL Data Library, April 1995
A:Reference number: S59820
A:Accession: S59820
A:Molecule type: DNA
A:Residues: 1-490 <MAD>
A:Cross-references: EMBL:U25279; NID:g805129; PIDN:AAC49982.1; PID:g805130
C:Genetics: SGD:MOT3; HMS1
A:Gene: YMR070w; SGD:S0004674
A:Cross-references: MIPS:YMR070w; SGD:S0004674
A:Map position: 13R

Query Match 74.1%; Score 43; DB 2; Length 490;
Best Local Similarity 83.3%; Pred. No. 30;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FVCPWC 8
| | | | |
Db 374 FLCPCWC 379

RESULT 6
C65202
probable formate acetyltransferase activating enzyme (EC 1.97.1.4), lyase 2-specific - Bt
C:Species: Escherichia coli
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: C65202
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: C65202
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-292 <BLAT>
A:Cross-references: UNIPROT:P32675; GB:AB000469; GB:U00096; NID:g1790385; PIDN:AAC76934.1
A:Experimental source: strain K-12, substrain M61655
C:Genetics:
A:Gene: pfic
C:Superfamily: pyruvate formate-lyase 2 activating enzyme; ferredoxin 2[4Fe-4S] homology
C:Keywords: oxidoreductase

Query Match 70.7%; Score 41; DB 1; Length 292;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VCPWCA 9
| | | | |
Db 50 LCPWCA 55

RESULT 7
F86086
hypothetical protein pfic [imported] - Escherichia coli (strain O157:H7, substrain EDL933;
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: F86086
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: F86086
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-292 <STO>

A;Cross-references: UNIPROT:Q8X748; GB:AE005174; NID:g12518871; PIDN:AAG59154.1.; GSPDB:C
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics: pfIC
A;Gene: pflC
C;Superfamily: pyruvate formate-lyase 2 activating enzyme; ferredoxin 2[4Fe-4S] homology

Query Match 70.7%; Score 41; DB 2; Length 292;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VCPWCA 9
:|||||
Db 50 LCPWCA 55

RESULT 8
A91239
hypothetical protein ECs4881 [imported] - Escherichia coli (strain O157:H7, substrain R1
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: A91239
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A39629; MUID:21156231; PMID:11258796
A;Accession: A91239
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-292 <HAY>
A;Cross-references: UNIPROT:Q8X748; GB:BA000007; PIDN:BAR38304.1; PID:g13364357; GSPDB:C
A;Experimental source: strain O157:H7, substrain R1MD 0509952
C;Genetics:
A;Gene: ECs4881
C;Superfamily: pyruvate formate-lyase 2 activating enzyme; ferredoxin 2[4Fe-4S] homology

Query Match 70.7%; Score 41; DB 2; Length 292;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VCPWCA 9
:|||||
Db 50 LCPWCA 55

RESULT 9
B75061
alpha chain of formate dehydrogenase PAB1389 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: B75061
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: B75061
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-686 <KAW>
A;Cross-references: UNIPROT:Q9UYM9; GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB5038
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1389
C;Superfamily: formate dehydrogenase

Query Match 70.7%; Score 41; DB 2; Length 686;
Best Local Similarity 83.3%; Pred. No. 75;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VCPWCA 9
:|||||
Db 9 VCPWCS 14

RESULT 10

B69421
methylviologen-reducing hydrogenase, subunit delta (vhuD) homolog - Archaeoglobus fulgid
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: B69421
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.;
Glocke, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.A.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: B69421
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-134 <KLE>
A;Cross-references: UNIPROT:O28897; GB:AB001009; GB:AE000782; NID:g2689332; PIDN:AAB8987
C;Superfamily: Methanobacterium thermoautotrophicum methyl viologen-reducing hydrogenase

Query Match 69.0%; Score 40; DB 2; Length 134;
Best Local Similarity 55.6%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LSPVCPWCA 9
:|||||
Db 4 IGFACQWCA 12

RESULT 11

S01449
hypothetical protein (xrn 5' region) - Halobacterium salinarum
C;Species: Halobacterium salinarum
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jul-2000
C;Accession: S01449
R;Mankin, A.S.; Kagramanova, V.K.
Nucleic Acids Res. 16, 4679-4692, 1988
A;Title: Complex promoter pattern of the single ribosomal RNA operon of an archaeobacteri
A;Reference number: S01449; MUID:88247769; PMID:3380693
A;Accession: S01449
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-170 <MAN>
A;Cross-references: EMBL:X06805
A;Note: the source is designated as Halobacterium halobium

Query Match 69.0%; Score 40; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VCPWC 8
:|||||
Db 146 VCPWC 150

RESULT 12

F87477
conserved hypothetical protein CC1843 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F87477
R;Niernman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87429; MUID:21173698; PMID:11259647
A;Accession: F87477
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-214 <STO>

A;Cross-references: UNIPROT:Q9A783; GB:AE005673; NID:gl3423282; PIDN:AAK23818.1; GSPDB:C
C;Genetics:
A;Gene: CC1843

Query Match 69.0%; Score 40; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VCPWC 8
|
|
|
|
Db 16 VCPWC 20

RESULT 13

frnE protein VCA0178 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: A82491
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Winn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B.

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: A82491
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-217 <HEI>
A;Cross-references: UNIPROT:Q9KMY8; GB:AE004358; GB:AE003853; NID:g9657566; PIDN:AAF9609
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0178
A;Map position: 2

Query Match 69.0%; Score 40; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VCPWC 8
|
|
|
|
Db 13 VCPWC 17

RESULT 14

frnE protein [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AI3595
R;DelVecchio, V.G.; Kapural, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AD3252; PMID:11756688
A;Accession: AI3595
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-224 <KUR>
A;Cross-references: UNIPROT:Q8YC42; UNIPROT:Q8FW83; GB:AE008918; PIDN:AAL53932.1; PID:gl
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI10690
A;Map position: 11

Query Match 69.0%; Score 40; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VCPWC 8
|
|
|
|
Db 15 VCPWC 19

RESULT 15

frnE protein VCA0178 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: G97573
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: G97573
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-242 <KUR>
A;Cross-references: UNIPROT:Q8UEI2; GB:AE007869; PIDN:AAK87544.1; PID:gl5156878; GSPDB:G

C;Genetics:
A;Gene: AGR_C_3262
A;Map position: circular chromosome

Query Match 69.0%; Score 40; DB 2; Length 242;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VCPWC 8
|
|
|
|
Db 33 VCPWC 37

Search completed: June 28, 2005, 21:27:50
Job time : 12.15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds
(without alignments)
59.826 Million cell updates/sec

Title: US-08-170-344-34

Perfect score: 58

Sequence: 1 LSFVCPWCA 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PT_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	17	15	US-10-432-465-103
2	58	100.0	17	16	US-10-433-091-72
3	58	100.0	105	16	US-10-433-091-4
4	58	100.0	105	16	US-10-800-023-28
5	58	100.0	118	16	US-10-472-724-8
6	58	100.0	227	13	US-10-000-903-16
7	58	100.0	227	13	US-10-000-903-19
8	58	100.0	227	17	US-10-899-771-16
9	58	100.0	227	17	US-10-899-771-19
10	58	100.0	383	13	US-10-000-903-23
11	58	100.0	383	17	US-10-899-771-23

12	54	93.1	9	17	US-10-751-845-150	Sequence 150, App
13	54	93.1	17	17	US-10-751-845-156	Sequence 156, App
14	54	93.1	119	17	US-10-751-845-159	Sequence 159, App
15	54	93.1	236	17	US-10-751-845-157	Sequence 157, App
16	54	93.1	237	17	US-10-751-845-158	Sequence 158, App
17	54	93.1	261	17	US-10-751-845-160	Sequence 160, App
18	51	87.9	11	15	US-10-447-161-146	Sequence 146, App
19	44	75.9	21	10	US-09-983-802-444	Sequence 444, App
20	44	75.9	21	10	US-09-984-490-444	Sequence 444, App
21	44	75.9	21	11	US-09-973-278-572	Sequence 572, App
22	44	75.9	149	10	US-09-983-802-443	Sequence 443, App
23	44	75.9	149	10	US-09-984-490-443	Sequence 443, App
24	44	75.9	149	11	US-09-973-278-571	Sequence 571, App
25	43	74.1	232	16	US-10-425-115-209517	Sequence 209517, App
26	42	72.4	56	16	US-10-437-963-196562	Sequence 196562, App
27	42	72.4	325	16	US-10-437-963-183537	Sequence 183537, App
28	41	70.7	13	15	US-10-447-161-145	Sequence 145, App
29	41	70.7	228	16	US-10-425-115-289517	Sequence 289517, App
30	41	70.7	240	14	US-10-029-386-32972	Sequence 32972, A
31	41	70.7	292	15	US-10-357-567-35	Sequence 35, Appl
32	41	70.7	686	15	US-10-369-493-21669	Sequence 21669, A
33	40	69.0	81	16	US-10-425-115-227037	Sequence 227037, A
34	40	69.0	83	16	US-10-437-963-194594	Sequence 194594, A
35	40	69.0	85	15	US-10-424-599-203179	Sequence 203179, A
36	40	69.0	107	11	US-09-864-408A-3052	Sequence 3052, Ap
37	40	69.0	112	16	US-10-437-963-112602	Sequence 112602, A
38	40	69.0	122	16	US-10-425-115-282360	Sequence 282360, A
39	40	69.0	135	16	US-10-425-115-319788	Sequence 319788, A
40	40	69.0	149	16	US-10-437-963-148419	Sequence 148419, A
41	40	69.0	154	16	US-10-767-701-47491	Sequence 47491, A
42	40	69.0	170	15	US-10-424-599-243062	Sequence 243062, A
43	40	69.0	213	15	US-10-424-599-243060	Sequence 243060, A
44	40	69.0	213	16	US-10-767-701-39526	Sequence 39526, A
45	40	69.0	217	16	US-10-425-115-354317	Sequence 354317, A

ALIGNMENTS

RESULT 1

US-10-432-465-103
; Sequence 103, Application US/10432465
; Publication No. US20040091479A1
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, John
; APPLICANT: Kaufmann, Andreas
; APPLICANT: Kather, Angela
; APPLICANT: Schinz, Manuela
; TITLE OF INVENTION: T-Cell Epitopes of the Papillomavirus L1
; TITLE OF INVENTION: Protein and E7 Protein and Their Use in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/077001
; CURRENT APPLICATION NUMBER: US/10432465
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/14037
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 10059631.2
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-432-465-103

Query Match 100.0%; Score 58; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9

Db 6 LSFVCPWCA 14

```

RESULT 2
US-10-433-091-72
; Sequence 72, Application US/10433091
; Publication No. US20040101533A1
; GENERAL INFORMATION:
; APPLICANT: MULLER, RAINER
; APPLICANT: NIELAND, JOHN
; APPLICANT: GABELSBERGER, JOSEF
; APPLICANT: HERBST, RUTH
; TITLE OF INVENTION: MEDICAMENT FOR PREVENTING OR TREATING TUMORS CAUSED BY
; FILE REFERENCE: 037067/0115
; CURRENT APPLICATION NUMBER: US/10/433,091
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: PCT/EP01/14038
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 100 59 630.4
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 72
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Human papillomavirus type 18
US-10-433-091-72

Query Match      100.0%; Score 58; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 6 LSFVCPWCA 14

RESULT 3
US-10-433-091-4
; Sequence 4, Application US/10433091
; Publication No. US20040101533A1
; GENERAL INFORMATION:
; APPLICANT: MULLER, RAINER
; APPLICANT: NIELAND, JOHN
; APPLICANT: GABELSBERGER, JOSEF
; APPLICANT: HERBST, RUTH
; TITLE OF INVENTION: MEDICAMENT FOR PREVENTING OR TREATING TUMORS CAUSED BY
; FILE REFERENCE: 037067/0115
; CURRENT APPLICATION NUMBER: US/10/433,091
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: PCT/EP01/14038
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 100 59 630.4
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 4
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Human papillomavirus type 18
US-10-433-091-4

Query Match      100.0%; Score 58; DB 16; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 94 LSFVCPWCA 102

RESULT 4
US-10-433-091-4
; Sequence 4, Application US/10433091
; Publication No. US20040101533A1
; GENERAL INFORMATION:
; APPLICANT: MULLER, RAINER
; APPLICANT: NIELAND, JOHN
; APPLICANT: GABELSBERGER, JOSEF
; APPLICANT: HERBST, RUTH
; TITLE OF INVENTION: MEDICAMENT FOR PREVENTING OR TREATING TUMORS CAUSED BY
; FILE REFERENCE: 037067/0115
; CURRENT APPLICATION NUMBER: US/10/433,091
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: PCT/EP01/14038
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 100 59 630.4
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 4
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Human papillomavirus type 18
US-10-433-091-4

Query Match      100.0%; Score 58; DB 16; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 94 LSFVCPWCA 102

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US-10-800-023-28
; Sequence 28, Application US/10800023
; Publication No. US20040258688A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Ralph
; APPLICANT: Nussenzweig, Michel
; APPLICANT: Hawiger, Daniel
; APPLICANT: Bonifaz, Laura
; TITLE OF INVENTION: Enhanced Antigen Delivery and Modulation
; TITLE OF INVENTION: of the Immune Response Therefrom
; FILE REFERENCE: 600-1-081CONCIP1
; CURRENT APPLICATION NUMBER: US/10/800,023
; CURRENT FILING DATE: 2004-03-14
; PRIOR APPLICATION NUMBER: 09/925,284
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/586,704
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: PCT/US96/01383
; PRIOR FILING DATE: 1996-01-31
; PRIOR APPLICATION NUMBER: 08/381,528
; PRIOR FILING DATE: 1995-01-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 105
; TYPE: PRT
; ORGANISM: human papilloma virus E7 protein
US-10-800-023-28

Query Match      100.0%; Score 58; DB 16; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 94 LSFVCPWCA 102

RESULT 5
US-10-472-724-8
; Sequence 8, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-8

Query Match      100.0%; Score 58; DB 16; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 99 LSFVCPWCA 107

RESULT 6
US-10-472-724-8

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US-10-000-903-16
; Sequence 16, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-16

Query Match      100.0%; Score 58; DB 13; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 207 LSFVCPWCA 215

RESULT 7
US-10-000-903-19
; Sequence 19, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-19

Query Match      100.0%; Score 58; DB 13; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 207 LSFVCPWCA 215

US-10-000-903-19
; Sequence 19, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-19

Query Match      100.0%; Score 58; DB 13; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 207 LSFVCPWCA 215

US-10-899-771-16
; Sequence 16, Application US/10000903
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and E7 from Human papilloma virus type
; OTHER INFORMATION: 18)
US-10-899-771-16

Query Match      100.0%; Score 58; DB 17; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 207 LSFVCPWCA 215

US-10-899-771-19
; Sequence 19, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and mutated E7 from Human papilloma
; OTHER INFORMATION: virus type 18)
US-10-899-771-19

Query Match      100.0%; Score 58; DB 17; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 207 LSFVCPWCA 215
```

RESULT 10

US-10-903-23
 ; Sequence 23, Application US/1000903
 ; Publication No. US20020182221A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bruck, Claudine
 ; APPLICANT: Cabezon Silva, Teresa
 ; APPLICANT: Delisse, Anne-Marie Eva Fernandez
 ; APPLICANT: Gerard, Catherine Marie Ghislaine
 ; APPLICANT: Lombardo-Bencheikh, Angela
 ; TITLE OF INVENTION: Vaccine
 ; FILE REFERENCE: B45107
 ; CURRENT APPLICATION NUMBER: US/10/000,903
 ; CURRENT FILING DATE: 2001-10-01
 ; PRIOR APPLICATION NUMBER: PCT/EP98/05285
 ; PRIOR FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: GB 9717953.5
 ; PRIOR FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 383
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-000-903-23

Query Match 100.0%; Score 58; DB 13; Length 383;
 Best Local Similarity 100.0%; Pred. No. 0.62;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LSFVCPWCA 9
 Db 363 LSFVCPWCA 371

RESULT 11

US-10-899-771-23
 ; Sequence 23, Application US/10899771
 ; Publication No. US20050031638A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dalemans, Wilfried L.J.
 ; APPLICANT: Gerard, Catherine Marie Ghislaine
 ; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
 ; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
 ; FILE REFERENCE: B45124
 ; CURRENT APPLICATION NUMBER: US/10/899,771
 ; CURRENT FILING DATE: 2004-07-27
 ; PRIOR APPLICATION NUMBER: US/09/581,976
 ; PRIOR FILING DATE: 2000-06-20
 ; PRIOR APPLICATION NUMBER: PCT/EP98/08563
 ; PRIOR FILING DATE: 1998-12-18
 ; PRIOR APPLICATION NUMBER: GB 9727262.9
 ; PRIOR FILING DATE: 1997-12-24
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 383
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
 ; OTHER INFORMATION: Influenzae B and B6E7 fusion from Human papilloma
 ; OTHER INFORMATION: virus type 18)
 US-10-899-771-23

Query Match 100.0%; Score 58; DB 17; Length 383;
 Best Local Similarity 100.0%; Pred. No. 0.62;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LSFVCPWCA 9
 Db 363 LSFVCPWCA 371

RESULT 12

US-10-751-845-150
 ; Sequence 150, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chicz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 150
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Human Papilloma virus
 US-10-751-845-150

Query Match 93.1%; Score 54; DB 17; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LSFVCPWC 8
 Db 2 LSFVCPWC 9

RESULT 13

US-10-751-845-156
 ; Sequence 156, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chicz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 156
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: Human Papilloma virus
 US-10-751-845-156

Query Match 93.1%; Score 54; DB 17; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LSFVCPWC 8
 Db 10 LSFVCPWC 17

RESULT 14

Search completed: June 29, 2005, 04:19:25
Job time : 58.85 secs

US-10-751-845-159
; Sequence 159, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-159

Query Match 93.1%; Score 54; DB 17; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LSFVCPWC 8
|||
Db 112 LSFVCPWC 119

RESULT 15
US-10-751-845-157
; Sequence 157, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-157

Query Match 93.1%; Score 54; DB 17; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LSFVCPWC 8
|||
Db 229 LSFVCPWC 236

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-34
Perfect score: 58
Sequence: 1 LSFVCPWCA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	29	US-08-934-915-66	Sequence 66, Appl
2	58	100.0	227	US-09-485-885-16	Sequence 16, Appl
3	58	100.0	227	US-09-485-885-19	Sequence 19, Appl
4	58	100.0	272	US-08-117-083-13	Sequence 13, Appl
5	58	100.0	383	US-09-485-885-23	Sequence 23, Appl
6	44	75.9	21	US-09-227-357-444	Sequence 444, App
7	44	75.9	149	US-09-227-357-443	Sequence 443, App
8	43	74.1	206	US-09-902-540-11760	Sequence 11760, A
9	41	70.7	292	US-09-323-872A-35	Sequence 35, Appl
10	41	70.7	292	US-09-072-433-37	Sequence 37, Appl
11	40	69.0	119	US-09-252-991A-24123	Sequence 24123, A
12	40	69.0	351	US-09-489-039A-7442	Sequence 7442, Ap
13	39.5	66.4	327	US-09-252-991A-30618	Sequence 30618, A
14	38	65.5	13	US-09-099-631A-4	Sequence 4, Appl
15	38	65.5	140	US-09-248-796A-16891	Sequence 16891, A
16	37	63.8	37	US-09-205-258-447	Sequence 447, App
17	37	63.8	81	US-09-621-976-7707	Sequence 7707, Ap
18	37	63.8	215	US-09-949-016-9485	Sequence 9485, Ap
19	37	63.8	238	US-09-252-991A-23069	Sequence 23069, A
20	37	63.8	258	US-09-583-110-4107	Sequence 4107, Ap
21	37	63.8	261	US-09-252-991A-19436	Sequence 19436, A
22	37	63.8	263	US-09-107-433-2968	Sequence 2968, Ap
23	37	63.8	323	US-09-543-681A-7304	Sequence 7304, Ap
24	37	63.8	344	US-08-818-112-69	Sequence 69, Appl
25	37	63.8	344	US-08-818-111-70	Sequence 70, Appl
26	37	63.8	344	US-09-056-556-69	Sequence 69, Appl
27	37	63.8	344	US-09-072-596-70	Sequence 70, Appl

28	37	63.8	344	4	US-09-072-967-69	Sequence 69, Appl
29	37	63.8	652	1	US-08-050-684-2	Sequence 2, Appl
30	37	63.8	652	1	US-08-582-719-2	Sequence 2, Appl
31	37	63.8	753	1	US-08-712-241-3	Sequence 3, Appl
32	37	63.8	753	1	US-08-026-143B-3	Sequence 3, Appl
33	37	63.8	753	5	PCT-US92-10621-3	Sequence 3, Appl
34	37	63.8	753	5	PCT-US94-02233-3	Sequence 3, Appl
35	36	62.1	45	4	US-09-270-767-33573	Sequence 33573, A
36	36	62.1	45	4	US-09-270-767-48790	Sequence 48790, A
37	36	62.1	49	4	US-09-270-767-35062	Sequence 35062, A
38	36	62.1	49	4	US-09-270-767-50279	Sequence 50279, A
39	36	62.1	54	4	US-08-732-210-930	Sequence 930, App
40	36	62.1	67	1	US-08-464-531-86	Sequence 86, Appl
41	36	62.1	67	2	US-08-461-598-86	Sequence 86, Appl
42	36	62.1	67	3	US-08-322-137-86	Sequence 86, Appl
43	36	62.1	157	4	US-09-252-991A-32848	Sequence 32848, A
44	36	62.1	169	4	US-09-902-540-10496	Sequence 10496, A
45	36	62.1	172	4	US-09-134-000C-4129	Sequence 4129, Ap

ALIGNMENTS

RESULT 1
US-08-934-915-66
; Sequence 66, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-66
Query Match 100.0%; Score 58; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 18 LSFVCPWCA 26

RESULT 2

US-09-485-885-16
; Sequence 16, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-16

Query Match 100.0%; Score 58; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 207 LSFVCPWCA 215

RESULT 3

US-09-485-885-19
; Sequence 19, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-19

Query Match 100.0%; Score 58; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9

Db 207 LSFVCPWCA 215

RESULT 4

US-08-117-083-13
; Sequence 13, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..272
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; the open reading frame."
US-08-117-083-13

Query Match 100.0%; Score 58; DB 1; Length 272;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFVCPWCA 9
Db 257 LSFVCPWCA 265

RESULT 5

US-09-485-885-23
; Sequence 23, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine

FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/05/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 383
TYPE: PRT
ORGANISM: Homo sapien
US-09-485-885-23

Query Match 100.0%; Score 58; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 LSFVCPWCA 9
Db 363 LSFVCPWCA 371
|||||

RESULT 6

US-09-227-357-444
Sequence 444, Application US/09227357
Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.

TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684

EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,932
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,916
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,930
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,918
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,920
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,733
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,795
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,919
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,928
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/055,722
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,948

EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,949
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,953
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,950
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,947
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,964
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/056,360
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,684
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,954
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 444
LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens
US-09-227-357-444

Query Match 75.9%; Score 44; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VCPWCA 9
Db 2 VCPWCA 7
|||||

RESULT 7
US-09-227-357-443
Sequence 443, Application US/09227357
Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,932
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,916

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; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 443
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-443

Query Match      75.9%; Score 44; DB 3; Length 149;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 VCPWCA 9
      :|||||
Db      11 VCPWCA 16

RESULT 8
US-09-902-540-11760
; Sequence 11760, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
```

```
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(115849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11760
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11760

Query Match      74.1%; Score 43; DB 4; Length 206;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 VCPWC 8
      :|||||
Db      13 VCPWC 18

RESULT 9
US-09-323-872A-35
; Sequence 35, Application US/09323872A
; Patent No. 6395539
; GENERAL INFORMATION:
; APPLICANT: Coschigano, Peter
; TITLE OF INVENTION: Compositions and Methods for Bioremediation
; FILE REFERENCE: OHU-03640
; CURRENT APPLICATION NUMBER: US/09/323,872A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/072,433
; PRIOR FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-323-872A-35

Query Match      70.7%; Score 41; DB 3; Length 292;
Best Local Similarity 83.3%; Pred. No. 42;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 VCPWCA 9
      :|||||
Db      50 LCPWCA 55

RESULT 10
US-09-072-433-37
; Sequence 37, Application US/09072433
; Patent No. 6551814
; GENERAL INFORMATION:
; APPLICANT: Coschigano, Peter W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: BIOREMEDIATION
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

; APPLICATION NUMBER: US/09/072,433
; FILING DATE: 04-MAY-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Peter G.
; REGISTRATION NUMBER: 32,837
; REFERENCES/DOCKET NUMBER: OHU-03344
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 292 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-072-433-37

Query Match 70.7%; Score 41; DB 4; Length 292;
Best Local Similarity 83.3%; Pred. No. 42;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VCPWCA 9
:|||||
DB 50 LCPWCA 55

RESULT 11
US-09-252-991A-24123
; Sequence 24123, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24123
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24123

Query Match 69.0%; Score 40; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CPWCA 9
:|||||
DB 17 CPWCA 21

RESULT 12
US-09-489-039A-7442
; Sequence 7442, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 7442
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7442

Query Match 69.0%; Score 40; DB 4; Length 351;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CPWCA 9
:|||||
DB 110 CPWCA 114

RESULT 13
US-09-252-991A-30618
; Sequence 30618, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30618
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30618

Query Match 66.4%; Score 38.5; DB 4; Length 327;
Best Local Similarity 70.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 LSFVC-PWCA 9
:|||||
DB 196 LSTICLPWCA 205

RESULT 14
US-09-099-631A-4
; Sequence 4, Application US/09099631A
; Patent No. 6444645
; GENERAL INFORMATION:
; APPLICANT: Seasted, Michael E.
; APPLICANT: Osapay, Kiara
; TITLE OF INVENTION: Crosslink-Stabilized Indolicidin Analogs
; FILE REFERENCE: P-UC 3050
; CURRENT APPLICATION NUMBER: US/09/099,631A
; CURRENT FILING DATE: 1998-06-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (13)
; OTHER INFORMATION: AMIDATION
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Construct
US-09-099-631A-4

Query Match 65.5%; Score 38; DB 4; Length 13;
Best Local Similarity 62.5%; Pred. No. 6.6;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSFVCPWC 8
| : |||
Db 2 LPWKCPWC 9

RESULT 15
US-09-248-796A-16891
; Sequence 16891, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16891
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16891

Query Match 65.5%; Score 38; DB 4; Length 140;
Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LSFVCPW 7
: || |||
Db 44 VSFACPW 50

Search completed: June 28, 2005, 21:33:29
Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-33
Perfect score: 43
Sequence: 1 LFLNTLSFV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	105	1 W7WL18	E7 protein - human
2	43	100.0	244	2 B36607	NS3-1 protein - po
3	43	100.0	244	2 B60076	hypothetical prote
4	43	100.0	244	2 S47425	hypothetical prote
5	43	100.0	244	2 B60007	hypothetical prote
6	43	100.0	251	2 JQ1722	3b protein - canin
7	38	88.4	106	2 S36562	E7 protein - human
8	38	88.4	244	2 S04890	hypothetical prote
9	35	81.4	197	2 C86748	hypothetical prote
10	35	81.4	270	2 S77574	oligopeptide trans
11	35	81.4	292	2 G01409	histamine N-methyl
12	35	81.4	302	2 A99074	hypothetical prote
13	34	79.1	92	1 S15622	E7 protein - human
14	34	79.1	176	2 B90343	hypothetical prote
15	33	76.7	206	2 T22816	hypothetical prote
16	33	76.7	239	2 D81335	ubiquinol-cytochro
17	33	76.7	272	2 S28745	uridylylate kinase (
18	33	76.7	289	2 C70169	hypothetical prote
19	33	76.7	305	2 B89500	protein P56B6.1 (i
20	33	76.7	458	2 E97349	membrane associate
21	33	76.7	1939	2 D97316	probable S-layer p
22	33	76.7	3844	2 T18402	asparagine/asparta
23	32	74.4	121	2 AF1730	hypothetical prote
24	32	74.4	214	2 S00832	finger protein (cl
25	32	74.4	242	2 C71006	hypothetical prote
26	32	74.4	290	2 G72203	sugar ABC transpor
27	32	74.4	293	2 B97194	probable protein o
28	32	74.4	307	2 T16457	hypothetical prote
29	32	74.4	408	2 T37929	probable major fac

30	74.4	608	2	T28301	ORF MSV140 hypothe
31	74.4	638	2	D69957	conserved hypothet
32	74.4	1086	2	AH2136	microcystin synthe
33	74.4	2133	2	T30637	hypothetical prote
34	72.1	37	2	C70186	hypothetical prote
35	72.1	94	2	A56555	trypsin inhibitor
36	72.1	107	2	A47487	serine proteinase
37	72.1	127	2	S08468	NADH2 dehydrogenas
38	72.1	146	2	F82180	conserved hypothet
39	72.1	170	2	E90221	hypothetical prote
40	72.1	194	2	D69885	phage-related prot
41	72.1	207	2	H72550	probable inorganic
42	72.1	262	2	S59078	conserved hypothet
43	72.1	321	2	T11088	NADH2 dehydrogenas
44	72.1	341	2	T41098	WD-repeat protein
45	72.1	362	2	T19285	hypothetical prote

ALIGNMENTS

RESULT 1

W7WL18
E7 protein - human papillomavirus type 18
C:Species: human papillomavirus type 18
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: B26165; H26251
R:Seedorf, K.; Olteradorf, T.; Kraemer, G.; Roewekamp, W.
EMBO J. 6, 139-144, 1987
A:Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)
A:Reference number: A91068; MUID:87218459; PMID:3034571
A:Accession: B26165
A:Molecule type: DNA
A:Residues: 1-105 <SEE>
A:Cross-references: UNIPROT:P06788; GB:X04773; MID:G60876; PIDN:CAA28467.1; PID:G60878
R:Cole, S.T.; Danos, O.
J. Mol. Biol. 193, 599-608, 1987
A:Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 18
A:Reference number: A92937; MUID:87283882; PMID:3039146
A:Accession: H26251
A:Molecule type: DNA
A:Residues: 1-105 <COL>
A:Cross-references: GB:X05015; MID:G60975; PIDN:CAA28665.1; PID:G60977
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 100.0%; Score 43; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LFLNTLSFV 9
|||
Db 89 LFLNTLSFV 97

RESULT 2

B36607
NS3-1 protein - porcine respiratory virus (strain RM4)
C:Species: porcine respiratory virus
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 09-Jul-2004
C:Accession: B36607
R:Rasschaert, D.; Duarte, M.; Laude, H.
J. Gen. Virol. 71, 2599-2607, 1990
A:Title: Porcine respiratory coronavirus differs from transmissible gastroenteritis virus
A:Reference number: A36607; MUID:91073120; PMID:2174956
A:Accession: B36607
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-244 <RAS>
A:Cross-references: UNIPROT:P24414; GB:Z24675; MID:G395057; PIDN:CAA80838.1; PID:G395059

Query Match 100.0%; Score 43; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.3;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9
| | | | | | | |
Db 5 LFLNTLSFV 13

RESULT 3
B60076
hypotheical protein 2 - porcine transmissible gastroenteritis virus (strain FS772/70)
C:Species: porcine transmissible gastroenteritis virus
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 09-Jul-2004
C:Accession: B60076; S08002
R:Britton, P.; Otin, C.L.; Alonso, J.M.M.; Parra, P.
Arch. Virol. 105, 165-178, 1989
A:Title: Sequence of the coding regions from the 3.0 kb and 3.9 kb mRNA. Subgenomic spec
A:Reference number: A60076; MUID:89321808; PMID:2546515
A:Accession: B60076
A:Molecule type: mRNA
A:Residues: 1-244 <BRI>
A:Cross-references: UNIPROT:P22656; EMBL:X14551; NID:G58990; PIDN:CAA32687.1; PID:G58992

Query Match 100.0%; Score 43; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9
| | | | | | | |
Db 5 LFLNTLSFV 13

RESULT 4
S47425
hypotheical protein 3b - porcine transmissible gastroenteritis virus
C:Species: porcine transmissible gastroenteritis virus
C>Date: 23-Nov-1994 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S65853; S47425
R:Chen, C.M.; Cavanagh, D.; Britton, P.
Virus Res. 38, 83-89, 1995
A:Title: Cloning and sequencing of a 8.4-kb region from the 3'-end of a Taiwanese virule
A:Reference number: S65850; MUID:96060227; PMID:8546012
A:Accession: S65853
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: genomic RNA
A:Residues: 1-244 <CH>
A:Cross-references: UNIPROT:Q88512; EMBL:X35758; NID:G529246; PIDN:CAA84808.1; PID:G52924
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994

Query Match 100.0%; Score 43; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9
| | | | | | | |
Db 5 LFLNTLSFV 13

RESULT 5
B60007
hypotheical protein B - porcine transmissible gastroenteritis virus (strain virulent M
C:Species: porcine transmissible gastroenteritis virus
C>Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C:Accession: B60007
R:Weasley, R.D.; Cheung, A.K.; Michael, D.D.; Woods, R.D.
Virus Res. 13, 87-100, 1989
A:Title: Nucleotide sequence of coronavirus TGEV genomic RNA: evidence for 3 mRNA specie
A:Reference number: A60007; MUID:89370816; PMID:2549745
A:Accession: B60007
A:Molecule type: mRNA
A:Residues: 1-244 <WES>
A:Cross-references: UNIPROT:Q85086; UNIPROT:Q84958; UNIPROT:Q88512; UNIPROT:Q85084; UNIF
C:Keywords: Glycoprotein
F:17,22,132/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 43; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9
| | | | | | | |
Db 5 LFLNTLSFV 13

RESULT 6
JQ1722
3b protein - canine coronavirus
C:Species: canine coronavirus
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: JQ1722
R:Horsburgh, B.C.; Brierley, I.; Brown, T.D.K.
J. Gen. Virol. 73, 2849-2862, 1992
A:Title: Analysis of a 9.6 kb sequence from the 3' end of canine coronavirus genomic RNA.
A:Reference number: PQ0481; MUID:93057357; PMID:1431811
A:Accession: JQ1722
A:Molecule type: mRNA
A:Residues: 1-251 <HOR>
A:Cross-references: DDBJ:D13096
A:Experimental source: strain Insavc-1

Query Match 100.0%; Score 43; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9
| | | | | | | |
Db 5 LFLNTLSFV 13

RESULT 7
S36562
E7 protein - human papillomavirus type 45
C:Species: human papillomavirus type 45
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36562
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36562
A:Molecule type: DNA
A:Residues: 1-106
A:Cross-references: UNIPROT:P21736; EMBL:X74479; NID:G397022; PIDN:CAA52574.1; PID:G39702
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 88.4%; Score 38; DB 2; Length 106;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9
| | | | | | | |
Db 90 LFLNTLSFV 98

RESULT 8
S04890
hypotheical protein, 27.7K - porcine transmissible gastroenteritis virus
C:Species: porcine transmissible gastroenteritis virus
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S04890
R:Kapke, P.A.; Tung, F.Y.T.; Brian, D.A.
submitted to the EMBL Data Library, September 1988
A:Description: Nucleotide sequence between the peplomer and matrix protein genes of the
A:Reference number: S04889
A:Accession: S04890
A:Molecule type: DNA


```
A;Residues: 1-244 <KAP>
A;Cross-references: UNIPROT:Q85086; EMBL:X12800; NID:G61373; PIDN:CAA31287.1; PID:G61375

Query Match      88.4%; Score 38; DB 2; Length 244;
Best Local Similarity 88.9%; Pred. No. 3.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFLNTLSFV 9
   |||:|||||
Db 5 LFLSTLSFV 13

RESULT 9
C66748
Hypothetical protein ykhd [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: C66748
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C66748
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-197 <STO>
A;Cross-references: UNIPROT:Q9CGV5; GB:AE005176; PID:g12723931; PIDN:AAK05085.1; GSPDB:C
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ykhd

Query Match      81.4%; Score 35; DB 2; Length 197;
Best Local Similarity 77.8%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LFLNTLSFV 9
   ||:|||||
Db 20 LFIGTLSFV 28

RESULT 10
S77574
oligopeptide transport protein homolog ophC - Agrobacterium tumefaciens plasmid pTiR10
N;Alternate names: oligopeptide permease homolog ophC
C;Species: Agrobacterium tumefaciens
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S77574
R;Fuqua, C.; Winans, S.C.
Mol. Microbiol. 20, 1199-1210, 1996
A;Title: Localization of OpcR-activated and Trar-activated promoters that express two AB
A;Reference number: S77571; MUID:96405643; PMID:8809772
A;Accession: S77574
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-270 <FUG>
A;Cross-references: UNIPROT:Q44374; EMBL:U48718; NID:g1215729; PIDN:AAC44510.1; PID:g121
A;Experimental source: strain RS10
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C;Genetics:
A;Gene: ophC
A;Genome: plasmid pTiR10
C;Superfamily: oligopeptide permease protein oppB
C;Keywords: oligopeptide transport

Query Match      81.4%; Score 35; DB 2; Length 270;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFLNTLSFV 9
   |||:|||||
Db 202 LFLSTLSFV 210
```

```
RESULT 11
G01409
histamine N-methyltransferase (EC 2.1.1.18) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G01409; JC4650
R;Otterness, D.M.
submitted to the EMBL Data Library, March 1994
A;Reference number: G06891
A;Accession: G01409
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-292 <OTT>
A;Cross-references: UNIPROT:P50135; EMBL:U08092; NID:G468258; PIDN:AAAL7423.1; PID:G4682
R;Akoy, S.; Raftogiannis, R.; Weinhiboum, R.
Biochem. Biophys. Res. Commun. 219, 548-554, 1996
A;Title: Human histamine N-methyltransferase gene: Structural characterization and chromo
A;Reference number: JC4650; MUID:96193689; PMID:8605025
A;Accession: JC4650
A;Molecule type: mRNA
A;Residues: 1-104 'T', 106-292 <AKS>
A;Cross-references: GB:U44106
C;Comment: This enzyme is an S-adenosyl-L-methionine-dependent cytosolic enzyme that cat
C;Genetics:
A;Gene: GDB:HNMT
A;Cross-references: GDB:328755
A;Map position: 19q13.2-19q13.4
A;Introns: 46/2; 64/1; 100/1; 143/3; 175/1
C;Keywords: methyltransferase; S-adenosylmethionine

Query Match      81.4%; Score 35; DB 2; Length 292;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LFLNTLSFV 9
   |||:|||||
Db 280 LFNNTLSFI 288

RESULT 12
A99074
Hypothetical protein ABC-MSP [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: A99074
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Es
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: A99074
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-302 <KUR>
A;Cross-references: UNIPROT:Q8DNN8; GB:AE007317; PIDN:AAL00422.1; PID:g15459288; GSPDB:G
C;Genetics:
A;Gene: ABC-MSP
C;Superfamily: inner membrane protein ugpa

Query Match      81.4%; Score 35; DB 2; Length 302;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FLNTLSFV 9
   |||:|||||
Db 82 FLNTLKVF 89

RESULT 13
S15622
E7 protein - human papillomavirus type 57
```

C;Species: human papillomavirus type 57
A;Note: host Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: S15622
R;Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
A;Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and
A;Reference number: S15614; MUID:91186699; PMID:1964523
A;Accession: S15622
A;Molecule type: DNA
A;Residues: 1-92 <HIR>
A;Cross-references: UNIPROT:P22160; EMBL:X55965; NID:G60882; PIDN:CAA39431.1; PID:G60884
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;55-91/Region: zinc finger CCCC motif

Query Match 79.1%; Score 34; DB 1; Length 92;
Best Local Similarity 77.8%; Pred. NO. 7.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LFLNLTLSFV 9
DB 79 LFLNLTLSFV 87

RESULT 14
B90343
Hypothetical protein SSO1805 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: B90343
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: B90343
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-176 <KUR>
A;Cross-references: UNIPROT:Q97XE0; GB:AE006641; NID:G13815057; PIDN:AAK42001.1; GSPDB:G
C;Genetics:
A;Gene: SSO1805

Query Match 79.1%; Score 34; DB 2; Length 176;
Best Local Similarity 75.0%; Pred. NO. 15;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFLNLTLSF 8
DB 112 LFLNLTLSF 119

RESULT 15
T22816
Hypothetical protein F57A10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22816
R;Gardner, A.
submitted to the EMBL Data Library, June 1997
A;Reference number: Z19619
A;Accession: T22816
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-206 <WIL>
A;Cross-references: UNIPROT:O17897; EMBL:Z96048; PIDN:CAB09421.1; GSPDB:GN000023; CESP:FS
A;Experimental source: clone F57A10
C;Genetics:
A;Gene: CESP:F57A10.4
A;Map position: 5
A;Introns: 53/2; 90/3; 137/1; 168/2

C;Superfamily: Caenorhabditis elegans hypothetical protein F57A10.4

Query Match 76.7%; Score 33; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. NO. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFLNLTLS 7
DB 49 LFLNLTLS 55

Search completed: June 28, 2005, 21:27:49
Job time : 12.15 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-33
Perfect score: 43
Sequence: 1 LFLNTLSFV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance-to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query #	Score	Match	Length	DB	ID	Description
1	43	100.0	40	2	Q39434	O39434	feline infe
2	43	100.0	52	2	Q9QEV4	Q9QEV4	porcine res
3	43	100.0	105	1	VE7_HPV18	P05788	human papil
4	43	100.0	105	2	Q6PGP1	Q6PGP1	homo sapien
5	43	100.0	178	2	Q9QEV7	Q9QEV7	porcine res
6	43	100.0	205	2	Q84959	Q84959	porcine res
7	43	100.0	239	2	Q9QEV6	Q9QEV6	porcine res
8	43	100.0	244	1	VNS3_CVFP	P22656	porcine tra
9	43	100.0	244	1	VNS3_CVPRM	P24414	porcine res
10	43	100.0	244	2	Q76WT3	Q76WT3	porcine res
11	43	100.0	244	2	Q84958	Q84958	porcine res
12	43	100.0	244	2	Q85084	Q85084	transmissib
13	43	100.0	244	2	Q88512	Q88512	transmissib
14	43	100.0	244	2	Q9QEV8	Q9QEV8	transmissib
15	43	100.0	244	2	Q9YRA6	Q9YRA6	transmissib
16	43	100.0	250	1	VNS3_CVCAI	P36695	canine ente
17	43	100.0	250	2	Q76T1	Q76T1	canine coro
18	39	90.7	391	2	Q8RN32	Q8RN32	campylobact
19	38	88.4	106	1	VE7_HPV45	P21736	human papil
20	38	88.4	106	2	Q9Y4Y3	Q9Y4Y3	homo sapien
21	38	88.4	106	2	O10609	O10609	human papil
22	38	88.4	244	2	Q85086	Q85086	transmissib
23	38	88.4	1073	2	Q8CE72	Q8CE72	mus musculu
24	37	86.0	63	2	Q89695	Q89695	porcine res
25	37	86.0	105	2	Q8V9K9	Q8V9K9	human papil
26	37	86.0	105	2	Q9QNPS	Q9QNPS	human papil
27	37	86.0	105	2	Q9QNP6	Q9QNP6	human papil
28	37	86.0	105	2	Q9QNP7	Q9QNP7	human papil
29	37	86.0	215	2	Q8QRR3	Q8QRR3	transmissib
30	36	83.7	107	2	Q81965	Q81965	human papil
31	36	83.7	355	2	Q9NFT2	Q9NFT2	drosophila

32 36 83.7 355 2 Q9VTD4 Q9vtd4 drosophila
33 35 81.4 109 1 VE7_HPV70 P50785 human papil
34 35 81.4 117 2 Q9PIY0 Q9piy0 homo sapien
35 35 81.4 117 2 Q9N2A8 Q9n2a8 gorilla gor
36 35 81.4 117 2 Q9N2A9 Q9n2a9 pan troglod
37 35 81.4 197 2 Q9CGV5 Q9cgv5 lactococcus
38 35 81.4 270 2 Q44374 Q44374 agrobacteri
39 35 81.4 274 2 Q981W1 Q981w1 rhizobium l
40 35 81.4 274 2 Q98CJ5 Q98cj5 rhizobium l
41 35 81.4 275 2 Q92NE9 Q92ne9 rhizobium m
42 35 81.4 292 1 HNMT_HUMAN P50135 homo sapien
43 35 81.4 302 2 Q8DNF8 Q8dnf8 streptococ
44 35 81.4 322 2 Q76LP9 Q76lp9 ixodes holo
45 35 81.4 477 2 Q7XUM6 Q7xum6 oryza sativ

ALIGNMENTS

RESULT 1
O39434 PRELIMINARY; PRT; 40 AA.
AC O39434;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE ORF 3b.
GN Name=ORF 3b;
OS Feline infectious peritonitis virus (FIPV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11135;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=79-1146;
RC MEDLINE=93318756; PubMed=9654687; DOI=10.1023/A:1008099209942;
RA Yamanaka M., Crisp T., Brown R., Dale B.;
RT "Nucleotide sequence of the inter-structural gene region of feline
infectious peritonitis virus."
RL Virus Genes 16:317-318(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=79-1146;
RC Yamanaka M.K., Dale B.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBAJ databases.
DR EMBL: AF033000; AAB87470.1; -
DR InterPro: IPR004293; Corona_NS3b.
DR Pfam: PF03053; Corona_NS3b; 1.
SQ SEQUENCE 40 AA; 4466 MW; 7750500AE7B52DEC CRC64;
Query Match 100.0%; Score 43; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LFLNTLSFV 9
Db 5 LFLNTLSFV 13
RESULT 2
Q9QEV4 PRELIMINARY; PRT; 52 AA.
AC Q9QEV4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Porcine respiratory coronavirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11146;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=BW155;
RX MEDLINE=20403263; PubMed=10948987;
RA Kim L., Hayes J., Lewis P., Parwani A.V., Chang K.O., Saif L.J.;
RT "Molecular characterization and pathogenesis of transmissible
RT gastroenteritis coronavirus (TGEV) and porcine respiratory coronavirus
RT (PRCV) field isolates co-circulating in a swine herd.";
RL Arch. Virol. 145:1133-1147(2000).
DR EMBL; AF179889; AAF02718.1; -;
DR InterPro; IPR004293; Corona_NS3b.
DR Pfam; PF03053; Corona_NS3b; 1.
KW Hypothetical protein.
SQ SEQUENCE 52 AA; 5879 MW; 98D0F7B3F7DE78F7 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.38; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 LFLNTLSFV 9
| | | | | | | | | |
Db 5 LFLNTLSFV 13
| | | | | | | | | |

RESULT 3
VE7 HPV18
ID VE7 HPV18 STANDARD; PRT; 105 AA.
AC P06788;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E7 protein.
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87283882; PubMed=3039146;
RA Cole S.R., Danos O.;
RT "Nucleotide sequence and comparative analysis of the human
RT papillomavirus type 18 genome. Phylogeny of papillomaviruses and
RT repeated structure of the E6 and E7 gene products.";
RL J. Mol. Biol. 193:599-608(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88188247; PubMed=2833614;
RA Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M.,
RA Sugimura T.;
RT "Nucleotide sequences of cDNAs for human papillomavirus type 18
RT transcripts in HeLa cells.";
RL J. Virol. 62:1640-1646(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87053870; PubMed=3023067;
RA Schneider-Gaedcke A., Schwarz E.;
RT "Different human cervical carcinoma cell lines show similar
RT transcription patterns of human papillomavirus type 18 early genes.";
RL EMBO J. 5:2285-2292(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=87218459; PubMed=3034571;
RA Seedorf K., Oltersdorf T., Kramer G., Roewekamp W.;
RT "Identification of early proteins of the human papilloma viruses type
RT 16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells.";
RL EMBO J. 6:139-144(1987).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X05015; CAA28665.1; -;
DR EMBL; M20324; AAA99513.1; -;
DR EMBL; M20325; AAA99515.1; -;
DR EMBL; M26798; AAA46947.1; -;
DR EMBL; X04773; CAA28467.1; -;
DR EMBL; A06324; CAA00540.1; -;
DR EMBL; A06328; CAA00543.1; -;
DR PIR; B26165; W7WL18.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW Transcription regulation.
FT SITE 63 66 C-XX-C motif-1.
FT SITE 98 101 C-XX-C motif-2.
FT CONFLICT 73 73 K -> E (in Ref. 1 and 4).
SQ SEQUENCE 105 AA; 11995 MW; 2CDB119534D0186A CRC64;

Query Match 100.0%; Score 43; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.74; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 LFLNTLSFV 9
| | | | | | | | | |
Db 89 LFLNTLSFV 97
| | | | | | | | | |

RESULT 4
O6PGP1
ID O6PGP1 PRELIMINARY; PRT; 105 AA.
AC Q6PGP1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056907; AAH56907.1; -;
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.

KW Hypothetical protein.
SQ SEQUENCE 105 AA; 11995 MW; 2CDB119534D0186A CRC64;

Query Match 100.0%; Score 43; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFLNTLSFV 9
|||||
DB 89 LFLNTLSFV 97

RESULT 5
Q9QEV7 PRELIMINARY; PRT; 178 AA.
AC Q9QEV7;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Porcine respiratory coronavirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11146;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BW126;
RX MEDLINE=20403263; PubMed=10948987;
RA Kim L., Hayes J., Lewis P., Parwani A.V., Chang K.O., Saif L.J.;
RT "Molecular characterization and pathogenesis of transmissible
RT gastroenteritis coronavirus (TGEV) and porcine respiratory coronavirus
RT (PRCV) field isolates co-circulating in a swine herd.";
RL Arch. Virol. 145:1133-1147(2000).
DR EMBL; AF179887; AAF02714.1; -;
DR InterPro; IPR004293; Corona_NS3b;
DR Pfam; PF03053; Corona_NS3b; 1.
KW Hypothetical protein.
SQ SEQUENCE 178 AA; 20448 MW; 12C1CF4674F72A65 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFLNTLSFV 9
|||||
DB 5 LFLNTLSFV 13

RESULT 6
Q84959 PRELIMINARY; PRT; 205 AA.
AC Q84959;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE ORF 3-1 gene.
OS Porcine respiratory coronavirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11146;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95222773; PubMed=7707547;
RA Vaughn E.M., Halbur P.G., Paul P.S.;
RT "Sequence comparison of porcine respiratory coronavirus isolates
RT reveals heterogeneity in the S, 3, and 3-1 genes.";
RL J. Virol. 69:3176-3184(1995).
DR EMBL; U26213; AAA67943.1; -;
DR InterPro; IPR004293; Corona_NS3b;
DR Pfam; PF03053; Corona_NS3b; 1.
SQ SEQUENCE 205 AA; 23234 MW; 09D8239E2BDDC76B CRC64;

Query Match 100.0%; Score 43; DB 2; Length 205;

Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFLNTLSFV 9
|||||
DB 5 LFLNTLSFV 13

RESULT 7
Q9QEV6 PRELIMINARY; PRT; 239 AA.
AC Q9QEV6;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Porcine respiratory coronavirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11146;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BW154;
RX MEDLINE=20403263; PubMed=10948987;
RA Kim L., Hayes J., Lewis P., Parwani A.V., Chang K.O., Saif L.J.;
RT "Molecular characterization and pathogenesis of transmissible
RT gastroenteritis coronavirus (TGEV) and porcine respiratory coronavirus
RT (PRCV) field isolates co-circulating in a swine herd.";
RL Arch. Virol. 145:1133-1147(2000).
DR EMBL; AF179888; AAF02716.1; -;
DR InterPro; IPR004293; Corona_NS3b;
DR Pfam; PF03053; Corona_NS3b; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 27198 MW; EF97BB42551D28F2_CRC64;

Query Match 100.0%; Score 43; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFLNTLSFV 9
|||||
DB 5 LFLNTLSFV 13

RESULT 8
VNS3_CVPFS STANDARD; PRT; 244 AA.
AC P22656;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Nonstructural protein 3-1 (X2B protein) (ORF 2).
GN Name=NS3-1;
OS Porcine transmissible gastroenteritis coronavirus (strain F8772/70)
OS (TGEV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11150;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89321808; PubMed=2546515;
RA Britton P., Lopez-Otin C., Alonso J.M.M., Parra F.;
RT "Sequence of the coding regions from the 3.0 kb and 3.9 kb mRNA.
RT Subgenomic species from a virulent isolate of transmissible
RT gastroenteritis virus.";
RL Arch. Virol. 105:165-178(1989).
CC -!- SIMILARITY: Belongs to the coronaviruses NS3b protein family.
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DR EMBL; X14551; CAA32687.1; -.

DR PIR; B60076; B60076.

DR InterPro; IPR004293; Corona_NS3b.

DR Pfam; PF03053; Corona_NS3b; 1.

KW Nonstructural protein_

KW Nonstructural protein_

SQ SEQUENCE 244 AA; 27624 MW; 2717B86EA0300A17 CRC64;

Query Match 100.0%; Score 43; DB 1; Length 244;

Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9

Db 5 LFLNTLSFV 13

RESULT 9

VNS3_CVPRM STANDARD; PRT; 244 AA.

ID VNS3_CVPRM

AC P24414;

DT 01-MAR-1992 (Rel. 21, Created)

DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Nonstructural protein 3-1.

GN Name=NS3-1;

OS Porcine respiratory coronavirus (strain RM4) (PRCOV) (PRCV).

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;

OC Coronaviridae; Coronavirus.

OX NCBI_TaxID=11148;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91073120; PubMed=2174956;

RA Raeschaert D., Duarte M., Laufer H.;

RT "Porcine respiratory coronavirus differs from transmissible gastroenteritis virus by a few genomic deletions.";

RL J. Gen. Virol. 71:2599-2607(1990).

CC -!- SIMILARITY: Belongs to the coronaviruses NS3b protein family.

CC -----

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DR EMBL; Z24675; CAA80838.1; -.

DR PIR; B36607; B36607.

DR InterPro; IPR004293; Corona_NS3b.

DR Pfam; PF03053; Corona_NS3b; 1.

KW Nonstructural protein.

SQ SEQUENCE 244 AA; 27686 MW; B623844CAF2F008C CRC64;

Query Match 100.0%; Score 43; DB 1; Length 244;

Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9

Db 5 LFLNTLSFV 13

RESULT 10

Q76WT3 PRELIMINARY; PRT; 244 AA.

ID Q76WT3

AC Q76WT3;

DT 05-JUL-2004 (TRENBLrel. 27, Created)

DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)

DE ORF-3.

OS Porcine respiratory coronavirus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;

OC Coronaviridae; Coronavirus; Group 1 species.

OX NCBI_TaxID=11148;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=86/137004; PubMed=1848593;

RX MEDLINE=91170940; Britton P.;

RA Page K.W., Mawditt K.L., Britton P.;

RT "Sequence comparison of the 5'-end of mRNA 3 from transmissible gastroenteritis virus and porcine respiratory coronavirus.";

RL J. Gen. Virol. 72:579-587(1991).

DR EMBL; D00658; BAA00549.1; -.

DR InterPro; IPR004293; Corona_NS3b.

DR Pfam; PF03053; Corona_NS3b; 1.

SQ SEQUENCE 244 AA; 27686 MW; B623844CAF2F008C CRC64;

Query Match 100.0%; Score 43; DB 2; Length 244;

Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9

Db 5 LFLNTLSFV 13

RESULT 11

Q84958 PRELIMINARY; PRT; 244 AA.

ID Q84958

AC Q84958;

DT 01-NOV-1996 (TRENBLrel. 01, Created)

DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE ORF 3b gene.

OS Porcine respiratory coronavirus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;

OC Coronaviridae; Coronavirus; Group 1 species.

OX NCBI_TaxID=11148;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9522773; PubMed=7707547;

RA Vaughn E.M., Haibur P.G., Paul P.S.;

RT "Sequence comparison of porcine respiratory coronavirus isolates reveals heterogeneity in the S, 3, and 3-1 genes.";

RL J. Virol. 69:3176-3184(1995).

DR EMBL; U26212; AAA67942.1; -.

DR PIR; B60007; B60007.

DR InterPro; IPR004293; Corona_NS3b.

DR Pfam; PF03053; Corona_NS3b; 1.

SQ SEQUENCE 244 AA; 27648 MW; 627E5D0DB0794BDA CRC64;

Query Match 100.0%; Score 43; DB 2; Length 244;

Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9

Db 5 LFLNTLSFV 13

RESULT 12

Q85084 PRELIMINARY; PRT; 244 AA.

ID Q85084

AC Q85084;

DT 01-NOV-1996 (TRENBLrel. 01, Created)

DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE ORF 3-1.

OS Transmissible gastroenteritis virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;

OC Coronaviridae; Coronavirus; Group 1 species.

OX NCBI_TaxID=11149;

RN [1]

```

RP SEQUENCE FROM N.A.
RX MEDLINE=95222773; PubMed=7707547;
RA Vaughn E.M., Halbur P.G., Paul P.S.;
RT "Sequence comparison of porcine respiratory coronavirus isolates
RT reveals heterogeneity in the S, 3, and 3'-1 genes.";
RL J. Virol. 69:3176-3184(1995).
DR EMBL; U26210; AA67951.1; -.
DR PIR; B60007; B60007.
DR InterPro; IPR004293; Corona_NS3b.
DR Pfam; PF03053; Corona_NS3b; 1.
SQ SEQUENCE 244 AA; 27691 MW; F6F11B654AF6BE81 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9
Db 5 LFLNTLSFV 13

RESULT 13
Q88512 PRELIMINARY; PRT; 244 AA.
AC Q88512;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE ORF-3b.
GN Name=ORF-3b;
OS Transmissible gastroenteritis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11149;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TFI;
RX MEDLINE=96060227; PubMed=8546012; DOI=10.1016/0168-1702(95)00046-S;
RA Chen C., Cavanagh D., Britton P.;
RT "Cloning and sequencing of a 8.4-kb region from the 3'-end of a
RT Taiwanese virulent isolate of the coronavirus transmissible
RT gastroenteritis virus.";
RL Virus Res. 38:83-89(1995).
DR EMBL; Z35758; CAA84808.1; -.
DR PIR; B60007; B60007.
DR PIR; S65853; S47425.
DR InterPro; IPR004293; Corona_NS3b.
DR Pfam; PF03053; Corona_NS3b; 1.
SQ SEQUENCE 244 AA; 27792 MW; 04016E1CA115123D CRC64;

Query Match 100.0%; Score 43; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9
Db 5 LFLNTLSFV 13

RESULT 14
Q9QEV8 PRELIMINARY; PRT; 244 AA.
AC Q9QEV8;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Hypothetical protein.
OS Transmissible gastroenteritis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11149;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=BW021898B;
RX MEDLINE=20403263; PubMed=10948987;
RA Kim L., Hayes J., Lewis P., Parwani A.V., Chang K.O., Saif L.J.;
RT "Molecular characterization and pathogenesis of transmissible
RT gastroenteritis coronavirus (TGEV) and porcine respiratory coronavirus
RT (PRCV) field isolates co-circulating in a swine herd.";
RL Arch. Virol. 145:1133-1147(2000).
DR EMBL; AF179886; AAF02712.1; -.
DR PIR; B60007; B60007.
DR InterPro; IPR004293; Corona_NS3b.
DR Pfam; PF03053; Corona_NS3b; 1.
KW Hypothetical protein.
SQ SEQUENCE 244 AA; 27642 MW; A32FC266AB74BC85 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9
Db 5 LFLNTLSFV 13

RESULT 15
Q9YRA6 PRELIMINARY; PRT; 244 AA.
AC Q9YRA6;
DT 01-MAY-1999 (TREMELrel. 10, Created)
DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Hypothetical protein.
OS Transmissible gastroenteritis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11149;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96-1933;
RX MEDLINE=99293500; PubMed=10365166;
RA McGoldrick A., Lowings J.P., Paton D.J.;
RT "Characterisation of a recent virulent transmissible gastroenteritis
RT virus from Britain with a deleted ORF 3a.";
RL Arch. Virol. 144:763-770(1999).
DR EMBL; AF104420; AAC96005.1; -.
DR InterPro; IPR004293; Corona_NS3b.
DR Pfam; PF03053; Corona_NS3b; 1.
KW Hypothetical protein.
SQ SEQUENCE 244 AA; 27685 MW; D94C8428B269B45D CRC64;

Query Match 100.0%; Score 43; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9
Db 5 LFLNTLSFV 13

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Search completed: June 28, 2005, 21:24:06
Job time : 56.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds

(without alignments)

59,826 Million cell updates/sec

Title: US-08-170-344-33

Perfect score: 43

Sequence: 1 LFLNTLSFV 9

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	10	17	US-10-751-845-146
2	43	100.0	17	15	US-10-432-465-103
3	43	100.0	17	16	US-10-433-091-72
4	43	100.0	17	17	US-10-751-845-156
5	43	100.0	20	15	US-10-432-465-102
6	43	100.0	20	16	US-10-433-091-71
7	43	100.0	105	16	US-10-433-091-4
8	43	100.0	118	16	US-10-472-724-8
9	43	100.0	119	17	US-10-751-845-159
10	43	100.0	227	13	US-10-000-903-16
11	43	100.0	227	13	US-10-000-903-19

12	43	100.0	227	17	US-10-899-771-16	Sequence 16, Appl
13	43	100.0	227	17	US-10-899-771-19	Sequence 15, Appl
14	43	100.0	236	17	US-10-751-845-157	Sequence 157, App
15	43	100.0	237	17	US-10-751-845-158	Sequence 158, App
16	43	100.0	261	17	US-10-751-845-160	Sequence 160, App
17	43	100.0	383	13	US-10-000-903-23	Sequence 23, Appl
18	43	100.0	383	17	US-10-899-771-23	Sequence 23, Appl
19	39	90.7	9	17	US-10-751-845-123	Sequence 123, App
20	37	86.0	105	16	US-10-800-023-28	Sequence 28, Appl
21	36	83.7	13	15	US-10-447-161-145	Sequence 145, App
22	35	83.4	292	9	US-09-919-497-71	Sequence 71, Appl
23	34	79.1	65	16	US-10-437-963-182385	Sequence 182385,
24	34	79.1	111	15	US-10-424-599-148582	Sequence 148582,
25	34	79.1	183	16	US-10-437-963-124028	Sequence 124028,
26	34	79.1	300	17	US-10-774-355A-2092	Sequence 2092, Ap
27	33	76.7	53	15	US-10-424-599-162043	Sequence 162043,
28	33	76.7	59	15	US-10-424-599-220841	Sequence 220841,
29	33	76.7	239	15	US-10-282-122A-54564	Sequence 54564, A
30	33	76.7	289	14	US-10-151-832-6	Sequence 6, Appli
31	33	76.7	289	18	US-10-986-427-6	Sequence 6, Appli
32	33	76.7	310	17	US-10-774-355A-1941	Sequence 1941, Ap
33	33	76.7	318	15	US-10-300-846-10	Sequence 10, Appl
34	33	76.7	319	17	US-10-774-355A-1383	Sequence 1383, Ap
35	33	76.7	442	15	US-10-369-493-9735	Sequence 9735, Ap
36	33	76.7	1668	15	US-10-424-599-214588	Sequence 214588,
37	32	74.4	52	16	US-10-425-115-223059	Sequence 223059,
38	32	74.4	64	15	US-10-424-599-153643	Sequence 153643,
39	32	74.4	103	15	US-10-424-599-190864	Sequence 190864,
40	32	74.4	157	16	US-10-767-701-39531	Sequence 39531, A
41	32	74.4	209	15	US-10-424-599-221962	Sequence 221962,
42	32	74.4	223	16	US-10-437-963-124750	Sequence 124750,
43	32	74.4	237	9	US-09-746-284-2	Sequence 2, Appli
44	32	74.4	318	17	US-10-774-355A-1977	Sequence 1977, Ap
45	32	74.4	328	9	US-09-886-055-301	Sequence 301, App

ALIGNMENTS

RESULT 1

US-10-751-845-146

; Sequence 146, Application US/10751845

; Publication No. US20050100928A1

; GENERAL INFORMATION:

; APPLICANT: Hedley, Mary Lynne

; APPLICANT: Urban, Robert G.

; APPLICANT: Chiciz, Roman M.

; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES

; FILE REFERENCE: 08191-013001

; CURRENT FILING DATE: 2004-01-05

; PRIOR APPLICATION NUMBER: US/10751.845

; PRIOR FILING DATE: 2000-08-18

; PRIOR APPLICATION NUMBER: US 60/169,846

; PRIOR FILING DATE: 1999-12-09

; PRIOR APPLICATION NUMBER: US 60/154,665

; PRIOR FILING DATE: 1999-09-16

; NUMBER OF SEQ ID NOS: 163

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 146

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Human Papilloma virus

US-10-751-845-146

Query Match 100.0%; Score 43; DB 17; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.14;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LFLNTLSFV 9

Db 2 LFLNTLSFV 10

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RESULT 2
US-10-432-465-103
; Sequence 103, Application US/10432465
; Publication No. US20040091479A1
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, John
; APPLICANT: Kather, Angela
; APPLICANT: Schinz, Manuela
; TITLE OF INVENTION: T-Cell Epitopes of the Papillomavirus L1
; TITLE OF INVENTION: Protein and E7 Protein and Their Use in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/077001
; CURRENT APPLICATION NUMBER: US/10/432,465
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/14037
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 10059631.2
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-432-465-103

Query Match      100.0%; Score 43; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFLNTLSFV 9
DB 1 LFLNTLSFV 9

RESULT 3
US-10-433-091-72
; Sequence 72, Application US/10433091
; Publication No. US20040101533A1
; GENERAL INFORMATION:
; APPLICANT: MULLER, RAINER
; APPLICANT: NIELAND, JOHN
; APPLICANT: GABELSBERGER, JOSEF
; APPLICANT: HERBST, RUTH
; TITLE OF INVENTION: MEDICAMENT FOR PREVENTING OR TREATING TUMORS CAUSED BY
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS TYPE 18
; FILE REFERENCE: 037067/0115
; CURRENT APPLICATION NUMBER: US/10/433,091
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: PCT/EP01/14038
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 100 59 630.4
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Human papillomavirus type 18
US-10-433-091-72

Query Match      100.0%; Score 43; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFLNTLSFV 9
DB 1 LFLNTLSFV 9

RESULT 4
US-10-433-091-71
; Sequence 71, Application US/10433091
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US-10-751-845-156
; Sequence 156, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-156

Query Match      100.0%; Score 43; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFLNTLSFV 9
DB 5 LFLNTLSFV 13

RESULT 5
US-10-432-465-102
; Sequence 102, Application US/10432465
; Publication No. US20040091479A1
; GENERAL INFORMATION:
; APPLICANT: Nieland, John
; APPLICANT: Kaufmann, Andreas
; APPLICANT: Kather, Angela
; APPLICANT: Schinz, Manuela
; TITLE OF INVENTION: T-Cell Epitopes of the Papillomavirus L1
; TITLE OF INVENTION: Protein and E7 Protein and Their Use in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/077001
; CURRENT APPLICATION NUMBER: US/10/432,465
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/14037
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 10059631.2
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-432-465-102

Query Match      100.0%; Score 43; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFLNTLSFV 9
DB 12 LFLNTLSFV 20

RESULT 6
US-10-433-091-71
; Sequence 71, Application US/10433091
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; Publication No. US20040101533A1
; GENERAL INFORMATION:
; APPLICANT: MULLER, RAINER
; APPLICANT: NIELAND, JOHN
; APPLICANT: GABELSBERGER, JOSEF
; APPLICANT: HERBST, RUTH
; TITLE OF INVENTION: MEDICAMENT FOR PREVENTING OR TREATING TUMORS CAUSED BY
; FILE REFERENCE: 037067/0115
; CURRENT APPLICATION NUMBER: US/10/433,091
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: PCT/EP01/14038
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 100 59 630.4
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 18
US-10-433-091-71

Query Match      100.0%; Score 43; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LFLNTLSFV 9
Db      12 LFLNTLSFV 20

RESULT 7
US-10-433-091-4
; Sequence 4, Application US/10433091
; Publication No. US20040101533A1
; GENERAL INFORMATION:
; APPLICANT: MULLER, RAINER
; APPLICANT: NIELAND, JOHN
; APPLICANT: GABELSBERGER, JOSEF
; APPLICANT: HERBST, RUTH
; TITLE OF INVENTION: MEDICAMENT FOR PREVENTING OR TREATING TUMORS CAUSED BY
; FILE REFERENCE: 037067/0115
; CURRENT APPLICATION NUMBER: US/10/433,091
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: PCT/EP01/14038
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 100 59 630.4
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Human papillomavirus type 18
US-10-433-091-4

Query Match      100.0%; Score 43; DB 16; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LFLNTLSFV 9
Db      89 LFLNTLSFV 97

RESULT 8
US-10-472-724-8
; Sequence 8, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
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; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-8
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Query Match      100.0%; Score 43; DB 16; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 LFLNTLSFV 9
Db      94 LFLNTLSFV 102
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RESULT 9
US-10-751-845-159
; Sequence 159, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-159
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Query Match      100.0%; Score 43; DB 17; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 LFLNTLSFV 9
Db      107 LFLNTLSFV 115
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RESULT 10
US-10-000-903-16
; Sequence 16, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezón Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
```

```
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-16
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Query Match 100.0%; Score 43; DB 13; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.5; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 LFLNTLSFV 9
Db 202 LFLNTLSFV 210
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RESULT 11
US-10-000-903-19
; Sequence 19, Application US/10000903
; Publication No. US2002182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernandez
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-19
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Query Match 100.0%; Score 43; DB 13; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.5; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 LFLNTLSFV 9
Db 202 LFLNTLSFV 210
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RESULT 12
US-10-899-771-16
; Sequence 16, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
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; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and E7 from Human papilloma virus type
; OTHER INFORMATION: 18)
US-10-899-771-16
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Query Match 100.0%; Score 43; DB 17; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.5; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 LFLNTLSFV 9
Db 202 LFLNTLSFV 210
|||||
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RESULT 13
US-10-899-771-19
; Sequence 19, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and mutated E7 from Human papilloma
; OTHER INFORMATION: virus type 18)
US-10-899-771-19
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Query Match 100.0%; Score 43; DB 17; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.5; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 LFLNTLSFV 9
Db 202 LFLNTLSFV 210
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RESULT 14
US-10-751-845-157
; Sequence 157, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
```

; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-157

Query Match 100.0%; Score 43; DB 17; Length 236;
Best Local Similarity 100.0%; Pred.No. 3.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9
| | | | | | | |
Db 224 LFLNTLSFV 232

RESULT 15
US-10-751-845-158
; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-158

Query Match 100.0%; Score 43; DB 17; Length 237;
Best Local Similarity 100.0%; Pred.No. 3.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9
| | | | | | | |
Db 225 LFLNTLSFV 233

Search completed: June 29, 2005, 04:19:24
Job time : 58.85 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-33
Perfect score: 43
Sequence: 1 LFLNLTSPV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	29	US-08-934-915-66	Sequence 66, Appl
2	43	100.0	227	US-09-485-885-16	Sequence 16, Appl
3	43	100.0	227	US-09-485-885-19	Sequence 19, Appl
4	43	100.0	272	US-08-117-083-13	Sequence 13, Appl
5	43	100.0	383	US-09-485-885-23	Sequence 23, Appl
6	35	81.4	263	US-09-902-540-16422	Sequence 16422, A
7	35	81.4	292	US-09-919-497-71	Sequence 71, Appl
8	35	81.4	292	US-09-949-016-6771	Sequence 6771, Ap
9	35	81.4	324	US-09-949-016-7132	Sequence 7132, Ap
10	33	76.7	224	US-09-543-681A-4894	Sequence 4894, Ap
11	33	76.7	289	US-10-151-832-6	Sequence 6, Appli
12	33	76.7	378	US-09-107-532A-6500	Sequence 6500, Ap
13	32	74.4	61	US-09-248-796A-27222	Sequence 27222, A
14	32	74.4	183	US-09-107-532A-5511	Sequence 5511, Ap
15	32	74.4	441	US-09-107-532A-4173	Sequence 4173, Ap
16	32	74.4	477	US-09-248-796A-26051	Sequence 26051, A
17	31	72.1	66	US-09-248-796A-22497	Sequence 22497, A
18	31	72.1	66	US-09-311-689B-42	Sequence 42, Appl
19	31	72.1	66	US-09-311-689B-43	Sequence 43, Appl
20	31	72.1	92	US-09-270-767-46770	Sequence 46770, A
21	31	72.1	127	US-09-270-767-45094	Sequence 45094, A
22	31	72.1	302	US-09-710-279-2980	Sequence 2980, Ap
23	31	72.1	350	US-09-134-001C-3383	Sequence 3383, Ap
24	31	72.1	434	US-09-328-352-4261	Sequence 4261, Ap
25	31	72.1	660	US-09-252-991A-22396	Sequence 22396, A
26	31	72.1	672	US-09-543-681A-5976	Sequence 5976, Ap
27	31	72.1	823	US-09-491-356C-23	Sequence 23, Appl

28	31	72.1	848	4	US-09-491-356C-22	Sequence 22, Appl
29	31	72.1	933	4	US-09-949-016-8386	Sequence 8386, Ap
30	31	72.1	953	4	US-09-949-016-8387	Sequence 8387, Ap
31	30	69.8	145	4	US-09-134-000C-5042	Sequence 5042, Ap
32	30	69.8	185	4	US-09-270-767-35241	Sequence 35241, A
33	30	69.8	185	4	US-09-270-767-50458	Sequence 50458, A
34	30	69.8	249	4	US-09-270-767-45034	Sequence 45034, A
35	30	69.8	283	4	US-09-270-767-61451	Sequence 61451, A
36	30	69.8	327	3	US-08-748-506-14	Sequence 14, Appl
37	30	69.8	327	3	US-08-748-506-24	Sequence 24, Appl
38	30	69.8	350	1	US-08-415-751-20	Sequence 20, Appl
39	30	69.8	387	4	US-09-328-352-5367	Sequence 5367, Ap
40	30	69.8	441	4	US-09-270-767-45465	Sequence 45465, A
41	30	69.8	452	2	US-08-984-171-3	Sequence 3, Appl1
42	30	69.8	576	4	US-09-248-796A-20352	Sequence 20352, A
43	30	69.8	581	3	US-08-619-812-6	Sequence 6, Appl1
44	30	69.8	608	4	US-09-949-016-9905	Sequence 9905, Ap
45	30	69.8	663	4	US-09-711-164-332	Sequence 332, App

ALIGNMENTS

RESULT 1
US-08-934-915-66
; Sequence 66, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-66
Query Match 100.0%; Score 43; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.093;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9
Db 13 LFLNTLSFV 21

RESULT 2
US-09-485-885-16
; Sequence 16, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-16

Query Match 100.0%; Score 43; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9
Db 202 LFLNTLSFV 210

RESULT 3
US-09-485-885-19
; Sequence 19, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-19

Query Match 100.0%; Score 43; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9

Db 202 LFLNTLSFV 210

RESULT 4
US-08-117-083-13
; Sequence 13, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..272
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-13

Query Match 100.0%; Score 43; DB 1; Length 272;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9
Db 252 LFLNTLSFV 260

RESULT 5
US-09-485-885-23
; Sequence 23, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine


```

; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-23

Query Match      100.0%; Score 43; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNLTSLFV 9
Db 358 LFLNLTSLFV 366

RESULT 6
US-09-902-540-16422
; Sequence 16422, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16422
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16422

Query Match      81.4%; Score 35; DB 4; Length 263;
Best Local Similarity 77.8%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 LFLNLTSLFV 9
Db 32 LFLNLTSLFV 40

RESULT 7
US-09-919-497-71
; Sequence 71, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-919-497-71
; Sequence 6771, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6771
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6771

Query Match      81.4%; Score 35; DB 4; Length 292;
Best Local Similarity 77.8%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 LFLNLTSLFV 9
Db 280 LFNLTSLFV 288

RESULT 8
US-09-949-016-6771
; Sequence 6771, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6771
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6771

Query Match      81.4%; Score 35; DB 4; Length 292;
Best Local Similarity 77.8%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 LFLNLTSLFV 9
Db 280 LFNLTSLFV 288

RESULT 9
US-09-949-016-7132
; Sequence 7132, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7132
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7132

Query Match      81.4%; Score 35; DB 4; Length 324;
Best Local Similarity 77.8%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

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APPLICANT: Keith weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

US-09-248-796A-27222

Query Match 74.4%; Score 32; DB 4; Length 61;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9
Db 36 VFLSTLSYV 44

RESULT 14

US-09-107-532A-5511
; Sequence 5511, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5511:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...183
; SEQUENCE DESCRIPTION: SEQ ID NO: 5511:
US-09-107-532A-5511

Query Match 74.4%; Score 32; DB 4; Length 183;
Best Local Similarity 44.4%; Pred. No. 83;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFLNTLSFV 9
Db 11 IFMNTLAYI 19

RESULT 15

US-09-107-532A-4173

; Sequence 4173, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4173:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...441
; SEQUENCE DESCRIPTION: SEQ ID NO: 4173:
US-09-107-532A-4173

Query Match 74.4%; Score 32; DB 4; Length 441;
Best Local Similarity 75.0%; Pred. No. 2,1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLNTLSFV 9
Db 55 FLNSLTFFV 62

Search completed: June 28, 2005, 21:33:28
Job time : 18 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-32

Perfect score: 44

Sequence: 1 QFLNLTSLF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	44	100.0	105	1	VE7 HPV18	P06788 human papillomavirus type 18
2	44	100.0	105	2	Q6PGP1	Q6PGP1 homo sapien
3	39	88.6	40	2	O39434	O39434 feline infe
4	39	88.6	52	2	Q9GEV4	Q9GEV4 porcine res
5	39	88.6	106	1	VE7 HPV45	P21736 human papillomavirus type 45
6	39	88.6	106	2	Q9Y4Y3	Q9Y4Y3 homo sapien
7	39	88.6	106	2	O10609	O10609 human papillomavirus type 18
8	39	88.6	178	2	Q9QEV7	Q9QEV7 porcine res
9	39	88.6	205	2	Q84959	Q84959 porcine res
10	39	88.6	239	2	Q9QEV6	Q9QEV6 porcine res
11	39	88.6	244	1	VNS3_CVPFS	P22656 porcine tra
12	39	88.6	244	1	VNS3_CVPRM	P24414 porcine res
13	39	88.6	244	2	Q76WT3	Q76WT3 porcine res
14	39	88.6	244	2	Q84958	Q84958 porcine res
15	39	88.6	244	2	Q85084	Q85084 transmissib
16	39	88.6	244	2	Q88512	Q88512 transmissib
17	39	88.6	244	2	Q9QEV8	Q9QEV8 transmissib
18	39	88.6	244	2	Q9Y4Y3	Q9Y4Y3 transmissib
19	39	88.6	250	1	VNS3_CVCAI	Q9Y4Y3 transmissib
20	39	88.6	250	2	Q7T6T1	P36695 canine ente
21	38	86.4	105	2	Q8V9K9	Q8V9K9 canine coro
22	38	86.4	105	2	Q9QNP5	Q9QNP5 human papillomavirus type 18
23	38	86.4	105	2	Q9QNP6	Q9QNP6 human papillomavirus type 18
24	38	86.4	105	2	Q9QNP7	Q9QNP7 human papillomavirus type 18
25	38	86.4	108	2	Q9WHG1	Q9WHG1 human papillomavirus type 18
26	37	84.1	107	2	Q81965	Q81965 human papillomavirus type 18
27	36	81.8	109	1	VE7 HPV70	P50785 human papillomavirus type 70
28	36	81.8	215	2	Q7QDL0	Q7QDL0 anopheles g
29	36	81.8	355	2	Q9NFT2	Q9NFT2 drosophila
30	36	81.8	355	2	Q9VTD4	Q9VTD4 drosophila
31	36	81.8	391	2	Q8RN32	Q8RN32 campylobact

32	36	81.8	497	2	Q6D8B4	Q6D8B4 erwinia car
33	36	81.8	1481	2	Q81BB3	Q81BB3 plasmodium
34	35	79.5	92	1	VE7 HPV57	P22160 human papillomavirus type 57
35	35	79.5	315	2	Q6U7U5	Q6U7U5 crinipellis
36	35	79.5	659	2	Q8XVB5	Q8XVB5 raletonia s
37	35	79.5	3531	2	Q7N120	Q7N120 photorhabdu
38	34	77.3	119	2	Q8EQ25	Q8EQ25 oceanobacil
39	34	77.3	138	2	Q866Q4	Q866Q4 sus scrofa
40	34	77.3	176	2	Q97XEO	Q97XEO sulfolobus
41	34	77.3	206	2	O17897	O17897 caenorhabdi
42	34	77.3	244	2	Q85086	Q85086 transmissib
43	34	77.3	252	2	Q99753	Q99753 homo sapien
44	34	77.3	270	2	Q44374	Q44374 agrobacteri
45	34	77.3	274	2	Q981W1	Q981W1 rhizobium 1

ALIGNMENTS

RESULT 1

VE7 HPV18 STANDARD; PRT; 105 AA.
AC P06788;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87283882; PubMed=3039146;
RA Cole S.T., Danos O.;
RT "Nucleotide sequence and comparative analysis of the human papillomavirus type 18 genome. Phylogeny of papillomaviruses and repeated structure of the E6 and E7 gene products."; J. Mol. Biol. 193:599-608(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88188247; PubMed=2833614;
RA Inagaki Y., Tsunokawa Y., Takebe N., Nakanishi S., Terada M., Sugimura T.;
RT "Nucleotide sequences of cDNAs for human papillomavirus type 18 transcripts in HeLa cells."; J. Virol. 62:1640-1646(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87053870; PubMed=3023067;
RA Schneider-Gaedcke A., Schwarz E.;
RT "Different human cervical carcinoma cell lines show similar transcription patterns of human papillomavirus type 18 early genes."; EMO J. 5:2285-2292(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=87218459; PubMed=3034571;
RA Sedorf K., Oltersdorf T., Kraemer G., Roewekamp W.;
RT "Identification of early proteins of the human papilloma viruses type 16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells."; EMO J. 6:1139-144(1987).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating activities.

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DR EMBL; X05015; CAA28665.1; -;
 DR EMBL; M20324; AAA99513.1; -;
 DR EMBL; M20325; AAA99515.1; -;
 DR EMBL; M26798; AAA46947.1; -;
 DR EMBL; X04773; CAA28467.1; -;
 DR EMBL; A06324; CAA00540.1; -;
 DR EMBL; A06328; CAA00543.1; -;
 DR PIR; B26165; W7WL18;
 DR InterPro; IPR000148; Papi_E7.
 DR Pfam; PF00527; E7; 1.
 KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
 KW Transcription regulation.
 FT SITE 63 66 C-XX-C motif-1.
 FT SITE 98 101 C-XX-C motif-2.
 FT CONFLICT 73 73 K -> E (in Ref. 1 and 4).
 SQ SEQUENCE 105 AA; 11995 MW; 2CDB119534D0186A CRC64;

Query Match 100.0%; Score 44; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 0.31;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLFLNTLSF 9
 DB 88 QLFLNTLSF 96

RESULT 2
 Q6PGP1 PRELIMINARY; PRT; 105 AA.
 AC Q6PGP1
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cervix;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska J., Schmutz J., Smalius D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cervix;
 RA Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC056907; AAH56907.1; -;
 DR InterPro; IPR000148; Papi_E7.
 DR Pfam; PF00527; E7; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 105 AA; 11995 MW; 2CDB119534D0186A CRC64;

Query Match 100.0%; Score 44; DB 2; Length 105;
 Best Local Similarity 100.0%; Pred. No. 0.31;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLFLNTLSF 9
 DB 88 QLFLNTLSF 96

RESULT 3
 O39434 PRELIMINARY; PRT; 40 AA.
 AC O39434
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE ORF 3b.
 GN Name=ORF 3b;
 OS Feline infectious peritonitis virus (FIPV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus; Group 1 species.
 OX NCBI_TaxID=11135;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=79-1146;
 RX MEDLINE=98318756; PubMed=9654687; DOI=10.1023/A:1008099209942;
 RA Yamanaka M., Crisp T., Brown R., Dale B.;
 RA "Nucleotide sequence of the inter-structural gene region of feline
 RT infectious peritonitis virus.";
 RL Virus Genes 16:317-318(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=79-1146;
 RA Yamanaka M.K., Dale B.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF033000; AAB87470.1; -;
 DR InterPro; IPR004293; Corona_NS3b.
 DR Pfam; PF03053; Corona_NS3b; 1.
 SQ SEQUENCE 40 AA; 4466 MW; 7750500AE7B52DEC CRC64;

Query Match 88.6%; Score 39; DB 2; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFLNTLSF 9
 DB 5 LFLNTLSF 12

RESULT 4
 Q9QEV4 PRELIMINARY; PRT; 52 AA.
 ID Q9QEV4
 AC Q9QEV4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Porcine respiratory coronavirus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus; Group 1 species.
 OX NCBI_TaxID=11146;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BWL55;
 RX Kim L., Hayes J., Lewis P., Farwani A.V., Chang K.O., Saif L.J.;
 RA "Molecular characterization and pathogenesis of transmissible
 RT gastroenteritis coronavirus (TGEV) and porcine respiratory coronavirus
 RT (PRCV) field isolates co-circulating in a swine herd.";
 RL Arch. Virol. 145:1133-1147(2000).
 DR EMBL; AF179889; AAF02718.1; -;
 DR InterPro; IPR004293; Corona_NS3b.
 DR Pfam; PF03053; Corona_NS3b; 1.

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KW Hypothetical protein.
SQ SEQUENCE 52 AA; 5879 MW; 98D0F7B3F7DE78F7 CRC64;

Query Match      88.6%; Score 39; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFLNTLSF 9
DB 5 LFLNTLSF 12

RESULT 5
VE7_HP45
ID VE7_HP45 STANDARD; PRT; 106 AA.
AC P21736;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sastre-Garau X., Favre M., Couturier J., Orth G.;
RT "Distinct patterns of alteration of myc genes associated with
RT integration of human papillomavirus type 16 oe type 45 in two genital
RT tumors.";
RL J. Gen. Virol. 81:198-199(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Favre M.G.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ242956; CAB44707.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 106 AA; 11977 MW; 1912D1DE742F6BED CRC64;

Query Match      88.6%; Score 39; DB 2; Length 106;
Best Local Similarity 88.9%; Pred. No. 3.4;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLFNTLSF 9
DB 89 QLFNTLSF 97

RESULT 7
OL0609
ID OL0609 PRELIMINARY; PRT; 106 AA.
AC O10609;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Oncoprotein E7.
OS Human papillomavirus type 45.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10593;
RN [1]
RP SEQUENCE FROM N.A.
RA Sastre-Garau X., Favre M., Couturier J., Orth G.;
RT "Distinct patterns of alteration of myc genes associated with
RT integration of HPV16 or HPV45 DNA in two genital tumors.";
RL J. Gen. Virol. 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RA Favre M.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y13218; CAA73661.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 106 AA; 11977 MW; 1912D1DE742F6BED CRC64;

Query Match      88.6%; Score 39; DB 2; Length 106;
Best Local Similarity 88.9%; Pred. No. 3.4;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLFNTLSF 9
DB 89 QLFNTLSF 97

RESULT 8
Q9QEV7
ID Q9QEV7 PRELIMINARY; PRT; 178 AA.
AC Q9QEV7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)

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DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Porcine respiratory coronavirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11146;
RN [1]_TaxID=11146;
RP SEQUENCE FROM N.A.
RC STRAIN=BW126;
RX MEDLINE=20403263; PubMed=10948987;
RA Kim L., Hayes J., Lewis P., Parwani A.V., Chang K.O., Saif L.J.;
RT "Molecular characterization and pathogenesis of transmissible
RT gastroenteritis coronavirus (TGEV) and porcine respiratory coronavirus
RT (PRCV) field isolates co-circulating in a swine herd.";
RL Arch. Virol. 145:1133-1147(2000).
DR EMBL; AF179887; AAF02714.1; -.
DR InterPro; IPR004293; Corona_NS3b.
DR Pfam; PF03053; Corona_NS3b; 1.
KW Hypothetical protein.
SQ SEQUENCE 178 AA; 20448 MW; 12C1CF4674F72A65 CRC64;

Query Match      88.6%; Score 39; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFLNTLSF 9
Db 5 LFLNTLSF 12

RESULT 9
ID Q84959 PRELIMINARY; PRT; 205 AA.
AC Q84959;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ORF 3-1 gene.
OS Porcine respiratory coronavirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11146;
RN [1]_TaxID=11146;
RP SEQUENCE FROM N.A.
RX MEDLINE=95222773; PubMed=7707547;
RA Vaughn E.M., Halbur P.G., Paul P.S.;
RT "Sequence comparison of porcine respiratory coronavirus isolates
RT reveals heterogeneity in the S, 3, and 3-1 genes.";
RL J. Virol. 69:3176-3184(1995).
DR EMBL; U26213; AAA67943.1; -.
DR InterPro; IPR004293; Corona_NS3b.
DR Pfam; PF03053; Corona_NS3b; 1.
SQ SEQUENCE 205 AA; 23234 MW; 09D8239E2BDDC76B CRC64;

Query Match      88.6%; Score 39; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFLNTLSF 9
Db 5 LFLNTLSF 12

RESULT 10
ID Q9QEV6 PRELIMINARY; PRT; 239 AA.
AC Q9QEV6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.

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OS Porcine respiratory coronavirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11146;
RN [1]_TaxID=11146;
RP SEQUENCE FROM N.A.
RC STRAIN=BW154;
RX MEDLINE=20403263; PubMed=10948987;
RA Kim L., Hayes J., Lewis P., Parwani A.V., Chang K.O., Saif L.J.;
RT "Molecular characterization and pathogenesis of transmissible
RT gastroenteritis coronavirus (TGEV) and porcine respiratory coronavirus
RT (PRCV) field isolates co-circulating in a swine herd.";
RL Arch. Virol. 145:1133-1147(2000).
DR EMBL; AF179888; AAF02716.1; -.
DR InterPro; IPR004293; Corona_NS3b.
DR Pfam; PF03053; Corona_NS3b; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 27198 MW; EF97BB42551D28F2 CRC64;

Query Match      88.6%; Score 39; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFLNTLSF 9
Db 5 LFLNTLSF 12

RESULT 11
VNS3_CVPFS STANDARD; PRT; 244 AA.
AC P22656;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Nonstructural protein 3-1 (X2B protein) (ORF 2).
GN Name=NS3-1;
OS Porcine transmissible gastroenteritis coronavirus (strain FS772/70)
OS (TGEV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11150;
RN [1]_TaxID=11150;
RP SEQUENCE FROM N.A.
RX MEDLINE=89321808; PubMed=2546515;
RA Britton P., Lopez-Otin C., Alonso J.M.M., Parra F.;
RT "Sequence of the coding regions from the 3.0 kb and 3.9 kb mRNA.
RT Subgenomic species from a virulent isolate of transmissible
RT gastroenteritis virus.";
RL Arch. Virol. 105:165-178(1989).
CC -1- SIMILARITY: Belongs to the coronaviruses NS3b protein family.
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-----
DR EMBL; X14551; CAA32687.1; -.
DR PIR; B60076; B60076.
DR InterPro; IPR004293; Corona_NS3b.
DR Pfam; PF03053; Corona_NS3b; 1.
KW Nonstructural protein.
SQ SEQUENCE 244 AA; 27624 MW; 2717B86EA0300A17 CRC64;

Query Match      88.6%; Score 39; DB 1; Length 244;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFLNTLSF 9
Db 5 LFLNTLSF 12

```



```
Db 5 LFLNTLSF 12

RESULT 12
VNS3 CVPRM STANDARD; PRT; 244 AA.
AC P244I4;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Nonstructural protein 3-1.
GN Name=NS3-1;
OS Porcine respiratory coronavirus (strain RM4) (PRCoV) (PRCV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11148;
RN [1]
RP SEQUENCE FROM N.A. PubMed=2174956;
RX MEDLINE=91073120; Duarte M., Laude H.;
RA Raschaert D., Duarte M., Laude H.;
RT "Porcine respiratory coronavirus differs from transmissible
RT gastroenteritis virus by a few genomic deletions.";
RL J. Gen. Virol. 71:2599-2607(1990).
CC - SIMILARITY: Belongs to the coronaviruses NS3b protein family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z24675; CAA80838.1; -.
DR PIR; B36607; B36607.
DR InterPro; IPR004293; Corona_NS3b.
DR Pfam; PF03053; Corona_NS3b; 1.
KW Nonstructural protein.
SQ SEQUENCE 244 AA; 27686 MW; B623844CAF2F008C CRC64;

Query Match 88.6%; Score 39; DB 1; Length 244;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LFLNTLSF 9
Db 5 LFLNTLSF 12

RESULT 13
Q76WT3 PRELIMINARY; PRT; 244 AA.
ID Q76WT3;
AC Q76WT3;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE ORF-3.
OS Porcine respiratory coronavirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=86/137004;
RX MEDLINE=91170940; PubMed=1848593;
RA Page K.W., Mawditt K.L., Britton P.;
RT "Sequence comparison of the 5'-end of mRNA 3 from transmissible
RT gastroenteritis virus and porcine respiratory coronavirus.";
RL J. Gen. Virol. 72:579-587(1991).
DR EMBL; D00658; BAA00549.1; -.
DR InterPro; IPR004293; Corona_NS3b.
DR Pfam; PF03053; Corona_NS3b; 1.
SQ SEQUENCE 244 AA; 27686 MW; B623844CAF2F008C CRC64;

Query Match 88.6%; Score 39; DB 1; Length 244;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LFLNTLSF 9
Db 5 LFLNTLSF 12

RESULT 14
Q84958 PRELIMINARY; PRT; 244 AA.
ID Q84958;
AC Q84958;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE ORF 3b gene.
OS Porcine respiratory coronavirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11148;
RN [1]
RP SEQUENCE FROM N.A. PubMed=7707547;
RX MEDLINE=95222773; Paul P.S.;
RA Vaughn E.M., Halbur P.G., Paul P.S.;
RT "Sequence comparison of porcine respiratory coronavirus isolates
RT reveals heterogeneity in the S, 3, and 3-1 genes.";
RL J. Virol. 69:3176-3184(1995).
DR EMBL; U26212; AAA67942.1; -.
DR PIR; B60007; B60007.
DR InterPro; IPR004293; Corona_NS3b.
DR Pfam; PF03053; Corona_NS3b; 1.
SQ SEQUENCE 244 AA; 27648 MW; 627E5D0DB0794BDA CRC64;

Query Match 88.6%; Score 39; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LFLNTLSF 9
Db 5 LFLNTLSF 12

RESULT 15
Q85084 PRELIMINARY; PRT; 244 AA.
ID Q85084;
AC Q85084;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE ORF 3-1.
OS Transmissible gastroenteritis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11149;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95222773; PubMed=7707547;
RA Vaughn E.M., Halbur P.G., Paul P.S.;
RT "Sequence comparison of porcine respiratory coronavirus isolates
RT reveals heterogeneity in the S, 3, and 3-1 genes.";
RL J. Virol. 69:3176-3184(1995).
DR EMBL; U26210; AAA67951.1; -.
DR PIR; B60007; B60007.
DR InterPro; IPR004293; Corona_NS3b.
DR Pfam; PF03053; Corona_NS3b; 1.
SQ SEQUENCE 244 AA; 27691 MW; F6F11B654AF6BE81 CRC64;

Query Match 88.6%; Score 39; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db 5 LFLNTLSF 12

Query Match 88.6%; Score 39; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LFLNTLSF 9
Db 5 LFLNTLSF 12

RESULT 14
Q84958 PRELIMINARY; PRT; 244 AA.
ID Q84958;
AC Q84958;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE ORF 3b gene.
OS Porcine respiratory coronavirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11148;
RN [1]
RP SEQUENCE FROM N.A. PubMed=7707547;
RX MEDLINE=95222773; Paul P.S.;
RA Vaughn E.M., Halbur P.G., Paul P.S.;
RT "Sequence comparison of porcine respiratory coronavirus isolates
RT reveals heterogeneity in the S, 3, and 3-1 genes.";
RL J. Virol. 69:3176-3184(1995).
DR EMBL; U26212; AAA67942.1; -.
DR PIR; B60007; B60007.
DR InterPro; IPR004293; Corona_NS3b.
DR Pfam; PF03053; Corona_NS3b; 1.
SQ SEQUENCE 244 AA; 27648 MW; 627E5D0DB0794BDA CRC64;

Query Match 88.6%; Score 39; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LFLNTLSF 9
Db 5 LFLNTLSF 12

RESULT 15
Q85084 PRELIMINARY; PRT; 244 AA.
ID Q85084;
AC Q85084;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE ORF 3-1.
OS Transmissible gastroenteritis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11149;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95222773; PubMed=7707547;
RA Vaughn E.M., Halbur P.G., Paul P.S.;
RT "Sequence comparison of porcine respiratory coronavirus isolates
RT reveals heterogeneity in the S, 3, and 3-1 genes.";
RL J. Virol. 69:3176-3184(1995).
DR EMBL; U26210; AAA67951.1; -.
DR PIR; B60007; B60007.
DR InterPro; IPR004293; Corona_NS3b.
DR Pfam; PF03053; Corona_NS3b; 1.
SQ SEQUENCE 244 AA; 27691 MW; F6F11B654AF6BE81 CRC64;

Query Match 88.6%; Score 39; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 LFLNTLSP 9
| | | | |
Db 5 LFLNTLSP 12

Search completed: June 28, 2005, 21:24:05
Job time : 57.1 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)

77.664 Million cell updates/sec

Title: US-08-170-344-32

Perfect score: 44

Sequence: 1 QLFNTLSF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	105	1 W7WL18	E7 protein - human
2	39	88.6	106	2 S36562	E7 protein - human
3	39	88.6	244	2 B36607	NS3-1 protein - po
4	39	88.6	244	2 B60076	hypothetical prote
5	39	88.6	244	2 S47425	hypothetical prote
6	39	88.6	244	2 B60007	hypothetical prote
7	39	88.6	251	2 J01722	3b protein - canin
8	35	79.5	92	1 S15622	E7 protein - human
9	34	77.3	176	2 B90343	hypothetical prote
10	34	77.3	206	2 T2816	hypothetical prote
11	34	77.3	244	2 S04890	hypothetical prote
12	34	77.3	270	2 S77574	oligopeptide trans
13	34	77.3	289	2 C70169	hypothetical prote
14	33	75.0	239	2 D81335	uridylyate kinase (
15	33	75.0	378	2 S55634	glycoprotein M - e
16	33	75.0	972	2 H84903	hypothetical prote
17	33	75.0	1939	2 D97316	probable S-layer p
18	32	72.7	214	2 S00832	finger protein (cl
19	32	72.7	282	2 T30729	hypothetical prote
20	32	72.7	290	2 G72203	sugar ABC transpor
21	32	72.7	291	2 T21475	hypothetical prote
22	32	72.7	292	2 G01409	histamine N-methyl
23	32	72.7	327	2 S54560	tom37 protein - ye
24	32	72.7	426	2 F81653	tolB protein, prob
25	32	72.7	545	2 T35429	hypothetical prote
26	32	72.7	1067	2 T06672	probable aminoacyl
27	32	72.7	1067	2 T48850	glycine-tRNA ligas
28	32	72.7	1086	2 AH2136	microcystin synth
29	32	72.7	1299	1 WMBEHS	membrane antigen p

ALIGNMENTS

RESULT 1

W7WL18

E7 protein - human papillomavirus type 18

C/Species: human papillomavirus type 18

C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004

C/Accession: B26165; H26251

R/Seedorf, K.; Olteradorf, T.; Kraemmer, G.; Roewekamp, W.

EMBO J. 6, 139-144, 1987

A/Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)

A/Reference number: A91068; MUID:87218459; PMID:3034571

A/Accession: B26165

A/Molecule type: DNA

A/Residues: 1-105 <SEE>

A/Cross-references: UNIPROT:P06788; GB:X04773; NID:G60876; PIDN:CAA28467.1; PID:G60878

R/Cole, S.T.; Danos, O.

J. Mol. Biol. 193, 599-608, 1987

A/Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 18

A/Reference number: A92937; MUID:87283882; PMID:3039146

A/Accession: H26251

A/Molecule type: DNA

A/Residues: 1-105 <COL>

A/Cross-references: GB:X05015; NID:G60975; PIDN:CAA28665.1; PID:G60977

C/Superfamily: papillomavirus E7 protein

C/Keywords: DNA binding; early protein; transcription regulation

Query Match 100.0%; Score 44; DB 1; Length 105;

Best Local Similarity 100.0%; Pred. No. 0.074;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLFNTLSF 9

Db 88 QLFNTLSF 96

RESULT 2

S36562

E7 protein - human papillomavirus type 45

C/Species: human papillomavirus type 45

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C/Accession: S36562

R/Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A/Description: Primer-directed sequencing of human papillomavirus types.

A/Reference number: S36469

A/Accession: S36562

A/Molecule type: DNA

A/Residues: 1-106

A/Cross-references: UNIPROT:P21736; EMBL:X74479; NID:G397022; PIDN:CAA52574.1; PID:G39702

C/Superfamily: papillomavirus E7 protein

C/Keywords: DNA binding; early protein; transcription regulation

Query Match

88.6%; Score 39; DB 2; Length 106;


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A:Molecule type: DNA
A:Residues: 1-92 <HIR>
A:Cross-References: UNIPROT:P22160; EMBL:X55965; NID:G60882; PIDN:CAA39431.1; PID:G60884
C:Species: papillomavirus E7 protein
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:55-91/Region: zinc finger CCCC motif

Query Match 79.5%; Score 35; DB 1; Length 92;
Best Local Similarity 87.5%; Pred. No. 4.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLFLNTLS 8
DB 78 QLFLNTLT 85

RESULT 9
B90343
Hypothetical protein SSO1805 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: B90343
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: B90343
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-176 <KUR>
A:Cross-References: UNIPROT:Q97XE0; GB:AE006641; NID:G13815057; PIDN:AAK42001.1; GSPDB:G
C:Genetics:
A:Gene: SSO1805

Query Match 77.3%; Score 34; DB 2; Length 176;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFLNTLSF 9
DB 112 IYLNLTSLF 119

RESULT 10
T22816
Hypothetical protein F57A10.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22816
R:Gardner, A.
submitted to the EMBL Data Library, June 1997
A:Reference number: Z19619
A:Accession: T22816
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-206 <WIL>
A:Cross-References: UNIPROT:O17897; EMBL:Z96048; PIDN:CAB09421.1; GSPDB:GN000023; CESP:FS
A:Experimental source: clone F57A10
C:Genetics:
A:Gene: CESP:F57A10.4
A:Map position: 5
A:Introns: 53/2; 90/3; 137/1; 168/2
C:Superfamily: Caenorhabditis elegans hypothetical protein F57A10.4

Query Match 77.3%; Score 34; DB 2; Length 206;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLFLNTLS 8
DB 48 RLFLNTLS 55
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RESULT 11

S04890
Hypothetical protein, 27.7K - porcine transmissible gastroenteritis virus
C:Species: porcine transmissible gastroenteritis virus
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S04890
R:Kapke, P.A.; Tung, F.Y.T.; Brian, D.A.
submitted to the EMBL Data Library, September 1988
A:Description: Nucleotide sequence between the peplomer and matrix protein genes of the
A:Reference number: S04889
A:Accession: S04890
A:Molecule type: DNA
A:Residues: 1-244 <KAP>
A:Cross-References: UNIPROT:Q85086; EMBL:X12800; NID:G61373; PIDN:CAA31387.1; PID:G61375

Query Match 77.3%; Score 34; DB 2; Length 244;
Best Local Similarity 87.5%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFLNTLSF 9
DB 5 LFLSTLSF 12

RESULT 12

S77574
oligopeptide transport protein homolog ophC - Agrobacterium tumefaciens plasmid pTiR10
N:Alternate names: oligopeptide permease homolog ophC
C:Species: Agrobacterium tumefaciens
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: S77574
R:Fuqua, C.; Winans, S.C.
Mol. Microbiol. 20, 1199-1210, 1996
A:Title: Localization of OckR-activated and Trar-activated promoters that express two ABC
A:Reference number: S77571; MUID:96405643; PMID:8809772
A:Accession: S77574
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-270 <FUQ>
A:Cross-References: UNIPROT:Q44374; EMBL:U48718; NID:G1215729; PIDN:AAC44510.1; PID:G1215
A:Experimental source: strain RS10
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C:Genetics:
A:Gene: ophC
A:Genome: plasmid pTiR10
C:Superfamily: oligopeptide permease protein oppB
C:Keywords: oligopeptide transport

Query Match 77.3%; Score 34; DB 2; Length 270;
Best Local Similarity 87.5%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFLNTLSF 9
DB 202 LFLSTLSF 209

RESULT 13

C70169
Hypothetical protein BB0556 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: C70169
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
i. Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: C70169

Search completed: June 28, 2005, 21:27:48
Job time : 12.15 secs

A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-289 <KLE>
A:Cross-references: UNIPROT:O51506; GB:AE001157; GB:AE000783; NID:g2688471; PIDN:AAC6692
A:Experimental source: strain B31

Query Match 77.3%; Score 34; DB 2; Length 289;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLFLNTLSF 9
::| | | | |
Db 184 KIFNTLSF 192

RESULT 14
D81335
uridylylate kinase (EC 2.7.4.-) Cj1274c [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: D81335
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillingworth, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell, A.; et al. 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervirulence
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: D81335
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-239 <PAR>
A:Cross-references: UNIPROT:O9PN24; GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB7352
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:

A:Gene: pyrH; Cj1274c
C:Superfamily: uridylylate kinase
C:Keywords: phosphotransferase

Query Match 75.0%; Score 33; DB 2; Length 239;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFLNTLSF 9
:| | | | | | |
Db 178 VFLNTLSY 185

RESULT 15
S55634
Glycoprotein M - equine herpesvirus 2
C:Species: equine herpesvirus 2
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S55634
R:Teiford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A:Title: The DNA sequence of equine herpesvirus 2.
A:Reference number: S55594; MUID:95302501; PMID:7783207
A:Accession: S55634
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-378 <TEL>
A:Cross-references: UNIPROT:P52371; GB:U20824; NID:g695172; PIDN:AAC13827.1; PID:g695212
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
C:Superfamily: cytomegalovirus UL100 protein
C:Keywords: glycoprotein

Query Match 75.0%; Score 33; DB 2; Length 378;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLFLNTLSF 9
| | | | | | |
Db 140 QLFIQTLSY 148

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds
(without alignments)
59.826 Million cell updates/sec

Title: US-08-170-344-32

Perfect score: 44

Sequence: 1 QLFNTLSF 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:**

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	9	17	US-10-751-845-123
2	44	100.0	10	17	US-10-751-845-146
3	44	100.0	17	17	US-10-751-845-152
4	44	100.0	20	15	US-10-432-465-106
5	44	100.0	20	16	US-10-433-091-71
6	44	100.0	105	16	US-10-433-091-4
7	44	100.0	118	16	US-10-472-724-8
8	44	100.0	119	17	US-10-751-845-159
9	44	100.0	227	13	US-10-000-903-16
10	44	100.0	227	13	US-10-000-903-19
11	44	100.0	227	17	US-10-899-771-16

12	44	100.0	227	17	US-10-899-771-19	Sequence 19, Appl
13	44	100.0	236	17	US-10-751-845-157	Sequence 157, App
14	44	100.0	237	17	US-10-751-845-158	Sequence 158, App
15	44	100.0	261	17	US-10-751-845-160	Sequence 160, App
16	44	100.0	383	13	US-10-000-903-23	Sequence 23, Appl
17	44	100.0	383	17	US-10-899-771-23	Sequence 23, Appl
18	39	88.6	17	15	US-10-432-465-103	Sequence 103, App
19	39	88.6	17	16	US-10-433-091-72	Sequence 72, Appl
20	38	86.4	105	16	US-10-800-023-28	Sequence 28, Appl
21	34	77.3	9	15	US-10-432-465-115	Sequence 115, App
22	34	77.3	9	17	US-10-751-845-149	Sequence 149, App
23	34	77.3	10	17	US-10-751-845-151	Sequence 151, App
24	34	77.3	67	16	US-10-437-963-186297	Sequence 186297,
25	34	77.3	300	17	US-10-774-355A-2092	Sequence 2092, Ap
26	34	77.3	442	15	US-10-369-493-9735	Sequence 9735, Ap
27	34	77.3	497	14	US-10-156-761-8691	Sequence 8691, Ap
28	34	77.3	520	16	US-10-437-963-197312	Sequence 197312,
29	33	75.0	131	16	US-10-425-115-283550	Sequence 283550,
30	33	75.0	239	15	US-10-282-122A-54564	Sequence 54564, A
31	33	75.0	289	14	US-10-151-832-6	Sequence 6, Appli
32	33	75.0	289	18	US-10-986-427-6	Sequence 6150, Ap
33	33	75.0	449	9	US-09-738-626-6150	Sequence 148574,
34	33	75.0	845	16	US-10-437-963-148574	Sequence 214588,
35	33	75.0	1668	15	US-10-424-599-214588	Sequence 145, App
36	32	72.7	13	15	US-10-447-161-145	Sequence 223059,
37	32	72.7	52	16	US-10-425-115-223059	Sequence 1051, Ap
38	32	72.7	63	11	US-09-833-245-1051	Sequence 1052, Ap
39	32	72.7	63	11	US-09-833-245-1052	Sequence 130864,
40	32	72.7	103	15	US-10-424-599-190864	Sequence 134750,
41	32	72.7	223	16	US-10-437-963-124750	Sequence 71, Appl
42	32	72.7	292	9	US-09-919-497-71	Sequence 42506, A
43	32	72.7	339	16	US-10-767-701-42506	Sequence 239449,
44	32	72.7	352	16	US-10-425-115-239449	Sequence 5902, Ap
45	32	72.7	1067	16	US-10-739-930-5902	

ALIGNMENTS

RESULT 1
US-10-751-845-123
; Sequence 123, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman W.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-123

Query Match 100.0%; Score 44; DB 17; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 QLFNTLSF 9

Db 1 QLFNTLSF 9

RESULT 2
US-10-751-845-146
; Sequence 146, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Robert G.
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiczo, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 146
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-146

Query Match 100.0%; Score 44; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QLFNTLSF 9
Db 1 QLFNTLSF 9

RESULT 3
US-10-751-845-156
; Sequence 156, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Robert G.
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiczo, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-156

Query Match 100.0%; Score 44; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QLFNTLSF 9
Db 4 QLFNTLSF 12

RESULT 4
US-10-432-465-102

; Sequence 102, Application US/10432465
; Publication No. US20040091479A1
; GENERAL INFORMATION:
; APPLICANT: Nieland, John
; APPLICANT: Kaufmann, Andreas
; APPLICANT: Kathner, Angela
; APPLICANT: Schinz, Manuela
; TITLE OF INVENTION: T-Cell Epitopes of the Papillomavirus L1
; TITLE OF INVENTION: Protein and E7 Protein and Their Use in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/077001
; CURRENT APPLICATION NUMBER: US/10/432,465
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/14037
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 10059631.2
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-432-465-102

Query Match 100.0%; Score 44; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QLFNTLSF 9
Db 11 QLFNTLSF 19

RESULT 5
US-10-433-091-71
; Sequence 71, Application US/10433091
; Publication No. US20040101533A1
; GENERAL INFORMATION:
; APPLICANT: MULLER, RAINER
; APPLICANT: NIELAND, JOHN
; APPLICANT: GABELSBERGER, JOSEF
; APPLICANT: HERBST, RUTH
; TITLE OF INVENTION: MEDICAMENT FOR PREVENTING OR TREATING TUMORS CAUSED BY
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS TYPE 18
; FILE REFERENCE: 037067/0115
; CURRENT APPLICATION NUMBER: US/10/433,091
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: PCT/EP01/14038
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 100 59 630.4
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 71
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 18
US-10-433-091-71

Query Match 100.0%; Score 44; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QLFNTLSF 9
Db 11 QLFNTLSF 19

RESULT 6
US-10-433-091-4
; Sequence 4, Application US/10433091
; Publication No. US20040101533A1


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; GENERAL INFORMATION:
; APPLICANT: MULLER, RAINER
; APPLICANT: NIELAND, JOHN
; APPLICANT: GABELSBERGER, JOSEF
; APPLICANT: HERBST, RUTH
; TITLE OF INVENTION: MEDICAMENT FOR PREVENTING OR TREATING TUMORS CAUSED BY
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS TYPE 18
; FILE REFERENCE: 037067/0115
; CURRENT APPLICATION NUMBER: US/10/433,091
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: PCT/EP01/14038
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 100 59 630.4
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Human papillomavirus type 18
US-10-433-091-4

Query Match          100.0%; Score 44; DB 16; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLFLNTLSF 9
Db 88 QLFLNTLSF 96

RESULT 7
US-10-472-724-8
; Sequence 8, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-8

Query Match          100.0%; Score 44; DB 16; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLFLNTLSF 9
Db 93 QLFLNTLSF 101

RESULT 8
US-10-751-845-159
; Sequence 159, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
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; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-159

Query Match          100.0%; Score 44; DB 17; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLFLNTLSF 9
Db 106 QLFLNTLSF 114

RESULT 9
US-10-000-903-16
; Sequence 16, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-16

Query Match          100.0%; Score 44; DB 13; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLFLNTLSF 9
Db 201 QLFLNTLSF 209

RESULT 10
US-10-000-903-19
; Sequence 19, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
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; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-19

Query Match      100.0%; Score 44; DB 13; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QLFNLTLSF 9
Db      201 QLFNLTLSF 209

RESULT 11
US-10-899-771-16
; Sequence 16, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E7 from Human papilloma virus type
; OTHER INFORMATION: 18)
US-10-899-771-16

Query Match      100.0%; Score 44; DB 17; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QLFNLTLSF 9
Db      201 QLFNLTLSF 209

RESULT 12
US-10-899-771-19
; Sequence 19, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E7 from Human papilloma virus type
; OTHER INFORMATION: 18)
US-10-899-771-16

Query Match      100.0%; Score 44; DB 17; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QLFNLTLSF 9
Db      201 QLFNLTLSF 209

RESULT 13
US-10-751-845-157
; Sequence 157, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-157

Query Match      100.0%; Score 44; DB 17; Length 236;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QLFNLTLSF 9
Db      223 QLFNLTLSF 231

RESULT 14
US-10-751-845-158
; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
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; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiccz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-158

Query Match 100.0%; Score 44; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLFNLTLSF 9
Db 224 QLFNLTLSF 232

RESULT 15
US-10-751-845-160
; Sequence 160, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiccz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160

Query Match 100.0%; Score 44; DB 17; Length 261;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLFNLTLSF 9
Db 248 QLFNLTLSF 256

Search completed: June 29, 2005, 04:19:23
Job time : 57.85 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-32

Perfect score: 44

Sequence: 1 QLFNLTLSF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
 - 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
 - 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
 - 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
 - 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
 - 6: /cgn2_6/ptodata/1/1aa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	44	100.0	29	2	US-08-934-915-66	Sequence 66, Appl
2	44	100.0	227	3	US-09-485-885-16	Sequence 16, Appl
3	44	100.0	227	3	US-09-485-885-19	Sequence 19, Appl
4	44	100.0	272	1	US-08-117-083-13	Sequence 13, Appl
5	44	100.0	383	3	US-09-485-885-23	Sequence 23, Appl
6	34	77.3	30	2	US-08-934-915-60	Sequence 60, Appl
7	34	77.3	281	4	US-09-540-236-2380	Sequence 2380, Ap
8	34	77.3	333	4	US-09-270-767-46066	Sequence 46066, A
9	33	75.0	289	4	US-10-151-832-6	Sequence 6, Appli
10	33	75.0	449	4	US-09-603-208A-42	Sequence 42, Appl
11	32	72.7	123	4	US-09-107-532A-3923	Sequence 3923, Ap
12	32	72.7	292	4	US-09-919-497-71	Sequence 71, Appl
13	32	72.7	292	4	US-09-949-016-6771	Sequence 6771, Ap
14	32	72.7	324	4	US-09-949-016-7132	Sequence 7132, Ap
15	32	72.7	378	4	US-09-107-532A-6500	Sequence 6500, Ap
16	32	72.7	633	3	US-09-041-991A-8	Sequence 8, Appli
17	32	72.7	633	3	US-09-041-991A-10	Sequence 10, Appl
18	32	72.7	633	4	US-09-608-533A-8	Sequence 8, Appli
19	32	72.7	633	4	US-09-608-533A-10	Sequence 10, Appl
20	31	70.5	66	4	US-09-248-796A-22497	Sequence 22497, A
21	31	70.5	127	4	US-09-270-767-45094	Sequence 45094, A
22	31	70.5	263	4	US-09-902-540-16422	Sequence 16422, A
23	31	70.5	302	4	US-09-710-279-23980	Sequence 23980, Ap
24	31	70.5	350	3	US-09-134-001C-3383	Sequence 3383, Ap
25	31	70.5	396	3	US-08-985-908-24	Sequence 24, Appli
26	31	70.5	581	3	US-08-619-812-6	Sequence 6, Appli
27	31	70.5	660	4	US-09-252-991A-22396	Sequence 22396, A

ALIGNMENTS

RESULT 1

US-08-934-915-66

; Sequence 66, Application US/08934915

; Patent No. 5932412

; GENERAL INFORMATION:

; APPLICANT: DILLNER, JOAKIM

; APPLICANT: DILLNER, LENA

; APPLICANT: CHENG, HWEE-MING

; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN

; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,

; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,

; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR

; TITLE OF INVENTION: DIAGNOSTIC PURPOSES

; NUMBER OF SEQUENCES: 193

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MASON & ASSOCIATES, P.A.

; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500

; CITY: CLEARWATER

; STATE: FLORIDA

; COUNTRY: U.S.A.

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 3.0

; SOFTWARE: Microsoft Word 6.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/934,915

; FILING DATE: 22-SEP-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/949,836

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: LOUISE A. Fouch

; REGISTRATION NUMBER: 37,133

; REFERENCE/POCKET NUMBER: 1946.6

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 813-538-3800

; TELEFAX: 813-538-3820

; TELEX:

; INFORMATION FOR SEQ ID NO: 66:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 29 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-934-915-66

Query Match

Best Local Similarity 100.0%; Score 44; DB 2; Length 29;

100.0%; Pred. No. 0.059;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLFNTLSF 9
| | | | |
Db 12 QLFNTLSF 20

RESULT 2
US-09-485-885-16
; Sequence 16, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-16

Query Match 100.0%; Score 44; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLFNTLSF 9
| | | | |
Db 201 QLFNTLSF 209

RESULT 3
US-09-485-885-19
; Sequence 19, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-19

Query Match 100.0%; Score 44; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLFNTLSF 9

Db 201 QLFNTLSF 209
| | | | |

RESULT 4
US-08-117-083-13
; Sequence 13, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..272
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-13

Query Match 100.0%; Score 44; DB 1; Length 272;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLFNTLSF 9
| | | | |
Db 251 QLFNTLSF 259

RESULT 5
US-09-485-885-23
; Sequence 23, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine

FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 383
TYPE: PRT
ORGANISM: Homo sapien
US-09-485-885-23

Query Match 100.0%; Score 44; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLFNLTSLF 9
Db 357 QLFNLTSLF 365

RESULT 6

US-08-934-915-60
Sequence 60, Application US/08934915
Patent No. 5932412

GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEI-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:

INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-60

Query Match

77.3%; Score 34; DB 2; Length 30;

Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLFNLTSL 7
Db 24 QLFNLTSL 30

RESULT 7

US-09-540-236-2380
Sequence 2380, Application US/09540236
Patent No. 6673910

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRI
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2380
LENGTH: 281
TYPE: PRT
ORGANISM: M.catarrhalis
US-09-540-236-2380

Query Match 77.3%; Score 34; DB 4; Length 281;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLFNLTSLF 9
Db 115 QLFNLTSLF 123

RESULT 8

US-09-270-767-46066
Sequence 46066, Application US/09270767
Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46066
LENGTH: 333
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-46066

Query Match 77.3%; Score 34; DB 4; Length 333;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLFNLTSL 8
Db 136 QLFNLTSL 143

RESULT 9

US-10-151-832-6
Sequence 6, Application US/10151832
Patent No. 6831206

GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Falco, Carl S.
APPLICANT: Tarczynski, Mitchell
TITLE OF INVENTION: Serine O-Acetyltransferase

FILE REFERENCE: BB1514
CURRENT APPLICATION NUMBER: US/10/151,832
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: 60/292,411
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Microsoft Office 97
SEQ ID NO 6
LENGTH: 289
TYPE: PRT
ORGANISM: Allium cepa
US-10-151-832-6

Query Match 75.0%; Score 33; DB 4; Length 289;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LFLNTLS 8
| | | | |
Db 80 LFLNTLS 86

RESULT 10
US-09-603-208A-42
Sequence 42, Application US/09603208A
Patent No. 6822084
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauser, Gregor
APPLICANT: Lee, Heung-Shick
APPLICANT: Kim, Hyung-Joon
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
TITLE OF INVENTION: RESISTANCE AND TOLERANCE PROTEINS
FILE REFERENCE: BGI-124CP
CURRENT APPLICATION NUMBER: US/09/603,208A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142692
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 60/151214
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19930429.7
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931413.6
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931457.8
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931541.8
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932209.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932230.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932914.1
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19940764.9
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19941382.7
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 306
SEQ ID NO 42
LENGTH: 449
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-603-208A-42

Query Match 75.0%; Score 33; DB 4; Length 449;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLENTLS 8
| | | | |
Db 354 QLENTLS 361

RESULT 11

US-09-107-532A-3923
Sequence 3923, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3923:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...123
SEQUENCE DESCRIPTION: SEQ ID NO: 3923:

US-09-107-532A-3923

Query Match 72.7%; Score 32; DB 4; Length 123;
Best Local Similarity 66.7%; Pred. No. 55;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QLENTLSF 9
| | | | |
Db 97 QLENTLDF 105

RESULT 12

US-09-919-497-71
Sequence 71, Application US/09919497
Patent No. 6773883
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER

FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-71

Query Match 72.7%; Score 32; DB 4; Length 292;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LFLNTLSF 9
Db 280 LFNNTLSF 287

RESULT 13
US-09-949-016-6771
; Sequence 6771, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6771
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6771

Query Match 72.7%; Score 32; DB 4; Length 292;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LFLNTLSF 9
Db 280 LFNNTLSF 287

RESULT 14
US-09-949-016-7132
; Sequence 7132, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7132
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7132

Query Match 72.7%; Score 32; DB 4; Length 324;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LFLNTLSF 9
Db 312 LFNNTLSF 319

RESULT 15
US-09-107-532A-6500
; Sequence 6500, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6500:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...378
SEQUENCE DESCRIPTION: SEQ ID NO: 6500:
US-09-107-532A-6500

Query Match 72.7%; Score 32; DB 4; Length 378;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LFLNTLSF 9

Db 275 LFLSTISF 282
|||:|:|

Search completed: June 28, 2005, 21:33:27
Job time : 17 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-31
Perfect score: 45
Sequence: 1 FQQLFLNTL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	45	100.0	105	1	VE7 HPV18	P06788 human papil
2	45	100.0	105	2	Q6PGP1	Q6pgp1 homo sapien
3	39	86.7	105	2	Q8V9K9	Q8v9k9 human papil
4	39	86.7	105	2	Q9QNPS	Q9qnp5 human papil
5	39	86.7	105	2	Q9QNPS	Q9qnp6 human papil
6	39	86.7	105	2	Q9QNPS	Q9qnp7 human papil
7	39	86.7	175	2	Q6IU21	Q6iu21 escherichia
8	39	86.7	441	2	Q87M06	Q87mq6 vibrio para
9	39	86.7	443	1	YHAO_ECOLI	P42628 escherichia
10	39	86.7	443	2	Q8ZLM4	Q8ziw4 salmonella
11	39	86.7	443	2	Q6LKM2	Q6lkm2 photobacter
12	39	86.7	443	2	Q7UBG9	Q7ubg9 shigella fl
13	39	86.7	443	2	Q83Q30	Q83q30 shigella fl
14	39	86.7	443	2	Q8XAF5	Q8xaf5 escherichia
15	39	86.7	471	2	Q8AB86	Q8ab86 proptontibac
16	37	82.2	588	2	Q7VFF0	Q7vff0 helicobacte
17	36	80.0	82	2	Q9UD98	Q9ud98 homo sapien
18	36	80.0	92	1	VE7 HPV57	P22160 human papil
19	36	80.0	343	2	Q9K1W3	Q9klw3 chlamydia p
20	36	80.0	344	2	Q9TS81	Q9ts81 chlamydia p
21	36	80.0	344	2	Q9Z6T2	Q9zet2 chlamydia p
22	36	80.0	429	2	Q88S17	Q88s17 lactobacill
23	36	80.0	603	1	RFCA_CHLRE	Q8a082 mus musculu
24	36	80.0	686	2	Q6A082	Q6a082 mus musculu
25	36	80.0	712	1	Y352 HUMAN	O15060 homo sapien
26	36	80.0	712	2	Q8PDK0	Q8pdk0 mus musculu
27	36	80.0	2931	2	Q8AE33	Q8ae33 dictyosteli
28	35	77.8	1022	1	C426_CHICK	P15988 gallus gall
29	34	75.6	106	1	VE7 HPV45	P21736 human papil
30	34	75.6	106	2	Q9Y4V3	Q9y4v3 homo sapien
31	34	75.6	106	2	O10609	O10609 human papil

32 34 75.6 173 2 Q9AN75 Q9an75 bradyrhizob
33 34 75.6 237 2 Q8MRM0 Q8mrmo drosophila
34 34 75.6 280 2 Q7Q4W9 Q7q4w9 anopheles g
35 34 75.6 457 1 LIPP MYOCO O64425 myocastor c
36 34 75.6 498 2 Q198Z5 Q198z5 caenorhabdi
37 34 75.6 570 2 Q832K7 Q832k7 enterococcu
38 34 75.6 823 2 Q7NW18 Q7nw18 chromobacte
39 34 75.6 1805 2 Q8II22 Q8i122 plasmodium
40 34 75.6 1834 2 Q73KT0 Q73kt0 treponema d
41 33 73.3 97 2 Q92LH2 Q92lh2 rhizobium m
42 33 73.3 108 2 Q9WHG1 Q9whg1 human papil
43 33 73.3 209 1 VATD_THEVO Q97cp8 thermoplasma
44 33 73.3 256 2 Q8YWAB Q8ywa8 anabaena sp
45 33 73.3 274 2 Q8IDQ1 Q8idq1 plasmodium

ALIGNMENTS

RESULT 1
VE7 HPV18
ID VE7 HPV18 STANDARD; PRT; 105 AA.
AC P06788; 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87283882; PubMed=3039146;
RA Cole S.T., Danos O.;
RT "Nucleotide sequence and comparative analysis of the human
papillomavirus type 18 genome. Phylogeny of papillomaviruses and
repeated structure of the E6 and E7 gene products.";
RL J. Mol. Biol. 193:599-608(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88188247; PubMed=2833614;
RA Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M.,
Sugimura T.;
RT "Nucleotide sequences of cDNAs for human papillomavirus type 18
transcripts in HeLa cells.";
RL J. Virol. 62:1640-1646(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87053870; PubMed=3023067;
RA Schneider-Gaedcke A., Schwarz E.;
RT "Different human cervical carcinoma cell lines show similar
transcription patterns of human papillomavirus type 18 early genes.";
RL EMBO J. 5:2285-2292(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=87218459; PubMed=3034571;
RA Seedorf K., Oltersdorf T., Kraemer G., Roewekamp W.;
RT "Identification of early proteins of the human papilloma viruses type
16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells.";
RL EMBO J. 6:139-144(1987).
RN [5]
RP FUNCTION: E7 protein has both transforming and trans-activating
activities.

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DR EMBL; X05015; CAA28665.1; -
DR EMBL; M20324; AAA99513.1; -
DR EMBL; M20325; AAA99515.1; -
DR EMBL; M26798; AAA46947.1; -
DR EMBL; X04773; CAA28467.1; -
DR EMBL; A06324; CAA00540.1; -
DR EMBL; A06328; CAA00543.1; -
DR PIR; B26165; W7WL18.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW Transcription regulation.
FT SITE 63 66 C-XX-C motif-1.
FT SITE 98 101 C-XX-C motif-2.
FT CONFLICT 73 73 K -> E (in Ref. 1 and 4).
SQ SEQUENCE 105 AA; 11995 MW; 2CDB119534D0186A CRC64;

Query Match 100.0%; Score 45; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
Db 86 FQQLFLNTL 94

RESULT 2
Q6PGP1 PRELIMINARY; PRT; 105 AA.
AC Q6PGP1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalski U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; EC056907; AAH56907.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW Hypothetical protein.
SQ SEQUENCE 105 AA; 11995 MW; 2CDB119534D0186A CRC64;

Query Match 100.0%; Score 45; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
Db 86 FQQLFLNTL 94

RESULT 3
Q8V9K9 PRELIMINARY; PRT; 105 AA.
AC Q8V9K9
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21568387; PubMed=11711624;
RX DOI=10.1128/JVI.75.24.12339-12346.2001;
RA Shera K.A., Shera C.A., McDougall J.K.;
RT "Small Tumor Virus Genomes Are Integrated near Nuclear Matrix
Attachment Regions in Transformed Cells.";
RL J. Virol. 75:12339-12346 (2001).
DR EMBL; AF339137; AAL34455.1; -
DR Pfam; PF00527; E7; 1.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 105 AA; 12036 MW; 2528DEA165850C71 CRC64;

Query Match 86.7%; Score 39; DB 2; Length 105;
Best Local Similarity 88.9%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
Db 86 FQQLFLNTL 94

RESULT 4
Q9QNP5 PRELIMINARY; PRT; 105 AA.
AC Q9QNP5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RA Laassri M., Gul'ko L., Vinokurova S., Kissel'ova N., Veiko V.,
RA Kissel'ev F.;
RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
Transformation Potential of E7 Gene and its Mutants.";
RL Virus Genes 182:139-149 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC Veiko V.P.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y18493; CAB53099.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 105 AA; 11952 MW; 247BF448A6BBB4FA CRC64;

Query Match 86.7%; Score 39; DB 2; Length 105;
Best Local Similarity 88.9%; Pred. No. 3.4;

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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQQLFLNLT 9
Db 86 FQQLFLKTL 94

RESULT 5
Q9QNP6 PRELIMINARY; PRT; 105 AA.
AC Q9QNP6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RA Laessli M., Gul'ko L., Vinokurova S., Kisseljova N., Veiko V.,
RA Kisseljev F.;
RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
RT Transformation Potential of E7 Gene and its Mutants.";
RL Virus Genes 182:139-149(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Veiko V.P.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y18492; CAB53097.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 105 AA; 12009 MW; C4979555DAD4A960 CRC64;

Query Match 86.7%; Score 39; DB 2; Length 105;
Best Local Similarity 88.9%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQQLFLNLT 9
Db 86 FQQLFLKTL 94

RESULT 6
Q9QNP7 PRELIMINARY; PRT; 105 AA.
AC Q9QNP7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RA Laessli M., Gul'ko L., Vinokurova S., Kisseljova N., Veiko V.,
RA Kisseljev F.;
RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
RT Transformation Potential of E7 Gene and its Mutants.";
RL Virus Genes 182:139-149(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Veiko V.P.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y18491; CAB53097.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 105 AA; 12010 MW; 24799BB534D4496A CRC64;

Query Match 86.7%; Score 39; DB 2; Length 105;

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Best Local Similarity 88.9%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQQLFLNLT 9
Db 86 FQQLFLKTL 94

RESULT 7
Q6IU21 PRELIMINARY; PRT; 175 AA.
AC Q6IU21;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE YhaO (Fragment).
OS Escherichia coli B.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=37762;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Bc251;
RC MEDLINE=22549866; PubMed=12664169; DOI=10.1007/s00239-002-2423-0;
RA Lenski R.E., Winkworth C.L., Riley M.A.;
RT "Rates of DNA sequence evolution in experimental populations of
RT Escherichia coli during 20,000 generations.";
RL J. Mol. Evol. 56:498-508(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=Bc251;
RC Lenski R.E., Winkworth C.L., Riley M.A.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY625128; AAT42482.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002422; AA/rel_permease2.
FT NON_TER 1
FT NON_TER 175
SQ SEQUENCE 175 AA; 19110 MW; 50388BC4D8D5F7A CRC64;

Query Match 86.7%; Score 39; DB 2; Length 175;
Best Local Similarity 77.8%; Pred. No. 5.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNLT 9
Db 52 FQRLFIINTL 60

RESULT 8
Q87MQ6 PRELIMINARY; PRT; 441 AA.
AC Q87MQ6;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Putative HAAP family transport protein.
GN OrderedLocusNames=VP2175;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=RIMD 2210633 / Serotype O3:K6;
RC MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Nejima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";

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RL Lancet 361:743-749(2003).
DR EMBL; AP005080; BAC60438.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002422; AA/rel_permease2.
DR InterPro; IPR002091; ARAA_permease.
DR PRINTS; PR00166; AROAAPRMEASE.
KW Complete proteome.
SQ SEQUENCE 441 AA; 47731 MW; F48994992623F3354 CRC64;

Query Match      86.7%; Score 39; DB 2; Length 441;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQQLFLNTL 9
DB 83 FQRLFIINTL 91

RESULT 9
YHAA_ECOLI
ID YHAA_ECOLI STANDARD; PRT; 443 AA.
AC P42628; Q6BF46;
DT 01-NOV-1995 (Rel. 32, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical transport protein yhaO.
GN Name=yhaO; OrderedLocusNames=b3110;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Valdes J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shaio Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP REVISIONS.
RA Arnaud M., Berlyn M.K.B., Blattner F.R., Galperin M.Y., Glasner J.D.,
RA Horiuchi T., Kosuge T., Mori H., Perna N.T., Plunkett G. III,
RA Riley M., Rudd K.E., Serres M.H., Thomas G.H., Wanner B.L.;
RT "Workshop on annotation of Escherichia coli K-12.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (potential).
CC -!- SIMILARITY: Belongs to the amino acid/polyamine transporter family
CC II. SdaC / tdc subfamily.
CC -!- CAUTION: Ref.1 (AA57914) sequence differs from that shown due to
CC frameshifts in positions 14 and 21.
CC -----
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CC -----
DR EMBL; U18997; AAA57914.1; ALT_FRAME.
DR EMBL; U00096; AAT48168.1; -.
DR EcoBASE; EB2609; -.
DR Ecogene; EG12754; yhaO.
DR InterPro; IPR002422; AA/rel_permease2.
DR InterPro; IPR002091; ARAA_permease.
DR InterPro; IPR004694; Ser transporter.
DR PRINTS; PR00166; AROAAPRMEASE.

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DR TIGRFAMs; TIGR00814; stp; 1.
KW Complete proteome; Hypothetical protein; Inner membrane;
KW Transmembrane; Transport.
FT TRANSMEM 49 69 Potential.
FT TRANSMEM 111 131 Potential.
FT TRANSMEM 150 170 Potential.
FT TRANSMEM 183 203 Potential.
FT TRANSMEM 215 235 Potential.
FT TRANSMEM 265 285 Potential.
FT TRANSMEM 298 318 Potential.
FT TRANSMEM 319 339 Potential.
FT TRANSMEM 368 388 Potential.
FT TRANSMEM 390 410 Potential.
FT TRANSMEM 422 442 Potential.
SQ SEQUENCE 443 AA; 48314 MW; B24A2D8E1A61E631 CRC64;

Query Match      86.7%; Score 39; DB 1; Length 443;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQQLFLNTL 9
DB 82 FQRLFIINTL 90

RESULT 10
Q8ZLW4
ID Q8ZLW4 PRELIMINARY; PRT; 443 AA.
AC Q8ZLW4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative HAAAP family transport protein.
GN Name=yhaO; OrderedLocusNames=STM3239;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
DR EMBL; AE008849; AAU22112.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR PRINTS; PR00166; AROAAPRMEASE.
DR TIGRFAMs; TIGR00814; stp; 1.
KW Complete proteome.
SQ SEQUENCE 443 AA; 48428 MW; 106150F2DC968877 CRC64;

Query Match      86.7%; Score 39; DB 2; Length 443;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQQLFLNTL 9
DB 82 FQRLFIINTL 90

RESULT 11
Q6LKM2
ID Q6LKM2 PRELIMINARY; PRT; 443 AA.

```

```

AC O6LKM2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transport system permease protein.
GN Name=SW3625; OrderedLocuNames=PPR80242;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; CR378675; CAG22115.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002422; AA/rel_permease2.
DR InterPro; IPR002091; AAA_permease.
DR PRINTS; PR00166; AROAAPMEASE.
KW Complete proteome.
SQ SEQUENCE 443 AA; 48358 MW; 207ADA97ACB29B16 CRC64;

Query Match 86.7%; Score 39; DB 2; Length 443;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
Db 85 FQKLFIINTL 93

RESULT 12
Q7UBG9 PRELIMINARY; PRT; 443 AA.
AC Q7UBG9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative transport system permease protein.
GN Name=yhaO; OrderedLocuNames=S3361;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
DR EMBL; AE016989; AAP18436.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002422; AA/rel_permease2.
DR InterPro; IPR004694; Ser_transporter.
DR TIGRFAMs; TIGR00814; stp; 1.
SQ SEQUENCE 443 AA; 48388 MW; B3E8BD8E1ACC3631 CRC64;

Query Match 86.7%; Score 39; DB 2; Length 443;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
Db 85 FQKLFIINTL 93

RESULT 12
Q7UBG9 PRELIMINARY; PRT; 443 AA.
AC Q7UBG9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative transport system permease protein.
GN Name=yhaO; OrderedLocuNames=S3361;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
DR EMBL; AE016989; AAP18436.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002422; AA/rel_permease2.
DR InterPro; IPR004694; Ser_transporter.
DR TIGRFAMs; TIGR00814; stp; 1.
SQ SEQUENCE 443 AA; 48388 MW; B3E8BD8E1ACC3631 CRC64;

Query Match 86.7%; Score 39; DB 2; Length 443;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
Db 82 FQRLFIINTL 90

RESULT 13
Q83Q30 PRELIMINARY; PRT; 443 AA.
AC Q83Q30;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative transport system permease protein.
GN Name=yhaO; OrderedLocuNames=SF3151;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=301 / Serotype 2a;
RX MEDLINE=2227406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
DR EMBL; AE015326; AAN44622.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002422; AA/rel_permease2.
DR InterPro; IPR002091; AAA_permease.
DR InterPro; IPR004694; Ser_transporter.
DR PRINTS; PR00166; AROAAPMEASE.
DR TIGRFAMs; TIGR00814; stp; 1.
KW Complete proteome.
SQ SEQUENCE 443 AA; 48404 MW; AB89A5F67ACC3623 CRC64;

Query Match 86.7%; Score 39; DB 2; Length 443;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
Db 82 FQRLFIINTL 90

RESULT 14
Q8XAF5 PRELIMINARY; PRT; 443 AA.
AC Q8XAF5; Q7AAM0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative transport system permease protein.
GN Name=yhaO; OrderedLocuNames=ECS3991, z4463;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;

```

RA MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick J.H.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayaishi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12";
RL DNA Res. 8:11-22(2001).
DR EMBL; AE005540; AAG58242.1; -;
DR EMBL; AP002564; BAB37414.1; -;
DR PIR; F85972; F85972.
DR PIR; G91127; G91127.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002422; AA/rel_permease2.
DR InterPro; IPR002091; ArAA_permease.
DR InterPro; IPR004694; Ser_transporter.
DR PRINTS; PR00166; AROAAPRMEASE.
DR TIGRFAMs; TIGR00814; stp; 1.
KW Complete proteome.
SQ SEQUENCE 443 AA; 48322 MW; 670BF2991168F1FA CRC64;

Query Match 86.7%; Score 39; DB 2; Length 443;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
Db 82 FQRLFIINTL 90
||:||||
||:||||

RESULT 15
Q6AB86 PRELIMINARY; PRT; 471 AA.
AC Q6AB86;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Putative transport protein.
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
GN OrderedLocustNames=PBA0218;
OS Propionibacterium acnes
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Propionibacterineae; Propionibacteriaceae; Propionibacterium.
OX NCBI_TaxID=1747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KPA171202 / DSM 16379;
RX PubMed=15286373; DOI=10.1126/science.1100330;
RA Brueggemann H., Henne A., Hoster F., Liesegang H., Wierer A.,
RA Strittmatter A., Hujer S., Duerre P., Gottschalk G.;
RT "The complete genome sequence of Propionibacterium acnes, a commensal
of human skin."
RL Science 305:671-673(2004).
DR EMBL; AE017283; AAT61980.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002422; AA/rel_permease2.

DR InterPro; IPR002091; ArAA_permease.
DR PRINTS; PR00166; AROAAPRMEASE.
KW Complete proteome.
SQ SEQUENCE 471 AA; 52424 MW; 4D441031C0F53F41 CRC64;

Query Match 86.7%; Score 39; DB 2; Length 471;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
Db 113 FQRLFIINTL 121
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||:||||

Search completed: June 28, 2005, 21:24:03
Job time : 56.1 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:23:53 ; Search time 11.15 Seconds
(without alignments)
77.664 Million cell updates/sec

Title: US-08-170-344-31
Perfect score: 45
Sequence: 1 FQQLFLNTL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	105	1 W7WL18	E7 protein - human
2	39	86.7	425	2 C65100	hypothetical 46.6
3	39	86.7	443	2 F85972	probable transport
4	39	86.7	443	2 G91127	probable transport
5	36	80.0	92	1 S15622	E7 protein - human
6	36	80.0	343	2 A81529	hypothetical prote
7	36	80.0	344	2 E72011	hypothetical prote
8	36	80.0	344	2 F86612	hypothetical prote
9	35	77.8	918	2 S23377	collagen alpha 2(V
10	35	77.8	1022	2 S04111	collagen alpha 2(V
11	34	75.6	106	2 S36562	E7 protein - human
12	34	75.6	457	2 I48206	triacylglycerol li
13	34	75.6	498	2 T16190	hypothetical prote
14	33	73.3	256	2 AE2019	hypothetical prote
15	33	73.3	424	2 JH0164	neurotensin recept
16	33	73.3	425	1 SAVVTL	satellite RNA-enco
17	33	73.3	454	2 F83748	hypothetical prote
18	33	73.3	633	2 C32053	parasporal crystal
19	33	73.3	633	2 D32053	parasporal crystal
20	33	73.3	1067	2 T06672	probable aminoacyl
21	33	73.3	1067	2 T48850	glycine-tRNA ligas
22	33	73.3	1204	2 A96676	hypothetical prote
23	33	73.3	1500	2 T03824	probable immediate
24	32	71.1	206	2 T22816	hypothetical prote
25	32	71.1	256	2 F75310	hypothetical prote
26	32	71.1	264	2 B46314	hypothetical prote
27	32	71.1	290	2 C84410	hypothetical prote
28	32	71.1	336	2 AF2162	UDP-glucose 4-epim
29	32	71.1	358	1 W2WL58	E2 protein - human

30 32 71.1 396 1 XNECD
31 32 71.1 396 2 AD0616
32 32 71.1 396 2 A85619
33 32 71.1 396 2 C90755
34 32 71.1 396 2 AD0172
35 32 71.1 572 2 AD1209
36 32 71.1 579 2 AB1829
37 32 71.1 839 2 B96998
38 32 71.1 1046 2 T34566
39 31 68.9 80 2 AB2755
40 31 68.9 111 2 S16556
41 31 68.9 188 2 S12393
42 31 68.9 200 2 S5280
43 31 68.9 251 2 AF0805
44 31 68.9 280 2 H83623
45 31 68.9 298 2 G89898

aspartate transami
aspartate aminotra
aspartate aminotra
aspartate transami
N-acetylmuramoyl-L
flavoprotein [limpo
phosphoenolpyruvat
hypothetical prote
host factor I [imp
E7 protein - human
hypothetical prote
probable membrane
vacu lipoprotein p
probable chemotaxi
hypothetical prote

ALIGNMENTS

RESULT 1

W7WL18
E7 protein - human papillomavirus type 18
C:Species: human papillomavirus type 18
C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: B26165; H26251
R:Seedorf, K.; Oltersdorf, T.; Kraemmer, G.; Roewekamp, W.
EMBO J. 6, 139-144, 1987
A>Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)
A:Reference number: A91068; MUID:87218459; PMID:3034571
A:Accession: B26165
A:Molecule type: DNA
A:Residues: 1-105 <SEE>
A:Cross-references: UNIPROT:P06788; GB:X04773; NID:G60876; PIDN:CAA28467.1; PID:G60878
J. Mol. Biol. 193, 593-608, 1987
A>Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 18
A:Reference number: A92937; MUID:87283882; PMID:3039146
A:Accession: H26251
A:Molecule type: DNA
A:Residues: 1-105 <COL>
A:Cross-references: GB:X05015; NID:G60975; PIDN:CAA28665.1; PID:G60977
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 100.0%; Score 45; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
|||
Db 86 FQQLFLNTL 94

RESULT 2

C65100
hypothetical 46.6 kD protein in exuR-tdcC intergenic region - Escherichia coli (strain K
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: C65100
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Coi
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: C65100
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-425 <BLAT>
A:Cross-references: GB:AE000392; GB:U00096; NID:g2367194; PIDN:AAC76145.1; PID:gl789497;
A:Experimental source: strain K-12, substrain MG1655.
C:Genetics:

A:Gene: yhaO
C:Superfamily: threonine-serine permease

Query Match 86.7%; Score 39; DB 2; Length 425;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
|:|:|:|:|
Db 64 FQRLFINL 72

RESULT 3

F85972 Probable transport system permease protein yhaO [imported] - Escherichia coli (strain O1

C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: F85972

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Natura 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: F85972

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-443 <STO>

A:Cross-references: UNIPROT:Q8XAF5; GB:AE005174; NID:g12517702; PIDN:AAG58242.1; GSPDB:C

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: yhaO

C:Superfamily: threonine-serine permease

Query Match 86.7%; Score 39; DB 2; Length 443;
Best Local Similarity 77.8%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
|:|:|:|:|
Db 82 FQRLFINL 90

RESULT 4

G91127 Probable transport system permease protein ECs3991 [imported] - Escherichia coli (strain

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C:Accession: G91127

R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: G91127

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-443 <HAY>

A:Cross-references: UNIPROT:Q8XAF5; GB:BA000007; PIDN:BA837414.1; PID:g13363464; GSPDB:C

A:Experimental source: strain O157:H7, substrain RIMD 0509952

C:Genetics:

A:Gene: ECs3991

C:Superfamily: threonine-serine permease

Query Match 86.7%; Score 39; DB 2; Length 443;
Best Local Similarity 77.8%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
|:|:|:|:|
Db 82 FQRLFINL 90

RESULT 5

S15622

E7 protein - human papillomavirus type 57

C:Species: human papillomavirus type 57

A:Note: host Homo sapiens (man)

C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004

C:Accession: S15622

R:Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.

Virus Res. 18, 81-98, 1990

A:Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and 5

A:Reference number: S15614; MUID:91186699; PMID:1964523

A:Accession: S15622

A:Molecule type: DNA

A:Residues: 1-92 <HIR>

A:Cross-references: UNIPROT:P22160; EMBL:X55965; NID:g60882; PIDN:CAA39431.1; PID:g60884

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:55-91/Region: zinc finger CCCC motif

Query Match 80.0%; Score 36; DB 1; Length 92;

Best Local Similarity 87.5%; Pred. No. 2.4;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QQLFLNTL 9

|:|:|:|:|

Db 77 EQLFLNTL 84

RESULT 6

A81529

hypothetical protein CP0879 [imported] - Chlamydomophila pneumoniae (strain AR39)

C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: A81529

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I.

, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A:Reference number: A81500; MUID:20150255; PMID:10684935

A:Accession: A81529

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-343 <REA>

A:Cross-references: UNIPROT:Q9KIW3; GB:AE002246; GB:AE002161; NID:g7189785; PIDN:AAF3866;

A:Experimental source: strain AR39, HL cells

C:Genetics:

A:Gene: CP0879

C:Superfamily: Chlamydia hypothetical protein Cpn0976

Query Match 80.0%; Score 36; DB 2; Length 343;

Best Local Similarity 77.8%; Pred. No. 9.6;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9

|:|:|:|:|

Db 296 FEQKFLNTL 304

RESULT 7

E72011

hypothetical protein - Chlamydomophila pneumoniae (strain CWL029)

C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: E72011

R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999

A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A:Reference number: A72000; MUID:99206606; PMID:10192388

A:Accession: E72011

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-344 <ARN>

A:Cross-references: UNIPROT:Q9Z6T2; GB:AE001678; GB:AE001363; NID:g4377301; PIDN:AAD1911;

A:Experimental source: strain CWL029

C;Genetics:
 A;Gene: CPN0977
 C;Superfamily: Chlamydia hypothetical protein CPN0976

Query Match 80.0%; Score 36; DB 2; Length 344;
 Best Local Similarity 77.8%; Pred. No. 9.6;
 Matches 7; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 FQQLFLNTL 9
 | : | | | | |
 Db 297 FEQKFLNTL 305

RESULT 8
 F86612
 Hypothetical protein CPj0977 [imported] - Chlamydomydia pneumoniae (strain J138)
 C;Species: Chlamydomydia pneumoniae, Chlamydia pneumoniae
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: F86612
 R;Shirai, M.; Mirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ie
 Nucleic Acids Res. 28, 2311-2314, 2000
 A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A;Reference number: A86491; MUID:20330349; PMID:10871362
 A;Accession: F86612
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-344 <STO>
 A;Cross-references: UNIPROT:Q9J881; GB:BA000008; NID:G8979350; PIDN:BAA99184.1; GSPDB:GN
 A;Experimental source: strain J138
 C;Genetics:
 A;Gene: CPj0977
 C;Superfamily: Chlamydia hypothetical protein CPN0976

Query Match 80.0%; Score 36; DB 2; Length 344;
 Best Local Similarity 77.8%; Pred. No. 9.6;
 Matches 7; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 FQQLFLNTL 9
 | : | | | | |
 Db 297 FEQKFLNTL 305

RESULT 9
 S23377
 collagen alpha 2(VI) chain short form precursor - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 22-Nov-1993 #sequence_revision 09-Mar-1996 #text_change 09-Jul-2004
 C;Accession: S23377; S15370
 R;Hayman, A.R.; Koppel, J.; Trueb, B.
 submitted to the EMBL Data Library, November 1990
 A;Description: Complete structure of the chicken alpha2(VI) collagen gene.
 A;Reference number: S23377
 A;Accession: S23377
 A;Molecule type: DNA
 A;Residues: 1-918 <HA1>
 A;Cross-references: UNIPROT:P15988; EMBL:X56659; NID:G62880; PIDN:CAA39981.1; PID:G62881
 R;Hayman, A.R.; Koppel, J.; Trueb, B.
 Eur. J. Biochem. 197, 177-184, 1991
 A;Title: Complete structure of the chicken alpha 2(VI) collagen gene.
 A;Accession: S15370
 A;Reference number: S15370; MUID:91200044; PMID:2015818
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 821-918 <HA2>
 A;Cross-references: EMBL:X56659
 C;Genetics:
 A;Introns: 39/3; 238/3; 245/3; 267/3; 285/3; 300/3; 309/3; 318/3; 333/3; 351/3; 372/3; 3
 C;Superfamily: collagen VI; von Willebrand factor type A repeat homology
 C;Keywords: alternative splicing; coiled coil; disulfide bond; extracellular matrix; gly
 F;1-27/Domain: signal sequence #status predicted <SIG>
 F;28-918/Product: collagen alpha 2(VI) chain short form #status predicted <MAT>
 F;28-255/Domain: non-collagenous NC2 #status predicted <NC2>
 F;44-216/Domain: von Willebrand factor type A repeat homology <VWA1>

F;256-590/Domain: collagenous #status predicted <COL>
 F;348-350/Region: cell attachment (R-G-D) motif
 F;366-368/Region: cell attachment (R-G-D) motif
 F;426-428/Region: cell attachment (R-G-D) motif
 F;444-446/Region: cell attachment (R-G-D) motif
 F;465-467/Region: cell attachment (R-G-D) motif
 F;489-491/Region: cell attachment (R-G-D) motif
 F;498-500/Region: cell attachment (R-G-D) motif
 F;591-918/Domain: non-collagenous NC1 #status predicted <NC1>
 F;613-789/Domain: von Willebrand factor type A repeat homology <VWA2>
 F;141,215,327,630/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 77.8%; Score 35; DB 2; Length 918;
 Best Local Similarity 77.8%; Pred. No. 44;
 Matches 7; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 FQQLFLNTL 9
 | : | | | | |
 Db 9 FQQLFLNTL 17

RESULT 10
 S04111
 collagen alpha 2(VI) chain long form precursor - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
 C;Accession: S23378; A36441; S14215; S04111; A31806
 R;Hayman, A.R.; Koppel, J.; Trueb, B.
 submitted to the EMBL Data Library, November 1990
 A;Description: Complete structure of the chicken alpha2(VI) collagen gene.
 A;Reference number: S23377
 A;Accession: S23378
 A;Molecule type: DNA
 A;Residues: 1-1022 <TR1>
 A;Cross-references: UNIPROT:P15988; EMBL:X56659; NID:G62880; PIDN:CAA39982.1; PID:G62882
 R;Hayman, A.R.; Koppel, J.; Winterhalter, K.H.; Trueb, B.
 J. Biol. Chem. 265, 9864-9868, 1990
 A;Title: The triple-helical domain of alpha2(VI) collagen is encoded by 19 short exons t
 A;Reference number: A36441; MUID:90277679; PMID:2351679
 A;Accession: A36441
 A;Molecule type: DNA
 A;Residues: 246-656 <TR2>
 A;Cross-references: GB:J05475
 R;Koller, E.; Hayman, A.R.; Trueb, B.
 Nucleic Acids Res. 19, 485-491, 1991
 A;Title: The promoter of the chicken alpha-2(VI) collagen gene has features characterist
 A;Reference number: S14215; MUID:91187664; PMID:2011522
 A;Accession: S14215
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 8-38 <TR3>
 A;Cross-references: EMBL:X56595; NID:G63321; PIDN:CAA39933.1; PID:G63322
 R;Koller, E.; Winterhalter, K.H.; Trueb, B.
 EMBO J. 8, 1073-1077, 1989
 A;Title: The globular domains of type VI collagen are related to the collagen-binding do
 A;Reference number: S04111; MUID:89305506; PMID:2787244
 A;Accession: S04111
 A;Molecule type: mRNA
 A;Residues: 1-1022 <TR4>
 A;Cross-references: EMBL:X15041; NID:G62876; PIDN:CAA33144.1; PID:G62877
 A;Note: it is uncertain whether Met-1 or Met-8 is the initiator
 R;Trueb, B.; Schaeren-Wiemers, N.; Schreier, T.; Winterhalter, K.H.
 J. Biol. Chem. 264, 136-140, 1989
 A;Title: Molecular cloning of chicken type VI collagen. Primary structure of the subunit
 A;Reference number: A31806; MUID:89079640; PMID:2451845
 A;Accession: A31806
 A;Molecule type: mRNA
 A;Residues: 77-796 <TR5>
 A;Cross-references: GB:J04425; NID:G211615; PIDN:AAA48705.1; PID:G211616
 C;Superfamily: collagen VI; von Willebrand factor type A repeat homology
 C;Keywords: Glycoprotein
 F;1-27/Domain: signal sequence #status predicted <SIG>
 F;28-1022/Product: collagen alpha 2(VI) chain #status predicted <MAT>

F:44-216/Domain: von Willebrand factor type A repeat homology <VWA1>
F:348-350/Region: cell attachment (R-G-D) motif
F:366-368/Region: cell attachment (R-G-D) motif
F:426-428/Region: cell attachment (R-G-D) motif
F:444-446/Region: cell attachment (R-G-D) motif
F:465-467/Region: cell attachment (R-G-D) motif
F:489-491/Region: cell attachment (R-G-D) motif
F:498-500/Region: cell attachment (R-G-D) motif
F:613-789/Domain: von Willebrand factor type A repeat homology <VWA2>
F:831-1005/Domain: von Willebrand factor type A repeat homology <VWA3>
F:141,215,327,630,897/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 77.8%; Score 35; DB 2; Length 1022;
Best Local Similarity 77.8%; Pred. No. 49;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQQLFLNTL 9
||| |||
Db 9 FQQLFLSTL 17

RESULT 11
S36562
E7 protein - human papillomavirus type 45
C:Species: human papillomavirus type 45
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36562
R:Delius, H.; Hofmann, B.
A:Submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36562
A:Molecule type: DNA
A:Residues: 1-106
A:Cross-references: UNIPROT:P21736; EMBL:X74479; NID:G997022; PIDN:CAA52574.1; PID:G9970
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 75.6%; Score 34; DB 2; Length 106;
Best Local Similarity 87.5%; Pred. No. 7.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QQLFLNTL 9
||| |||
Db 88 QQLFLSTL 95

RESULT 12
I48206
triacylglycerol lipase (EC 3.1.1.3) - nutria (fragment)
C:Species: Myocastor coypus (nutria, coypu)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48206
R:Thirstrup, K.; Carriere, F.; Hjorth, S.A.; Rasmussen, P.B.; Nielsen, P.F.; Ladefoged, Eur. J. Biochem. 227, 186-193, 1995
A:Title: Cloning and expression in insect cells of two pancreatic lipases and a procolip
A:Reference number: I48204; MUID:95154288; PMID:7851384
A:Accession: I48206
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-457 <RES>
A:Cross-references: UNIPROT:O64425; EMBL:X82999; NID:G599870; PIDN:CAA58120.1; PID:G5998
C:Superfamily: triacylglycerol lipase
C:Keywords: carboxylic ester hydrolase

Query Match 75.6%; Score 34; DB 2; Length 457;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQQLFLNTL 8
||| |||
Db 331 FQQLFLNT 338

RESULT 13
T16190
hypothetical protein F27D9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16190
R:Bentley, D.
submitted to the EMBL Data Library, February 1996
A:Description: The sequence of C. elegans cosmid F27D9.
A:Reference number: Z18473
A:Accession: T16190
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-498 <BEN>
A:Cross-references: UNIPROT:Q19845; EMBL:U49829; NID:G1203924; PID:G1203930; PIDN:AAA9336
C:Genetics:
A:Gene: CESP:F27D9.2
A:Introns: 31/3; 69/3; 151/1; 256/3; 287/2; 334/2; 371/1; 393/3; 427/3; 468/3

Query Match 75.6%; Score 34; DB 2; Length 498;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQQLFLNT 8
||| |||
Db 276 FQQLFLNT 283

RESULT 14
AE2019
hypothetical protein all1707 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AE2019
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE2019
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-256 <KUR>
A:Cross-references: UNIPROT:Q8VWA8; GB:BA000019; PIDN:BA878073.1; PID:G17135527; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all1707

Query Match 73.3%; Score 33; DB 2; Length 256;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQQLFLN 7
||| |||
Db 162 FQQLFLN 168

RESULT 15
JH0164
neurotensin receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: JH0164
R:Tanaka, K.; Masu, M.; Nakanishi, S.
Neuron 4, 847-854, 1990
A:Title: Structure and functional expression of the cloned rat neurotensin receptor.
A:Reference number: JH0164; MUID:90297956; PMID:1694443
A:Accession: JH0164
A:Molecule type: mRNA
A:Residues: 1-424 <TAN>
A:Cross-references: UNIPROT:P20789

C;Comment: Neurotensin receptor belongs to the family of G protein-coupled receptor. This
ter (neuromodulator in the brain and as a hormone) cellular mediator in peripheral tissue
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
P:65-87/Domain: transmembrane #status predicted <TM1>
P:97-121/Domain: transmembrane #status predicted <TM2>
P:144-165/Domain: transmembrane #status predicted <TM3>
P:189-210/Domain: transmembrane #status predicted <TM4>
P:236-260/Domain: transmembrane #status predicted <TM5>
P:309-330/Domain: transmembrane #status predicted <TM6>
P:348-372/Domain: transmembrane #status predicted <TM7>
P:4,38,42/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 73.3%; Score 33; DB 2; Length 424;
Best Local Similarity 66.7%; Pred. No. 50;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
|:|:|:|:
Db 376 FRQVFLSTL 384

Search completed: June 28, 2005, 21:27:47
Job time : 12.15 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds
(without alignments)
59.826 Million cell updates/sec

Title: US-08-170-344-31

Perfect score: 45

Sequence: 1 FQQLFLNTL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_PUB.pdb.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pdb.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pdb.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pdb.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pdb.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pdb.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pdb.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pdb.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pdb.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pdb.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pdb.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pdb.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pdb.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pdb.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	9	15	US-10-432-465-115
2	45	100.0	9	17	US-10-751-845-149
3	45	100.0	10	17	US-10-751-845-151
4	45	100.0	17	17	US-10-751-845-156
5	45	100.0	20	15	US-10-432-465-102
6	45	100.0	20	16	US-10-433-091-71
7	45	100.0	105	16	US-10-433-091-4
8	45	100.0	118	16	US-10-472-724-8
9	45	100.0	119	17	US-10-751-845-159
10	45	100.0	227	13	US-10-000-903-16
11	45	100.0	227	13	US-10-000-903-19

12	45	100.0	227	17	US-10-899-771-16	Sequence 16, Appl
13	45	100.0	227	17	US-10-899-771-19	Sequence 19, Appl
14	45	100.0	236	17	US-10-751-845-157	Sequence 157, Appl
15	45	100.0	237	17	US-10-751-845-158	Sequence 158, Appl
16	45	100.0	261	17	US-10-751-845-160	Sequence 160, Appl
17	45	100.0	383	13	US-10-000-903-23	Sequence 23, Appl
18	45	100.0	383	13	US-10-899-771-23	Sequence 23, Appl
19	39	86.7	105	16	US-10-800-023-28	Sequence 28, Appl
20	36	80.0	358	15	US-10-289-762-1049	Sequence 1049, Appl
21	34	75.6	9	17	US-10-751-845-123	Sequence 123, Appl
22	34	75.6	10	17	US-10-751-845-146	Sequence 146, Appl
23	34	75.6	1688	15	US-10-424-599-214588	Sequence 214588, Appl
24	33	73.3	60	9	US-09-993-844-69	Sequence 69, Appl
25	33	73.3	60	9	US-09-993-844-70	Sequence 70, Appl
26	33	73.3	60	9	US-09-993-844-71	Sequence 71, Appl
27	33	73.3	60	19	US-11-026-435-69	Sequence 69, Appl
28	33	73.3	60	19	US-11-026-435-70	Sequence 70, Appl
29	33	73.3	60	19	US-11-026-435-71	Sequence 71, Appl
30	33	73.3	65	16	US-10-425-115-354133	Sequence 354133, Appl
31	33	73.3	122	16	US-10-425-115-356344	Sequence 356344, Appl
32	33	73.3	133	14	US-10-083-357-786	Sequence 786, Appl
33	33	73.3	174	16	US-10-804-219-7	Sequence 7, Appl
34	33	73.3	424	17	US-10-915-157-7	Sequence 7, Appl
35	33	73.3	632	14	US-10-040-906A-2	Sequence 2, Appl
36	33	73.3	632	14	US-10-040-906A-4	Sequence 2, Appl
37	33	73.3	632	15	US-10-428-961-2	Sequence 2, Appl
38	33	73.3	633	14	US-10-040-906A-8	Sequence 8, Appl
39	33	73.3	633	14	US-10-198-478-18	Sequence 18, Appl
40	33	73.3	633	16	US-10-782-020-8	Sequence 8, Appl
41	33	73.3	633	16	US-10-782-141-9	Sequence 9, Appl
42	33	73.3	633	16	US-10-781-979-11	Sequence 11, Appl
43	33	73.3	633	17	US-10-926-819-12	Sequence 12, Appl
44	33	73.3	634	14	US-10-198-478-2	Sequence 2, Appl
45	33	73.3	634	14	US-10-198-478-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-10-432-465-115
; Sequence 115, Application US/10432465
; Publication No. US20040091479A1
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, John
; APPLICANT: Kaufmann, Andreas
; APPLICANT: Schinz, Manuela
; TITLE OF INVENTION: T-Cell Epitopes of the Papillomavirus L1
; TITLE OF INVENTION: Protein and E7 Protein and Their Use in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/077001
; CURRENT APPLICATION NUMBER: US/10/432,465
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/14037
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 10059631.2
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 115
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-432-465-115

Query Match 100.0%; Score 45; DB 15; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.6e+06; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FQQLFLNTL 9

1 FQQLFLNTL 9

RESULT 2

US-10-751-845-149
; Sequence 149, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-149

Query Match 100.0%; Score 45; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQQLFLNTL 9
| | | | |
DB 1 FQQLFLNTL 9

RESULT 3

US-10-751-845-151
; Sequence 151, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-151

Query Match 100.0%; Score 45; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQQLFLNTL 9
| | | | |
DB 2 FQQLFLNTL 10

RESULT 4

US-10-751-845-151

US-10-751-845-156
; Sequence 156, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-156

Query Match 100.0%; Score 45; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQQLFLNTL 9
| | | | |
DB 2 FQQLFLNTL 10

RESULT 5

US-10-432-465-102
; Sequence 102, Application US/10432465
; Publication No. US20040091479A1
; GENERAL INFORMATION:
; APPLICANT: Nieland, John
; APPLICANT: Kaufmann, Andreas
; APPLICANT: Kather, Angela
; APPLICANT: Schinz, Manuela
; TITLE OF INVENTION: T-Cell Epitopes of the Papillomavirus L1
; TITLE OF INVENTION: Protein and E7 Protein and Their Use in Diagnosis and
; FILE REFERENCE: 50125/077001
; CURRENT APPLICATION NUMBER: US/10/432,465
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/14037
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 10059631.2
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-432-465-102

Query Match 100.0%; Score 45; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQQLFLNTL 9
| | | | |
DB 9 FQQLFLNTL 17

RESULT 6

US-10-433-091-71
; Sequence 71, Application US/10433091


```

; Publication No. US20040101533A1
; GENERAL INFORMATION:
; APPLICANT: MULLER, RAINER
; APPLICANT: NIELAND, JOHN
; APPLICANT: GABELSBERGER, JOSEF
; APPLICANT: HERBST, RUTH
; TITLE OF INVENTION: MEDICAMENT FOR PREVENTING OR TREATING TUMORS CAUSED BY
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS TYPE 18
; FILE REFERENCE: 037067/0115
; CURRENT APPLICATION NUMBER: US/10/433,091
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: PCT/EP01/14038
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 100 59 630.4
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 18
US-10-433-091-71

Query Match      100.0%; Score 45; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
Db 9 FQQLFLNTL 17

RESULT 7
US-10-433-091-4
; Sequence 4, Application US/10433091
; Publication No. US20040101533A1
; GENERAL INFORMATION:
; APPLICANT: MULLER, RAINER
; APPLICANT: NIELAND, JOHN
; APPLICANT: GABELSBERGER, JOSEF
; APPLICANT: HERBST, RUTH
; TITLE OF INVENTION: MEDICAMENT FOR PREVENTING OR TREATING TUMORS CAUSED BY
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS TYPE 18
; FILE REFERENCE: 037067/0115
; CURRENT APPLICATION NUMBER: US/10/433,091
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: PCT/EP01/14038
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 100 59 630.4
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Human papillomavirus type 18
US-10-433-091-4

Query Match      100.0%; Score 45; DB 16; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
Db 86 FQQLFLNTL 94

RESULT 8
US-10-472-724-8
; Sequence 8, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel

```

```

; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-8

Query Match      100.0%; Score 45; DB 16; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
Db 91 FQQLFLNTL 99

RESULT 9
US-10-751-845-159
; Sequence 159, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-159

Query Match      100.0%; Score 45; DB 17; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
Db 104 FQQLFLNTL 112

RESULT 10
US-10-000-903-16
; Sequence 16, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande

```

; APPLICANT: Gerard, Catherine Marie Ghislaine
 ; APPLICANT: Lombardo-Bencheikh, Angela
 ; TITLE OF INVENTION: Vaccine
 ; FILE REFERENCE: B45107
 ; CURRENT APPLICATION NUMBER: US/10/000,903
 ; CURRENT FILING DATE: 2001-10-01
 ; PRIOR APPLICATION NUMBER: PCT/EP98/05285
 ; PRIOR FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: GB 9717953.5
 ; PRIOR FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 16
 ; LENGTH: 227
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
 ; OTHER INFORMATION: Influenzae B and E7 from Human papilloma virus type
 ; OTHER INFORMATION: 18)
 US-10-000-903-16

Query Match 100.0%; Score 45; DB 13; Length 227;
 Best Local Similarity 100.0%; Pred. No. 1.6; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQQLFLNTL 9
 |||||
 Db 199 FQQLFLNTL 207

RESULT 11

US-10-000-903-19
 ; Sequence 19, Application US/10000903
 ; Publication No. US20020182221A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bruck, Claudine
 ; APPLICANT: Cabezon Silva, Teresa
 ; APPLICANT: Delisse, Anne-Marie Eva Fernande
 ; APPLICANT: Gerard, Catherine Marie Ghislaine
 ; APPLICANT: Lombardo-Bencheikh, Angela
 ; TITLE OF INVENTION: Vaccine
 ; FILE REFERENCE: B45107
 ; CURRENT APPLICATION NUMBER: US/10/000,903
 ; CURRENT FILING DATE: 2001-10-01
 ; PRIOR APPLICATION NUMBER: PCT/EP98/05285
 ; PRIOR FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: GB 9717953.5
 ; PRIOR FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 19
 ; LENGTH: 227
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
 ; OTHER INFORMATION: Influenzae B and mutated E7 from Human papilloma
 ; OTHER INFORMATION: virus type 18)
 US-10-000-903-19

Query Match 100.0%; Score 45; DB 13; Length 227;
 Best Local Similarity 100.0%; Pred. No. 1.6; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQQLFLNTL 9
 |||||
 Db 199 FQQLFLNTL 207

RESULT 12

US-10-899-771-16
 ; Sequence 16, Application US/10899771
 ; Publication No. US20050031638A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dalemans, Wilfried L.J.
 ; APPLICANT: Gerard, Catherine Marie Ghislaine
 ; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
 ; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
 ; FILE REFERENCE: B45124
 ; CURRENT APPLICATION NUMBER: US/10/899,771

; CURRENT FILING DATE: 2004-07-27
 ; PRIOR APPLICATION NUMBER: US/09/581,976
 ; PRIOR FILING DATE: 2000-06-20
 ; PRIOR APPLICATION NUMBER: PCT/EP98/08563
 ; PRIOR FILING DATE: 1998-12-18
 ; PRIOR APPLICATION NUMBER: GB 9727262.9
 ; PRIOR FILING DATE: 1997-12-24
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 16
 ; LENGTH: 227
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
 ; OTHER INFORMATION: Influenzae B and E7 from Human papilloma virus type
 ; OTHER INFORMATION: 18)
 US-10-899-771-16

Query Match 100.0%; Score 45; DB 17; Length 227;
 Best Local Similarity 100.0%; Pred. No. 1.6; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQQLFLNTL 9
 |||||
 Db 199 FQQLFLNTL 207

RESULT 13

US-10-899-771-19
 ; Sequence 19, Application US/10899771
 ; Publication No. US20050031638A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dalemans, Wilfried L.J.
 ; APPLICANT: Gerard, Catherine Marie Ghislaine
 ; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
 ; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
 ; FILE REFERENCE: B45124
 ; CURRENT APPLICATION NUMBER: US/10/899,771
 ; CURRENT FILING DATE: 2004-07-27
 ; PRIOR APPLICATION NUMBER: US/09/581,976
 ; PRIOR FILING DATE: 2000-06-20
 ; PRIOR APPLICATION NUMBER: PCT/EP98/08563
 ; PRIOR FILING DATE: 1998-12-18
 ; PRIOR APPLICATION NUMBER: GB 9727262.9
 ; PRIOR FILING DATE: 1997-12-24
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 19
 ; LENGTH: 227
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
 ; OTHER INFORMATION: Influenzae B and mutated E7 from Human papilloma
 ; OTHER INFORMATION: virus type 18)
 US-10-899-771-19

Query Match 100.0%; Score 45; DB 17; Length 227;
 Best Local Similarity 100.0%; Pred. No. 1.6; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQQLFLNTL 9
 |||||
 Db 199 FQQLFLNTL 207

RESULT 14

US-10-751-845-157
 ; Sequence 157, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne

; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-157

Query Match 100.0%; Score 45; DB 17; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 FQQLFLNTL 9
Db 221 FQQLFLNTL 229

RESULT 15
US-10-751-845-158
; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-158

Query Match 100.0%; Score 45; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 FQQLFLNTL 9
Db 222 FQQLFLNTL 230

Search completed: June 29, 2005, 04:19:23
Job time : 58.85 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	45	100.0	39	2	US-08-934-915-66	Sequence 66, Appl
2	45	100.0	20	2	US-08-934-915-60	Sequence 60, Appl
3	45	100.0	227	3	US-09-485-885-16	Sequence 16, Appl
4	45	100.0	227	3	US-09-485-885-19	Sequence 19, Appl
5	45	100.0	272	1	US-08-117-083-13	Sequence 13, Appl
6	45	100.0	383	3	US-09-485-885-23	Sequence 23, Appl
7	39	86.7	448	4	US-09-543-681A-7245	Sequence 7245, Ap
8	36	80.0	358	4	US-09-198-452A-1049	Sequence 1049, Ap
9	36	80.0	358	4	US-09-438-185A-978	Sequence 978, App
10	34	75.6	153	4	US-09-270-767-42027	Sequence 42027, A
11	34	75.6	222	4	US-09-107-532A-4879	Sequence 4879, Ap
12	34	75.6	469	4	US-09-270-767-44482	Sequence 44482, A
13	34	75.6	591	4	US-09-134-000C-5327	Sequence 5327, Ap
14	33	73.3	174	4	US-09-645-593-7	Sequence 7, Appli
15	33	73.3	242	4	US-09-270-767-58952	Sequence 58952, A
16	33	73.3	333	4	US-09-270-767-46066	Sequence 46066, A
17	33	73.3	353	1	US-08-118-270-45	Sequence 45, Appl
18	33	73.3	353	5	PCT-US93-08528-45	Sequence 45, Appl
19	33	73.3	619	4	US-09-134-000C-5525	Sequence 45, Appl
20	33	73.3	632	4	US-09-661-322A-2	Sequence 5525, Ap
21	33	73.3	633	3	US-09-041-991A-8	Sequence 2, Appli
22	33	73.3	633	3	US-09-041-991A-10	Sequence 8, Appli
23	33	73.3	633	4	US-09-186-002-18	Sequence 10, Appl
24	33	73.3	633	4	US-09-608-533A-8	Sequence 18, Appl
25	33	73.3	633	4	US-09-608-533A-10	Sequence 8, Appli
26	33	73.3	634	4	US-09-186-002-2	Sequence 10, Appl
27	33	73.3	634	4	US-09-186-002-12	Sequence 2, Appli
						Sequence 12, Appl

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
| | | | |
Db 10 FQQLFLNTL 18

RESULT 2

US-08-934-915-60
; Sequence 60, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Fouch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-934-915-60
Query Match 100.0%; Score 45; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
| | | | |
Db 22 FQQLFLNTL 30

RESULT 3

US-09-485-885-16
; Sequence 16, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine

; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-16

Query Match 100.0%; Score 45; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
| | | | |
Db 199 FQQLFLNTL 207

RESULT 4

US-09-485-885-19
; Sequence 19, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-19

Query Match 100.0%; Score 45; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
| | | | |
Db 199 FQQLFLNTL 207

RESULT 5

US-08-117-083-13
; Sequence 13, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58783
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..272
OTHER INFORMATION: /note="xaa refers to stop codon in the open reading frame."
US-08-117-083-13

Query Match 100.0%; Score 45; DB 1; Length 272;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQQLFLNLT 9
|||
DB 249 FQQLFLNLT 257

RESULT 6
US-09-485-895-23
; Sequence 23, Application US/09485895
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,895
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-895-23

Query Match 100.0%; Score 45; DB 3; Length 383;

Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FQQLFLNLT 9
|||
DB 355 FQQLFLNLT 363
RESULT 7
US-09-543-681A-7245
; Sequence 7245, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7245
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7245

Query Match 86.7%; Score 39; DB 4; Length 448;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQQLFLNLT 9
|||
DB 90 FQQLFLNLT 98

RESULT 8
US-09-198-452A-1049
; Sequence 1049, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1049
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1049

Query Match 80.0%; Score 36; DB 4; Length 358;
Best Local Similarity 77.8%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQQLFLNLT 9
|||
DB 311 FQQLFLNLT 319

RESULT 9
US-09-438-185A-978
; Sequence 978, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue

; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 978
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0977
US-09-438-185A-978

Query Match 80.0%; Score 36; DB 4; Length 358;
Best Local Similarity 77.8%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
|:|:|||||
Db 311 FEQKFLNTL 319

RESULT 10
US-09-270-767-42027
; Sequence 42027, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42027
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42027

Query Match 75.6%; Score 34; DB 4; Length 153;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNT 8
|:|:|||||
Db 34 FEQLFLNS 41

RESULT 11
US-09-107-532A-4879
; Sequence 4879, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA

ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4879:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...222
SEQUENCE DESCRIPTION: SEQ ID NO: 4879:
US-09-107-532A-4879

Query Match 75.6%; Score 34; DB 4; Length 222;
Best Local Similarity 77.8%; Pred. No. 48;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
|:|:|||||
Db 112 FQQLIDTL 120

RESULT 12
US-09-270-767-44482
; Sequence 44482, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44482
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44482

Query Match 75.6%; Score 34; DB 4; Length 469;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLNT 8
|:|:|||||
Db 183 FEQLFLNS 190

RESULT 13
US-09-134-000C-5327
; Sequence 5327, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5327
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5327

Query Match 75.6%; Score 34; DB 4; Length 591;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQQLFLN 7
| | | | |
Db 295 FQQLFMN 301

RESULT 14
US-09-645-593-7
; Sequence 7, Application US/09645593
; Patent No. 677591
; GENERAL INFORMATION:
; APPLICANT: Chaudhary, Sarita
; APPLICANT: van Rooijen, Gijb
; APPLICANT: Moloney, Maurice
; APPLICANT: Singh, Surinder
; TITLE OF INVENTION: Flax Seed Specific Promoters
; FILE REFERENCE: 9369-151
; CURRENT APPLICATION NUMBER: US/09/645,593
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,044
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/161,722
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Linum usitatissimum
US-09-645-593-7

Query Match 73.3%; Score 33; DB 4; Length 174;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
| | | | |
Db 93 FEQLFVTTL 101

RESULT 15
US-09-270-767-58952
; Sequence 58952, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58952
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-58952

Query Match 73.3%; Score 33; DB 4; Length 242;
Best Local Similarity 66.7%; Pred. No. 81;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FQQLFLNTL 9
| | | | |
Db 103 FQQLFTNNI 111

Search completed: June 28, 2005, 21:33:27
Job time : 18 secs

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Qy 1 TLQDIVLHL 9

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Db      1 TLQDIVLHL 9
|||||
RESULT 2
US-10-053-520-315
; Sequence 315, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Ouerfelli, Ouathak
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 315
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-520-315
Query Match      100.0%; Score 44; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TLQDIVLHL 9
|||||
Db      1 TLQDIVLHL 9
|||||
RESULT 3
US-10-053-498B-315
; Sequence 315, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Ouerfelli, Ouathak
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 315
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-498B-315
Query Match      100.0%; Score 44; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TLQDIVLHL 9
|||||
Db      1 TLQDIVLHL 9
|||||
RESULT 4
US-10-367-580-89
; Sequence 89, Application US/10367580
; Publication No. US20040071720A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461061
; CURRENT APPLICATION NUMBER: US/10/367,580
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,832
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-580-89
Query Match      100.0%; Score 44; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TLQDIVLHL 9
|||||
Db      1 TLQDIVLHL 9
|||||
RESULT 5
US-10-367-593-89
; Sequence 89, Application US/10367593
; Publication No. US20040071721A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461012
; CURRENT APPLICATION NUMBER: US/10/367,593
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479

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; PRIOR FILING DATE: 1995-08-18
 ; NUMBER OF SEQ ID NOS: 349
 ; SOFTWARE: WordPerfect 8.0 for Windows
 ; SEQ ID NO 89
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic peptide
 US-10-367-593-89

Query Match 100.0%; Score 44; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLQDIVLHL 9
 |||||
 Db 1 TLQDIVLHL 9

RESULT 6

US-10-367-594-89
 ; Sequence 89, Application US/10367594
 ; Publication No. US2004007172A1
 ; GENERAL INFORMATION:

; APPLICANT: Rothman, James E.
 ; APPLICANT: Hartl, F. Ulrich
 ; APPLICANT: Hoe, Mee H.
 ; APPLICANT: Houghton, Alan
 ; APPLICANT: Takechi, Yoshizumi
 ; APPLICANT: Mayhew, Mark

; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
 ; FILE REFERENCE: 11746/461041
 ; CURRENT APPLICATION NUMBER: US/10/367,594

; CURRENT FILING DATE: 2003-02-14
 ; PRIOR FILING DATE: 2000-10-05
 ; PRIOR APPLICATION NUMBER: US 09/680,806
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: PCT/US96/13363
 ; PRIOR FILING DATE: 1996-08-16
 ; PRIOR APPLICATION NUMBER: US 60/002,490
 ; PRIOR FILING DATE: 1995-08-18
 ; PRIOR APPLICATION NUMBER: US 60/002,479
 ; PRIOR FILING DATE: 1995-08-18
 ; NUMBER OF SEQ ID NOS: 349
 ; SOFTWARE: WordPerfect 8.0 for Windows

; SEQ ID NO 89
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic peptide
 US-10-367-594-89

Query Match 100.0%; Score 44; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLQDIVLHL 9
 |||||
 Db 1 TLQDIVLHL 9

RESULT 7

US-10-367-654-89
 ; Sequence 89, Application US/10367654
 ; Publication No. US2004007172A1
 ; GENERAL INFORMATION:

; APPLICANT: Rothman, James E.
 ; APPLICANT: Hartl, F. Ulrich
 ; APPLICANT: Hoe, Mee H.
 ; APPLICANT: Houghton, Alan

; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies

; APPLICANT: Takechi, Yoshizumi
 ; APPLICANT: Mayhew, Mark
 ; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
 ; FILE REFERENCE: 11746/461032
 ; CURRENT APPLICATION NUMBER: US/10/367,654
 ; CURRENT FILING DATE: 2003-02-14
 ; PRIOR APPLICATION NUMBER: US 10/171,734
 ; PRIOR FILING DATE: 2002-06-13
 ; PRIOR APPLICATION NUMBER: US 09/636,295
 ; PRIOR FILING DATE: 2000-08-10
 ; PRIOR APPLICATION NUMBER: US 09/011,645
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: PCT/US96/13363
 ; PRIOR FILING DATE: 1996-08-16
 ; PRIOR APPLICATION NUMBER: US 60/002,490
 ; PRIOR FILING DATE: 1995-08-18
 ; PRIOR APPLICATION NUMBER: US 60/002,479
 ; PRIOR FILING DATE: 1995-08-18
 ; NUMBER OF SEQ ID NOS: 349
 ; SOFTWARE: WordPerfect 8.0 for Windows
 ; SEQ ID NO 89
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic peptide
 US-10-367-654-89

Query Match 100.0%; Score 44; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLQDIVLHL 9
 |||||
 Db 1 TLQDIVLHL 9

RESULT 8

US-10-367-658-89
 ; Sequence 89, Application US/10367658
 ; Publication No. US2004007172A1
 ; GENERAL INFORMATION:

; APPLICANT: Rothman, James E.
 ; APPLICANT: Hartl, F. Ulrich
 ; APPLICANT: Hoe, Mee H.
 ; APPLICANT: Houghton, Alan
 ; APPLICANT: Takechi, Yoshizumi
 ; APPLICANT: Mayhew, Mark

; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
 ; FILE REFERENCE: 11746/461051
 ; CURRENT APPLICATION NUMBER: US/10/367,658
 ; CURRENT FILING DATE: 2003-02-14

; PRIOR APPLICATION NUMBER: US 09/794,529
 ; PRIOR FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: US 09/011,645
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: PCT/US96/13363
 ; PRIOR FILING DATE: 1996-08-16
 ; PRIOR APPLICATION NUMBER: US 60/002,490
 ; PRIOR FILING DATE: 1995-08-18
 ; PRIOR APPLICATION NUMBER: US 60/002,479
 ; PRIOR FILING DATE: 1995-08-18
 ; NUMBER OF SEQ ID NOS: 349
 ; SOFTWARE: WordPerfect 8.0 for Windows
 ; SEQ ID NO 89
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic peptide
 US-10-367-658-89

Query Match

100.0%; Score 44; DB 15; Length 9;

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; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-674-89

Query Match          100.0%; Score 44; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLQDIVLHL 9
Db 1 TLQDIVLHL 9

RESULT 11
US-10-815-514-10
; Sequence 10, Application US/10815514
; Publication No. US20040204361A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/815,514
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/696,872
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: papillomavirus
US-10-815-514-10

Query Match          100.0%; Score 44; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLQDIVLHL 9
Db 1 TLQDIVLHL 9

RESULT 12
US-10-877-930-10
; Sequence 10, Application US/10877930
; Publication No. US20040235129A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/877,930
; CURRENT FILING DATE: 2004-05-25
; PRIOR APPLICATION NUMBER: US/09/696,070
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
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Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLQDIVLHL 9
Db 1 TLQDIVLHL 9

RESULT 9
US-10-367-668-89
; Sequence 89, Application US/10367668
; Publication No. US20040071725A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461072
; CURRENT APPLICATION NUMBER: US/10/367,668
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,517
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-668-89

Query Match          100.0%; Score 44; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLQDIVLHL 9
Db 1 TLQDIVLHL 9

RESULT 10
US-10-367-674-89
; Sequence 89, Application US/10367674
; Publication No. US2004012784A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/4610211
; CURRENT APPLICATION NUMBER: US/10/367,674
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 10/170,738
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/552,868
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
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; LENGTH: 9
; TYPE: PRT
; ORGANISM: papillomavirus
US-10-877-930-10

Query Match      100.0%; Score 44; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
Db 1 TLQDIVLHL 9

RESULT 13
US-10-873-594-10
; Sequence 10, Application US/10873594
; Publication No. US20050095667A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: A31488-I-1 065360.0152
; CURRENT APPLICATION NUMBER: US/10/873,594
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/09/800,358
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/696,070
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: 09/124,671
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-873-594-10

Query Match      100.0%; Score 44; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
Db 1 TLQDIVLHL 9

RESULT 14
US-10-751-845-144
; Sequence 144, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus

US-10-751-845-144
; Sequence 145, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-145

Query Match      100.0%; Score 44; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
Db 2 TLQDIVLHL 10

Search completed: June 29, 2005, 04:19:22
Job time : 58.85 secs
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-30
Perfect score: 44
Sequence: 1 TLQDIVLHL 9

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/iaa/ECTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	9	3	US-09-124-671-10
2	44	100.0	20	4	US-09-794-529B-14
3	44	100.0	20	4	US-09-794-529B-15
4	44	100.0	20	4	US-09-794-517A-14
5	44	100.0	20	4	US-09-794-517A-15
6	44	100.0	20	4	US-09-011-645E-14
7	44	100.0	20	4	US-09-011-645E-15
8	44	100.0	20	4	US-09-794-832-14
9	44	100.0	20	4	US-09-794-832-15
10	44	100.0	20	4	US-09-680-806A-14
11	44	100.0	20	4	US-09-680-806A-15
12	44	100.0	20	4	US-09-552-868-14
13	44	100.0	20	4	US-09-552-868-15
14	44	100.0	20	4	US-09-636-295-14
15	44	100.0	20	4	US-09-636-295-15
16	44	100.0	30	2	US-08-934-915-61
17	44	100.0	227	3	US-09-485-885-16
18	44	100.0	227	3	US-09-485-885-19
19	44	100.0	272	1	US-08-117-083-13
20	44	100.0	383	3	US-09-485-885-23
21	37	84.1	1003	4	US-09-252-991A-24069
22	36	81.8	579	4	US-08-851-567B-51
23	36	81.8	715	4	US-09-489-039A-10710
24	36	81.8	2516	4	US-08-851-567B-47
25	36	81.8	2516	4	US-09-817-514A-2
26	36	81.8	2522	3	US-09-251-645-13
27	34	77.3	573	4	US-08-851-567B-55

28	34	77.3	2504	4	US-08-851-567B-12	Sequence 12, Appl
29	34	77.3	2504	4	US-09-817-514A-8	Sequence 8, Appl
30	33	75.0	82	4	US-09-270-767-45813	Sequence 45813, A
31	33	75.0	96	4	US-09-513-999C-5998	Sequence 5998, Ap
32	33	75.0	319	4	US-09-634-238-243	Sequence 243, App
33	33	75.0	351	4	US-09-538-092-1256	Sequence 1256, Ap
34	33	75.0	405	4	US-09-270-767-44068	Sequence 44068, A
35	33	75.0	504	4	US-09-252-991A-26180	Sequence 26180, A
36	33	75.0	700	4	US-09-543-681A-6902	Sequence 6902, Ap
37	33	75.0	748	4	US-09-252-991A-21696	Sequence 21696, A
38	33	75.0	1332	4	US-09-270-767-59785	Sequence 59785, A
39	33	75.0	1375	3	US-09-722-139-2	Sequence 2, Appl
40	33	75.0	1375	3	US-09-721-832-2	Sequence 2, Appl
41	33	75.0	1375	4	US-09-721-689-2	Sequence 2, Appl
42	33	75.0	1607	4	US-09-270-767-44362	Sequence 44362, A
43	33	75.0	1657	1	US-08-287-959-1	Sequence 1, Appl
44	33	75.0	1657	4	US-09-949-016-6427	Sequence 6427, Ap
45	33	75.0	1678	4	US-09-949-016-9445	Sequence 9445, Ap

ALIGNMENTS

RESULT 1
US-09-124-671-10
; Sequence 10, Application US/09124671A
; Patent No. 6160088
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/09/124.671A
; CURRENT FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: papillomavirus
US-09-124-671-10

Query Match 100.0%; Score 44; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.le+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TLQDIVLHL 9
Db	1	TLQDIVLHL 9

RESULT 2
US-09-794-529B-14
; Sequence 14, Application US/09794529B
; Patent No. 6641812
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; ROTHMAN, James E.
; HARTL, F. Ulrich
; HOE, Mee H.
; HOUGHTON, Alan
; TAKECHI, Yoshizumi
; MAYHEW, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: One Broadway
; CITY: New York
; STATE: NY
; COUNTRY: US


```
;
; STATE: NY
; COUNTRY: US
; ZIP: 10004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Perfect
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/794,517A
; FILING DATE: 19-Oct-2001
; CLASSIFICATION: 536
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,479
; FILING DATE: August 18, 1995
; APPLICATION NUMBER: 60/002,490
; FILING DATE: August 18, 1995
; APPLICATION NUMBER: PCT/US96/13363
; FILING DATE: August 16, 1996
; APPLICATION NUMBER: 09/011,645
; FILING DATE: February 13, 1998
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Delucia, Richard L.
; REGISTRATION NUMBER: 28,839
; REFERENCE/DOCKET NUMBER: 11746/13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 425-7200
; TELEFAX: (212) 425-5288
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: yes
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: <Unknown>
;
; FEATURE:
;
; OTHER INFORMATION: hybrid peptide for human papilloma
; virus vaccine
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-794-517A-14

Query Match 100.0%; Score 44; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
Db 1 TLQDIVLHL 9

RESULT 5
US-09-794-517A-15
; Sequence 15, Application US/09794517A
; Patent No. 6656679
;
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; ROTHMAN, James E.
; HARTL, P. Ulrich
; HOE, Mee H.
; HOUGHTON, Alan
; TAKECHI, Yoshizumi
; MAYHEW, Mark
;
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and
; Immunotherapies
;
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: One Broadway
```

```
;
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Perfect
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/794,517A
; FILING DATE: 19-Oct-2001
; CLASSIFICATION: 536
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,479
; FILING DATE: August 18, 1995
; APPLICATION NUMBER: 60/002,490
; FILING DATE: August 18, 1995
; APPLICATION NUMBER: PCT/US96/13363
; FILING DATE: August 16, 1996
; APPLICATION NUMBER: 09/011,645
; FILING DATE: February 13, 1998
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Delucia, Richard L.
; REGISTRATION NUMBER: 28,839
; REFERENCE/DOCKET NUMBER: 11746/13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 425-7200
; TELEFAX: (212) 425-5288
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: yes
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: <Unknown>
;
; FEATURE:
;
; OTHER INFORMATION: hybrid peptide for human papilloma
; virus vaccine
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-794-517A-15

Query Match 100.0%; Score 44; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
Db 12 TLQDIVLHL 20

RESULT 6
US-09-011-645E-14
; Sequence 14, Application US/09011645E
; Patent No. 6663868
;
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; ROTHMAN, James E.
; HARTL, P. Ulrich
; HOE, Mee H.
; HOUGHTON, Alan
; TAKECHI, Yoshizumi
; MAYHEW, Mark
;
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and
; Immunotherapies
;
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
```

STREET: One Broadway
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,645E
FILING DATE: 13-Feb-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/002,479
FILING DATE: August 18, 1995
APPLICATION NUMBER: 60/002,490
FILING DATE: August 18, 1995
APPLICATION NUMBER: PCT/US96/13363
FILING DATE: August 16, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Delucia, Richard L.
REGISTRATION NUMBER: 28,839
REFERENCE/DOCKET NUMBER: 11746/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: yes
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: <Unknown>
FEATURE:
OTHER INFORMATION: hybrid peptide for human papilloma
virus vaccine
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-011-645E-14
Query Match 100.0%; Score 44; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TLQDIVLHL 9
Db 1 TLQDIVLHL 9
RESULT 7
US-09-011-645E-15
Sequence 15, Application US/09011645E
Patent No. 6663868
GENERAL INFORMATION:
APPLICANT: Sloan-Kettering Institute for Cancer Research
ROTHMAN, James E.
HARTL, F. Ulrich
HOUGHTON, Alan
TAKECHI, Yoshizumi
MAYHEW, Mark
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and
Immunotherapies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway

CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,645E
FILING DATE: 13-Feb-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/002,479
FILING DATE: August 18, 1995
APPLICATION NUMBER: 60/002,490
FILING DATE: August 18, 1995
APPLICATION NUMBER: PCT/US96/13363
FILING DATE: August 16, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Delucia, Richard L.
REGISTRATION NUMBER: 28,839
REFERENCE/DOCKET NUMBER: 11746/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: yes
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: <Unknown>
FEATURE:
OTHER INFORMATION: hybrid peptide for human papilloma
virus vaccine
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-011-645E-15
Query Match 100.0%; Score 44; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TLQDIVLHL 9
Db 12 TLQDIVLHL 20
RESULT 8
US-09-794-832-14
Sequence 14, Application US/09794832
Patent No. 6673348
GENERAL INFORMATION:
APPLICANT: Sloan-Kettering Institute for Cancer Research
ROTHMAN, James E.
HARTL, F. Ulrich
HOUGHTON, Alan
TAKECHI, Yoshizumi
MAYHEW, Mark
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and
Immunotherapies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York

STATE: NY
COUNTRY: US
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794,832
FILING DATE: 27-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/011,645
FILING DATE: 13-Feb-1998
APPLICATION NUMBER: 60/002,479
FILING DATE: August 18, 1995
APPLICATION NUMBER: 60/002,490
FILING DATE: August 18, 1995
APPLICATION NUMBER: PCT/US96/13363
FILING DATE: August 16, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Delucia, Richard L.
REGISTRATION NUMBER: 28,839
REFERENCE/DOCKET NUMBER: 11746/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: yes
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: <Unknown>
FEATURE:
OTHER INFORMATION: hybrid peptide for human papilloma virus vaccine
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-794-832-14
Query Match 100.0%; Score 44; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TLQDIVLHL 9
Db 1 TLQDIVLHL 9
RESULT 9
US-09-794-832-15
Sequence 15, Application US/09794832
Patent No. 6673348
GENERAL INFORMATION:
APPLICANT: Sloan-Kettering Institute for Cancer Research
ROTHMAN, James E.
HARTL, F. Ulrich
HOE, Mee H.
HOUGHTON, Alan
TAKECHI, Yoshizumi
MAYHEW, Mark
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway

CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794,832
FILING DATE: 27-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/011,645
FILING DATE: 13-Feb-1998
APPLICATION NUMBER: 60/002,479
FILING DATE: August 18, 1995
APPLICATION NUMBER: 60/002,490
FILING DATE: August 18, 1995
APPLICATION NUMBER: PCT/US96/13363
FILING DATE: August 16, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Delucia, Richard L.
REGISTRATION NUMBER: 28,839
REFERENCE/DOCKET NUMBER: 11746/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: yes
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: <Unknown>
FEATURE:
OTHER INFORMATION: hybrid peptide for human papilloma virus vaccine
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-794-832-15
Query Match 100.0%; Score 44; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TLQDIVLHL 9
Db 12 TLQDIVLHL 20
RESULT 10
US-09-680-806A-14
Sequence 14, Application US/09680806A
Patent No. 6719974
GENERAL INFORMATION:
APPLICANT: Sloan-Kettering Institute for Cancer Research
ROTHMAN, James E.
HARTL, F. Ulrich
HOE, Mee H.
HOUGHTON, Alan
TAKECHI, Yoshizumi
MAYHEW, Mark
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon

```

; STREET: One Broadway
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Perfect
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,806A
; FILING DATE: 05-Oct-2000
; CLASSIFICATION: 424
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,479
; FILING DATE: August 18, 1995
; APPLICATION NUMBER: 60/002,490
; FILING DATE: August 18, 1995
; APPLICATION NUMBER: PCT/US96/13363
; FILING DATE: August 16, 1996
; APPLICATION NUMBER: 09/011,645
; FILING DATE: February 13, 1998
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Delucia, Richard L.
; REGISTRATION NUMBER: 28,839
; REFERENCE/DOCKET NUMBER: 11746/10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 425-7200
; TELEFAX: (212) 425-5288
; TELEX: <Unknown>
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; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
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; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: yes
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: <Unknown>
; FEATURE:
; OTHER INFORMATION: hybrid peptide for human papilloma
; virus vaccine
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-680-806A-14
Query Match 100.0%; Score 44; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLQDIVLHL 9
Db 1 TLQDIVLHL 9

RESULT 11
US-09-680-806A-15
; Sequence 15, Application US/09680806A
; Patent No. 6719974
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; ROTHMAN, James E.
; HARTL, F. Ulrich
; HOE, Mee H.
; HOUGHTON, Alan
; TAKECHI, Yoshizumi
; MAYHEW, Mark
;
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and
; Immunotherapies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:

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; ADDRESSEE: Kenyon & Kenyon
; STREET: One Broadway
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS
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; APPLICATION NUMBER: US/09/680,806A
; FILING DATE: 05-Oct-2000
; CLASSIFICATION: 424
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,479
; FILING DATE: August 18, 1995
; APPLICATION NUMBER: 60/002,490
; FILING DATE: August 18, 1995
; APPLICATION NUMBER: PCT/US96/13363
; FILING DATE: August 16, 1996
; APPLICATION NUMBER: 09/011,645
; FILING DATE: February 13, 1998
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Delucia, Richard L.
; REGISTRATION NUMBER: 28,839
; REFERENCE/DOCKET NUMBER: 11746/10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 425-7200
; TELEFAX: (212) 425-5288
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: yes
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: <Unknown>
; FEATURE:
; OTHER INFORMATION: hybrid peptide for human papilloma
; virus vaccine
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-680-806A-15
Query Match 100.0%; Score 44; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLQDIVLHL 9
Db 12 TLQDIVLHL 20

RESULT 12
US-09-552-868-14
; Sequence 14, Application US/09552868
; Patent No. 6761892
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; ROTHMAN, James E.
; HARTL, F. Ulrich
; HOE, Mee H.
; HOUGHTON, Alan
; TAKECHI, Yoshizumi
; MAYHEW, Mark
;
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and
; Immunotherapies
; NUMBER OF SEQUENCES: 30

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;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: One Broadway
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Perfect
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/552,868
; FILING DATE: 20-Apr-2000
; CLASSIFICATION: 424
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,479
; FILING DATE: August 18, 1995
; APPLICATION NUMBER: 60/002,490
; FILING DATE: August 18, 1995
; APPLICATION NUMBER: PCT/US96/13363
; FILING DATE: August 16, 1996
; APPLICATION NUMBER: 09/011,645
; FILING DATE: February 13, 1998
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Delucia, Richard L.
; REGISTRATION NUMBER: 28,839
; REFERENCE/DOCKET NUMBER: 11746/8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 425-7200
; TELEFAX: (212) 425-5288
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: yes
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: <Unknown>
; FEATURE:
; OTHER INFORMATION: hybrid peptide for human papilloma
; virus vaccine
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-552-868-14
Query Match 100.0%; Score 44; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
Db 1 TLQDIVLHL 9

RESULT 13
US-09-552-868-15
; Sequence 15, Application US/09552868
; Patent No. 6761892
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; ROTHMAN, James E.
; HARTL, F. Ulrich
; HOE, Mee H.
; HOUGHTON, Alan
; TAKECHI, Yoshizumi
; MAYHEW, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and
; Immunotherapies

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; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: One Broadway
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
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; APPLICATION NUMBER: US/09/552,868
; FILING DATE: 20-Apr-2000
; CLASSIFICATION: 424
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,479
; FILING DATE: August 18, 1995
; APPLICATION NUMBER: 60/002,490
; FILING DATE: August 18, 1995
; APPLICATION NUMBER: PCT/US96/13363
; FILING DATE: August 16, 1996
; APPLICATION NUMBER: 09/011,645
; FILING DATE: February 13, 1998
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Delucia, Richard L.
; REGISTRATION NUMBER: 28,839
; REFERENCE/DOCKET NUMBER: 11746/8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 425-7200
; TELEFAX: (212) 425-5288
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: yes
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: <Unknown>
; FEATURE:
; OTHER INFORMATION: hybrid peptide for human papilloma
; virus vaccine
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-552-868-15
Query Match 100.0%; Score 44; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLQDIVLHL 9
Db 12 TLQDIVLHL 20

RESULT 14
US-09-636-295-14
; Sequence 14, Application US/09636295
; Patent No. 6773707
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; ROTHMAN, James E.
; HARTL, F. Ulrich
; HOE, Mee H.
; HOUGHTON, Alan
; TAKECHI, Yoshizumi
; MAYHEW, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and

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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-3
Perfect score: 47
Sequence: 1 QLCTELQTT 9

Scoring table: BLOSUM62
Gapop 10.0., Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	138	2 Q919D2	Q919D2 human papil
2	47	100.0	143	2 Q919B6	Q919B6 human papil
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4	47	100.0	151	2 Q778I6	Q778I6 human papil
5	47	100.0	151	2 Q773C7	Q773C7 human papil
6	47	100.0	151	2 Q772J5	Q772J5 human papil
7	47	100.0	151	2 Q80963	Q80963 human papil
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10	47	100.0	151	2 Q89755	Q89755 human papil
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12	47	100.0	151	2 Q8B564	Q8B564 human papil
13	47	100.0	151	2 Q8BB19	Q8BB19 human papil
14	47	100.0	151	2 Q8BB20	Q8BB20 human papil
15	47	100.0	151	2 Q9W8C3	Q9W8C3 human papil
16	47	100.0	151	2 Q9W931	Q9W931 human papil
17	47	100.0	151	2 Q9WMP4	Q9WMP4 human papil
18	47	100.0	151	2 Q9WMP5	Q9WMP5 human papil
19	47	100.0	158	1 V86_HPV16	V86_HPV16 human papil
20	47	100.0	158	2 Q8QHP5	Q8QHP5 human papil
21	47	100.0	158	2 Q8QHT0	Q8QHT0 human papil
22	47	100.0	158	2 Q8QRD6	Q8QRD6 human papil
23	47	100.0	158	2 Q8QRD7	Q8QRD7 human papil
24	47	100.0	158	2 Q8QRD8	Q8QRD8 human papil
25	47	100.0	158	2 Q8QRD9	Q8QRD9 human papil
26	47	100.0	158	2 Q8QRE0	Q8QRE0 human papil
27	47	100.0	158	2 Q8QRE1	Q8QRE1 human papil
28	47	100.0	158	2 Q71B17	Q71B17 human papil
29	47	100.0	158	2 Q9QDH3	Q9QDH3 human papil
30	47	100.0	158	2 Q9QDH5	Q9QDH5 human papil
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34 47 100.0 161 2 Q919B1 Q919B1 human papil
35 47 100.0 161 2 Q919C6 Q919C6 human papil
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ALIGNMENTS

RESULT 1

Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404694; AAL01345.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
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Query Match 100.0%; Score 47; DB 2; Length 138;

Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELQTT 9

Db 1 QLCTELQTT 9

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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).

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DR EMBL; AF404702; AAL01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3B6BE2AC CRC64;

Query Match          100.0%; Score 47; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

Qy 1 QLCTELOTT 9
Db 6 QLCTELOTT 14

RESULT 3
Q919C4
ID Q919C4 PRELIMINARY; PRT; 143 AA.
AC Q919C4;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404698; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match          100.0%; Score 47; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

Qy 1 QLCTELOTT 9
Db 6 QLCTELOTT 14

RESULT 4
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ID Q778I6 PRELIMINARY; PRT; 151 AA.
AC Q778I6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388056; CAB45104.1; -.
DR EMBL; AJ388061; CAB45114.1; -.
DR EMBL; AJ388066; CAB45124.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18320 MW; 617D2A2FDB4F8C17 CRC64;

Query Match          100.0%; Score 47; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

Qy 1 QLCTELOTT 9
Db 14 QLCTELOTT 22

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ID Q77JC7 PRELIMINARY; PRT; 151 AA.
AC Q77JC7;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Early transforming protein E6 variant (Transforming protein E6).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Xinjiang;
RA Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang P.;
RT "Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma Biopsies in Xinjiang.";
RL Sheng Wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan 0:0-0(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22242222; PubMed=12355268; DOI=10.1007/s00239-002-2344-y;
RA DeFilippis V.R., Ayala F.J., Villarreal L.P.;
RT "Evidence of diversifying selection in human papillomavirus type 16 E6 but not E7 oncogenes.";
RL J. Mol. Evol. 55:491-499(2002).
RN [4]
RP SEQUENCE FROM N.A.
RA Cruz M., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S., Martins C.R.F.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Cruz M.R., Martins C.R.F.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF327851; AAG45940.1; -.
DR EMBL; AJ388057; CAB45106.1; -.
DR EMBL; AJ388059; CAB45130.1; -.
DR EMBL; AY089951; AAM11875.1; -.
DR EMBL; AY089954; AAM11881.1; -.
DR EMBL; AY112663; AAM51854.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18320 MW; 617D2A2FDB4F8C17 CRC64;

Query Match          100.0%; Score 47; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.12;
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DR EMBL; AJ388066; CAB45124.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;

Query Match          100.0%; Score 47; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

Qy 1 QLCTELOTT 9
Db 14 QLCTELOTT 22

RESULT 5
Q77JC7
ID Q77JC7 PRELIMINARY; PRT; 151 AA.
AC Q77JC7;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Early transforming protein E6 variant (Transforming protein E6).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Xinjiang;
RA Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang P.;
RT "Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma Biopsies in Xinjiang.";
RL Sheng Wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan 0:0-0(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22242222; PubMed=12355268; DOI=10.1007/s00239-002-2344-y;
RA DeFilippis V.R., Ayala F.J., Villarreal L.P.;
RT "Evidence of diversifying selection in human papillomavirus type 16 E6 but not E7 oncogenes.";
RL J. Mol. Evol. 55:491-499(2002).
RN [4]
RP SEQUENCE FROM N.A.
RA Cruz M., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S., Martins C.R.F.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Cruz M.R., Martins C.R.F.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF327851; AAG45940.1; -.
DR EMBL; AJ388057; CAB45106.1; -.
DR EMBL; AJ388059; CAB45130.1; -.
DR EMBL; AY089951; AAM11875.1; -.
DR EMBL; AY089954; AAM11881.1; -.
DR EMBL; AY112663; AAM51854.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18320 MW; 617D2A2FDB4F8C17 CRC64;

Query Match          100.0%; Score 47; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.12;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLCTELQTT 9
 Db 14 QLCTELQTT 22

RESULT 6
 Q772J5 PRELIMINARY; PRT; 151 AA.
 AC Q772J5;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "sequence variations and viral genomic state of human papillomavirus
 type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 DR EMBL; AF003019; AAB70736.1; -;
 DR EMBL; AF003018; AAB70735.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18221 MW; 60CD2A34DAF48CB7 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLCTELQTT 9
 Db 14 QLCTELQTT 22

RESULT 7
 Q80963 PRELIMINARY; PRT; 151 AA.
 AC Q80963;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Early transforming protein E6.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96079021; PubMed=7494284;
 RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
 RA Jenison S.A.;
 RT "Human papillomavirus type 16 variant lineages in United States
 RT populations characterized by nucleotide sequence analysis of the E6,
 RT L2, and L1 coding segments.";
 RL J. Virol. 69:7743-7753(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX Farmer A.D.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

QY 1 QLCTELQTT 9
 Db 14 QLCTELQTT 22

RESULT 8
 Q89640 PRELIMINARY; PRT; 151 AA.
 AC Q89640;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Early transforming protein E6.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96079021; PubMed=7494284;
 RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
 RA Jenison S.A.;
 RT "Human papillomavirus type 16 variant lineages in United States
 RT populations characterized by nucleotide sequence analysis of the E6,
 RT L2, and L1 coding segments.";
 RL J. Virol. 69:7743-7753(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Farmer A.D.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

QY 1 QLCTELQTT 9
 Db 14 QLCTELQTT 22

RESULT 9
 Q89648 PRELIMINARY; PRT; 151 AA.
 AC Q89648; O12653; O12654; O12928; O12929;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Early transforming protein E6.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;

DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18291 MW; 97C7028D5169382D CRC64;

Query Match 100.0%; Score 47; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLCTELQTT 9
 Db 14 QLCTELQTT 22

RESULT 8
 Q89640 PRELIMINARY; PRT; 151 AA.
 AC Q89640;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Early transforming protein E6.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96079021; PubMed=7494284;
 RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
 RA Jenison S.A.;
 RT "Human papillomavirus type 16 variant lineages in United States
 RT populations characterized by nucleotide sequence analysis of the E6,
 RT L2, and L1 coding segments.";
 RL J. Virol. 69:7743-7753(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Farmer A.D.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

QY 1 QLCTELQTT 9
 Db 14 QLCTELQTT 22

RESULT 9
 Q89648 PRELIMINARY; PRT; 151 AA.
 AC Q89648; O12653; O12654; O12928; O12929;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Early transforming protein E6.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;

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RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=96079021; PubMed=7494284;
RA  Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RT  "Human papillomavirus type 16 variant lineages in United States
RT  populations characterized by nucleotide sequence analysis of the E6,
RT  L2, and L1 coding segments.";
RL  J. Virol. 69:7743-7753(1995).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  Farmer A.D.;
RL  Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR  EMBL; U34110; AAA91657.1; -
DR  EMBL; U34109; AAA91656.1; -
DR  EMBL; U34113; AAA91660.1; -
DR  EMBL; U34135; AAA91682.1; -
DR  GO; GO:0042025; C:host cell nucleus; IEA.
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  InterPro; IPR001334; E6.
DR  Pfam; PF00518; E6; 1.
SQ  SEQUENCE 151 AA; 18221 MW; 60CD2A34DAF48CB7 CRC64;

Query Match      100.0%; Score 47; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 QLCTELOTT 9
DB  14 QLCTELOTT 22

RESULT 10
Q89755
ID  Q89755      PRELIMINARY;      PRT; 151 AA.
AC  Q89755;
DT  01-NOV-1996 (TRENBLrel. 01, Created)
DT  01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT  05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE  Early transforming protein E6.
OS  Human papillomavirus.
OC  Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC  Papillomavirus.
OX  NCBI_TaxID=10566;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RT  "Human papillomavirus type 16 variant lineages in United States
RT  populations characterized by nucleotide sequence analysis of the E6,
RT  L2, and L1 coding segments.";
RL  J. Virol. 69:7743-7753(1995).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  Farmer A.D.;
RL  Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR  EMBL; U34126; AAA91673.1; -
DR  EMBL; U34111; AAA91658.1; -
DR  EMBL; U34121; AAA91668.1; -
DR  EMBL; U34123; AAA91670.1; -
DR  GO; GO:0042025; C:host cell nucleus; IEA.
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  InterPro; IPR001334; E6.
DR  Pfam; PF00518; E6; 1.
SQ  SEQUENCE 151 AA; 18334 MW; FF9F2A2FCBBA6C02 CRC64;

Query Match      100.0%; Score 47; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 QLCTELOTT 9
DB  14 QLCTELOTT 22

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```

DB  14 QLCTELOTT 22

RESULT 11
Q89852
ID  Q89852      PRELIMINARY;      PRT; 151 AA.
AC  Q89852;
DT  01-NOV-1996 (TRENBLrel. 01, Created)
DT  01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT  05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE  Early transforming protein E6.
OS  Human papillomavirus.
OC  Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC  Papillomavirus.
OX  NCBI_TaxID=10566;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RT  "Human papillomavirus type 16 variant lineages in United States
RT  populations characterized by nucleotide sequence analysis of the E6,
RT  L2, and L1 coding segments.";
RL  J. Virol. 69:7743-7753(1995).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  Farmer A.D.;
RL  Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR  EMBL; U34134; AAA91681.1; -
DR  EMBL; U34127; AAA91674.1; -
DR  EMBL; U34133; AAA91680.1; -
DR  GO; GO:0042025; C:host cell nucleus; IEA.
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  InterPro; IPR001334; E6.
DR  Pfam; PF00518; E6; 1.
SQ  SEQUENCE 151 AA; 18320 MW; 617D2A2FDB4F8C17 CRC64;

Query Match      100.0%; Score 47; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 QLCTELOTT 9
DB  14 QLCTELOTT 22

RESULT 12
Q89564
ID  Q89564      PRELIMINARY;      PRT; 151 AA.
AC  Q89564;
DT  01-MAR-2003 (TRENBLrel. 23, Created)
DT  01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT  01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE  E6 protein.
OS  Human papillomavirus.
OC  Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC  Papillomavirus.
OX  NCBI_TaxID=10566;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Ponglikitmongkol M., Vaeteewootacharn K.;
RL  Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF548023; AA016239.1; -
DR  GO; GO:0042025; C:host cell nucleus; IEA.
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  InterPro; IPR001334; E6.
DR  Pfam; PF00518; E6; 1.
SQ  SEQUENCE 151 AA; 18348 MW; FE3F2D5FCD7A69B2 CRC64;

Query Match      100.0%; Score 47; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 QLCTELQTT 9
Db 14 QLCTELQTT 22

RESULT 13

Q8BB19 PRELIMINARY; PRT; 151 AA.
AC Q8BB19
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22242222; PubMed=12355268; DOI=10.1007/s00239-002-2344-Y;
RA Defilippis V.R., Ayala F.J., Villarreal L.P.;
RT "Evidence of diversifying selection in human papillomavirus type 16 E6 but not E7 oncogenes.";
RL J. Mol. Evol. 55:491-499(2002).
DR EMBL; AY089955; AAM11883.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18319 MW; 6P9D2A2FD5AF88F7 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELQTT 9
Db 14 QLCTELQTT 22

RESULT 14

Q8BB20 PRELIMINARY; PRT; 151 AA.
AC Q8BB20
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22242222; PubMed=12355268; DOI=10.1007/s00239-002-2344-Y;
RA Defilippis V.R., Ayala F.J., Villarreal L.P.;
RT "Evidence of diversifying selection in human papillomavirus type 16 E6 but not E7 oncogenes.";
RL J. Mol. Evol. 55:491-499(2002).
DR EMBL; AY089953; AAM11879.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18319 MW; 7CBD23EFCF4F8C17 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELQTT 9
Db 14 QLCTELQTT 22

RESULT 15

Q9W8C3 PRELIMINARY; PRT; 151 AA.
AC Q9W8C3
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388064; CAB45120.1; -.
DR EMBL; AJ388082; CAB45116.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18360 MW; FF9A2A3ADDBA7902 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELQTT 9
Db 14 QLCTELQTT 22

Search completed: June 28, 2005, 19:19:20
Job time : 56.3 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 01:35:30 ; Search time 57.55 Seconds
(without alignments)
60.138 Million cell updates/sec

Title: US-08-170-344-3
Perfect score: 47
Sequence: 1 QLTRELQTT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	47	100.0	21	16	US-10-476-570-8
4	47	100.0	30	16	US-10-476-570-53
5	47	100.0	30	17	US-10-858-384-4
6	47	100.0	32	16	US-10-476-570-9
7	47	100.0	33	16	US-10-476-570-19
8	47	100.0	151	14	US-10-177-390-6
9	47	100.0	151	17	US-10-484-063-20
10	47	100.0	151	17	US-10-484-063-27
11	47	100.0	158	17	US-10-858-384-2

12	47	100.0	158	17	US-10-367-057-16	Sequence 16, Appl
13	47	100.0	171	16	US-10-472-724-2	Sequence 2, Appl
14	47	100.0	266	9	US-09-367-309A-1	Sequence 1, Appl
15	47	100.0	273	13	US-10-000-903-4	Sequence 4, Appl
16	47	100.0	273	17	US-10-899-771-4	Sequence 4, Appl
17	47	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
18	47	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
19	47	100.0	371	13	US-10-000-903-6	Sequence 6, Appl
20	47	100.0	371	17	US-10-899-771-6	Sequence 6, Appl
21	47	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
22	47	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
23	47	100.0	536	15	US-10-367-095-10	Sequence 10, Appl
24	47	100.0	536	15	US-10-368-046-10	Sequence 10, Appl
25	47	100.0	536	16	US-10-367-367-10	Sequence 10, Appl
26	47	100.0	536	17	US-10-918-337-10	Sequence 10, Appl
27	37	78.7	48	9	US-09-925-299-1386	Sequence 1386, Ap
28	37	78.7	48	10	US-09-925-299-1386	Sequence 1386, Ap
29	37	78.7	587	16	US-10-437-363-115784	Sequence 115784,
30	37	78.7	853	16	US-10-437-363-122232	Sequence 122232,
31	36	76.6	55	15	US-10-424-599-191823	Sequence 191823,
32	36	76.6	470	15	US-10-369-493-1712	Sequence 1712, Ap
33	35	74.5	158	15	US-10-282-122A-70249	Sequence 70249, A
34	35	74.5	158	17	US-10-857-625-567	Sequence 567, App
35	34	72.3	104	13	US-10-424-599-246277	Sequence 246277,
36	34	72.3	120	16	US-10-767-701-37218	Sequence 37218, A
37	34	72.3	202	14	US-10-127-816-9	Sequence 9, Appl
38	34	72.3	202	14	US-10-127-816-11	Sequence 11, Appl
39	34	72.3	202	14	US-10-142-717-12	Sequence 12, Appl
40	34	72.3	202	15	US-10-420-034A-60	Sequence 60, Appl
41	34	72.3	202	15	US-10-420-034A-62	Sequence 62, Appl
42	34	72.3	202	16	US-10-691-923-8	Sequence 8, Appl
43	34	72.3	202	16	US-10-691-923-10	Sequence 10, Appl
44	34	72.3	202	17	US-10-914-772-8	Sequence 8, Appl
45	34	72.3	202	17	US-10-914-772-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
; Sequence 20, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POURVILLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 17-31
US-10-476-570-20

Query Match 100.0%; Score 47; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 QLCTELQTT 9
      |||||
Db      5 QLCTELQTT 13

RESULT 2
US-10-476-570-21
; Sequence 21, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: Papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 20-34
US-10-476-570-21

Query Match      100.0%; Score 47; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QLCTELQTT 9
      |||||
Db      2 QLCTELQTT 10

RESULT 3
US-10-476-570-8
; Sequence 8, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: Papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-34
US-10-476-570-8

Query Match      100.0%; Score 47; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QLCTELQTT 9
      |||||
Db      2 QLCTELQTT 10

RESULT 4
US-10-476-570-53
; Sequence 53, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: Papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 30
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 15-44
US-10-476-570-53

Query Match      100.0%; Score 47; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QLCTELQTT 9
      |||||
Db      7 QLCTELQTT 15

RESULT 5
US-10-858-384-4
; Sequence 4, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence

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FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E6 of HPV
US-10-858-384-4

Query Match 100.0%; Score 47; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.16; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 QLCTELOTT 9

Db 7 QLCTELOTT 15

RESULT 6

US-10-476-570-9
; Sequence 9, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; PRIOR FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-45
US-10-476-570-9

Query Match 100.0%; Score 47; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.2; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 QLCTELOTT 9

Db 8 QLCTELOTT 16

RESULT 7

US-10-476-570-19
; Sequence 19, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; PRIOR FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-46
US-10-476-570-19

Query Match 100.0%; Score 47; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.2; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 QLCTELOTT 9

Db 8 QLCTELOTT 16

RESULT 8

US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerps Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match 100.0%; Score 47; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.91; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 QLCTELOTT 9

Db 14 QLCTELOTT 22

RESULT 9

US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match 100.0%; Score 47; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.91; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 QLCTELOTT 9
Db 14 QLCTELOTT 22

RESULT 10
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match 100.0%; Score 47; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.91; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 QLCTELOTT 9
Db 14 QLCTELOTT 22

RESULT 11
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGALT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 100.0%; Score 47; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.96; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 QLCTELOTT 9
Db 21 QLCTELOTT 29

RESULT 12
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraSeqlist version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 100.0%; Score 47; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.96; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 QLCTELOTT 9
Db 21 QLCTELOTT 29

RESULT 13
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Zur Hausen, Harald
; APPLICANT: Cid-Arregui, Angel
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 100.0%; Score 47; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 QLCTELOTT 9
Db 26 QLCTELOTT 34

RESULT 14
US-09-367-309A-1

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; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080,
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1
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Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  QLCTELOTT 9
Db      21  QLCTELOTT 29
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RESULT 15

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US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4
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Query Match          100.0%; Score 47; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  QLCTELOTT 9
Db     127  QLCTELOTT 135
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OM protein - protein search, using sw model

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Title: US-08-170-344-3
Perfect score: 47
Sequence: 1 QLCTELQTT 9

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	47	100.0	30	US-08-363-586-4	Sequence 4, Appli
3	47	100.0	30	US-09-980-523A-4	Sequence 4, Appli
4	47	100.0	158	US-09-980-523A-2	Sequence 2, Appli
5	47	100.0	162	US-08-316-239B-3	Sequence 3, Appli
6	47	100.0	162	US-08-316-239B-4	Sequence 4, Appli
7	47	100.0	172	US-08-860-165-14	Sequence 14, Appli
8	47	100.0	172	US-09-359-382-14	Sequence 14, Appli
9	47	100.0	182	US-08-117-083-10	Sequence 10, Appli
10	47	100.0	266	US-08-860-165-10	Sequence 10, Appli
11	47	100.0	266	US-09-359-382-10	Sequence 10, Appli
12	47	100.0	266	US-09-367-302A-1	Sequence 1, Appli
13	47	100.0	273	US-09-485-885-4	Sequence 4, Appli
14	47	100.0	292	US-09-485-885-10	Sequence 10, Appli
15	47	100.0	371	US-09-485-885-6	Sequence 6, Appli
16	47	100.0	390	US-09-485-885-14	Sequence 14, Appli
17	34	72.3	4019	US-09-854-133-425	Sequence 425, App
18	33	70.2	32	US-08-466-285-2	Sequence 2, Appli
19	33	70.2	32	US-08-164-768-2	Sequence 2, Appli
20	33	70.2	141	US-09-270-767-33527	Sequence 33527, A
21	33	70.2	141	US-09-270-767-48744	Sequence 48744, A
22	33	70.2	158	US-08-247-904B-10	Sequence 10, Appli
23	33	70.2	158	US-08-767-942A-19	Sequence 19, Appli
24	33	70.2	271	US-08-117-083-14	Sequence 14, Appli
25	33	70.2	278	US-09-485-885-21	Sequence 21, Appli
26	33	70.2	383	US-09-485-885-23	Sequence 23, Appli
27	33	70.2	1104	US-09-793-998-11	Sequence 11, Appli

28 32 68.1 9 1 US-08-787-547-101 Sequence 101, App
29 32 68.1 9 4 US-09-601-729-274 Sequence 274, App
30 32 68.1 203 4 US-09-248-796A-17743 Sequence 17743, A
31 32 68.1 211 4 US-09-543-681A-8111 Sequence 8111, Ap
32 32 68.1 236 4 US-09-634-137-32 Sequence 32, Appl
33 32 68.1 251 4 US-09-270-767-33015 Sequence 33015, A
34 32 68.1 469 4 US-09-543-681A-5423 Sequence 5423, Ap
35 32 68.1 771 3 US-09-121-964-9 Sequence 9, Appli
36 31 66.0 9 3 US-08-159-339A-320 Sequence 320, App
37 31 66.0 14 3 US-08-271-539-3 Sequence 3, Appli
38 31 66.0 56 4 US-09-513-999C-6885 Sequence 6885, Ap
39 31 66.0 108 1 US-08-234-812-3 Sequence 3, Appli
40 31 66.0 108 2 US-08-663-809-3 Sequence 3, Appli
41 31 66.0 129 1 US-08-049-503-1 Sequence 1, Appli
42 31 66.0 129 1 US-08-225-224-2 Sequence 2, Appli
43 31 66.0 129 1 US-08-470-299-21 Sequence 21, Appli
44 31 66.0 129 2 US-08-874-697-1 Sequence 1, Appli
45 31 66.0 129 3 US-08-722-258-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-934-915-159
; Sequence 159, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-159
Query Match 100.0%; Score 47; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELOTT 9
| | | | |
Db 5 QLCTELOTT 13

RESULT 2

US-08-363-586-4
; Sequence 4, Application US/08363586
; Patent No. 5629161
; GENERAL INFORMATION:
; APPLICANT: Mueller, Martin
; APPLICANT: Gissmann, Lutz
; TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
; TITLE OF INVENTION: Peptides for the Diagnostic Purpose
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,586
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/909,296
; FILING DATE: 09-JUL-1992
; APPLICATION NUMBER: EP 9111720.8
; FILING DATE: 13-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wadler, Linda A.
; REGISTRATION NUMBER: 33,218
; REFERENCE/DOCKET NUMBER: 02481-1195-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-363-586-4

Query Match 100.0%; Score 47; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELOTT 9
| | | | |
Db 14 QLCTELOTT 22

RESULT 3

US-09-980-523A-4
; Sequence 4, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE

; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/01 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PPT
; ORGANISM: Human Papillomavirus
US-09-980-523A-4

Query Match 100.0%; Score 47; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELOTT 9
| | | | |
Db 7 QLCTELOTT 15

RESULT 4

US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/01 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PPT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 47; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELOTT 9
| | | | |
Db 21 QLCTELOTT 29

RESULT 5

US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Farmer, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an

;; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
;; TITLE OF INVENTION: Cervical Cancer
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Jagtiani & Associates
;; STREET: 6126 Rocky Way Court
;; CITY: Centreville
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 20120-3400
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/316,239B
;; FILING DATE: 30-SEP-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jagtiani, Ajay A.
;; REGISTRATION NUMBER: 35,205
;; REFERENCE/DOCKET NUMBER: UNME-0001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 817-9453
;; TELEFAX: (703) 803-9387
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 162 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; US-08-316-239B-3

Query Match 100.0%; Score 47; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELOTT 9
Db 21 QLCTELOTT 29

RESULT 6
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jagtiani, Ajay A.
;; REGISTRATION NUMBER: 35,205
;; REFERENCE/DOCKET NUMBER: UNME-0001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 817-9453
;; TELEFAX: (703) 803-9387
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 162 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; US-08-316-239B-4

Query Match 100.0%; Score 47; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELOTT 9
Db 21 QLCTELOTT 29

RESULT 7
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
; US-08-860-165-14

Query Match 100.0%; Score 47; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELOTT 9
Db 90 QLCTELOTT 98

RESULT 8
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148

```

; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match      100.0%; Score 47; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QLCTELOTT 9
DB      90 QLCTELOTT 98

RESULT 9
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Bournell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58763
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note="Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-10

Query Match      100.0%; Score 47; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QLCTELOTT 9
DB      90 QLCTELOTT 98

RESULT 9
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Bournell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58763
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note="Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-10

Query Match      100.0%; Score 47; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QLCTELOTT 9
DB      22 QLCTELOTT 30

RESULT 10
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match      100.0%; Score 47; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QLCTELOTT 9
DB      21 QLCTELOTT 29

RESULT 11
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10
```


Query Match 100.0%; Score 47; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELOTT 9
| | | | | | | |
Db 21 QLCTELOTT 29

RESULT 12
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODRICK I.
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 47; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELOTT 9
| | | | | | | |
Db 21 QLCTELOTT 29

RESULT 13
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 47; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELOTT 9
| | | | | | | |

Db 127 QLCTELOTT 135
RESULT 14
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match 100.0%; Score 47; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELOTT 9
| | | | | | | |
Db 146 QLCTELOTT 154

RESULT 15
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match 100.0%; Score 47; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCTELOTT 9
| | | | | | | |
Db 127 QLCTELOTT 135

Search completed: June 28, 2005, 19:29:01
Job time : 18.15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds
(without alignments)
59.826 Million cell updates/sec

Title: US-08-170-344-29

Perfect score: 47
Sequence: 1 LTNTGLYNL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*

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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	9	17 US-10-751-845-135	Sequence 135, App
2	47	100.0	10	17 US-10-751-845-134	Sequence 134, App
3	47	100.0	10	17 US-10-751-845-142	Sequence 142, App
4	47	100.0	27	17 US-10-751-845-153	Sequence 153, App
5	47	100.0	119	17 US-10-751-845-159	Sequence 159, App
6	47	100.0	158	16 US-10-800-023-27	Sequence 27, Appl
7	47	100.0	172	16 US-10-472-724-6	Sequence 6, Appl
8	47	100.0	236	17 US-10-751-845-157	Sequence 157, App
9	47	100.0	237	17 US-10-751-845-158	Sequence 158, App
10	47	100.0	261	17 US-10-751-845-160	Sequence 160, App
11	47	100.0	278	13 US-10-000-903-21	Sequence 21, Appl

12	47	100.0	278	17	US-10-899-771-21	Sequence 21, Appl
13	47	100.0	383	13	US-10-000-903-23	Sequence 23, Appl
14	47	100.0	383	17	US-10-899-771-23	Sequence 23, Appl
15	38	80.9	12	15	US-10-356-257-95	Sequence 95, Appl
16	37	78.7	173	16	US-10-767-701-62514	Sequence 62514, A
17	37	78.7	289	15	US-10-424-599-165644	Sequence 165644, A
18	37	78.7	523	16	US-10-437-963-151032	Sequence 151032, A
19	37	78.7	534	16	US-10-425-115-343736	Sequence 343736, A
20	35	74.5	47	16	US-10-437-963-146238	Sequence 146238, A
21	35	74.5	189	16	US-10-767-701-56572	Sequence 56572, A
22	35	74.5	233	16	US-10-425-115-197706	Sequence 197706, A
23	35	74.5	386	16	US-10-437-963-176280	Sequence 176280, A
24	35	74.5	427	15	US-10-424-599-155545	Sequence 155545, A
25	35	74.5	516	16	US-10-425-115-197705	Sequence 197705, A
26	35	74.5	529	15	US-10-425-114-67463	Sequence 67463, A
27	35	74.5	1721	15	US-10-282-122A-62548	Sequence 62548, A
28	35	74.5	2204	15	US-10-282-122A-64364	Sequence 64364, A
29	34	72.3	17	9	US-09-813-329-19	Sequence 19, Appl
30	34	72.3	17	9	US-09-813-329-20	Sequence 20, Appl
31	34	72.3	27	9	US-09-813-329-54	Sequence 54, Appl
32	34	72.3	27	9	US-09-813-329-64	Sequence 64, Appl
33	34	72.3	68	16	US-10-437-963-175271	Sequence 175271, A
34	34	72.3	181	16	US-10-767-701-42359	Sequence 42359, A
35	34	72.3	211	9	US-09-925-257-484	Sequence 484, App
36	34	72.3	213	15	US-10-094-749-1949	Sequence 1949, App
37	34	72.3	258	15	US-10-104-047-3590	Sequence 3590, App
38	34	72.3	356	15	US-10-085-198-24	Sequence 24, Appl
39	34	72.3	390	16	US-10-425-115-304104	Sequence 304104, A
40	34	72.3	393	13	US-10-062-254-294	Sequence 294, App
41	34	72.3	406	9	US-09-813-329-4	Sequence 4, Appl
42	34	72.3	409	9	US-09-813-329-6	Sequence 6, Appl
43	34	72.3	442	13	US-10-016-768-8	Sequence 8, Appl
44	34	72.3	689	14	US-10-113-085-2	Sequence 2, Appl
45	34	72.3	836	14	US-10-281-867-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-10-751-845-135
; Sequence 135, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751.845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-135

Query Match 100.0%; Score: 47; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTNTGLYNL 9

Db 1 LTNTGLYNL 9

```

RESULT 2
US-10-751-845-134
; Sequence 134, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-134

```

```

Query Match      100.0%; Score 47; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LTNTGLYNL 9
Db 2 LTNTGLYNL 10

```

```

RESULT 3
US-10-751-845-142
; Sequence 142, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-142

```

```

Query Match      100.0%; Score 47; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LTNTGLYNL 9
Db 1 LTNTGLYNL 9

```

```

RESULT 4
US-10-751-845-153

```

```

; Sequence 153, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-153

```

```

Query Match      100.0%; Score 47; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LTNTGLYNL 9
Db 10 LTNTGLYNL 18

```

```

RESULT 5
US-10-751-845-159
; Sequence 159, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-159

```

```

Query Match      100.0%; Score 47; DB 17; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LTNTGLYNL 9
Db 52 LTNTGLYNL 60

```

```

RESULT 6
US-10-800-023-27
; Sequence 27, Application US/10800023

```

; Publication No. US20040258688A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Ralph
; APPLICANT: Nussenzeiwig, Michel
; APPLICANT: Hawiger, Daniel
; APPLICANT: Bonifaz, Laura
; TITLE OF INVENTION: Enhanced Antigen Delivery and Modulation
; FILE REFERENCE: 600-1-081CONCIPI
; CURRENT APPLICATION NUMBER: US/10/800,023
; CURRENT FILING DATE: 2004-03-14
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,284
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: PCT/US96/01383
; PRIOR FILING DATE: 1996-01-31
; PRIOR APPLICATION NUMBER: 08/381,528
; PRIOR FILING DATE: 1995-01-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 158
; TYPE: PRT
; ORGANISM: human papilloma virus E6 protein
US-10-800-023-27

Query Match 100.0%; Score 47; DB 16; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.38; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 LTNTGLYNL 9
Db 93 LTNTGLYNL 101
|||||

RESULT 7
US-10-472-724-6
; Sequence 6, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-6

Query Match 100.0%; Score 47; DB 16; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.42; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 LTNTGLYNL 9
Db 99 LTNTGLYNL 107
|||||

RESULT 8
US-10-751-845-157
; Sequence 157, Application US/10751845

; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-157

Query Match 100.0%; Score 47; DB 17; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.6; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 LTNTGLYNL 9
Db 169 LTNTGLYNL 177
|||||

RESULT 9
US-10-751-845-158
; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-158

Query Match 100.0%; Score 47; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.6; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 LTNTGLYNL 9
Db 170 LTNTGLYNL 178
|||||

RESULT 10
US-10-751-845-160

```

; Sequence 160, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160

Query Match      100.0%; Score 47; DB 17; Length 261;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTNTGLYNL 9
Db 194 LTNTGLYNL 202

RESULT 11
US-10-000-903-21
; Sequence 21, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-21

Query Match      100.0%; Score 47; DB 13; Length 278;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTNTGLYNL 9
Db 204 LTNTGLYNL 212

RESULT 12
US-10-899-771-21
; Sequence 21, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and E6 from Human papilloma virus type
US-10-899-771-21

Query Match      100.0%; Score 47; DB 17; Length 278;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTNTGLYNL 9
Db 204 LTNTGLYNL 212

RESULT 13
US-10-000-903-23
; Sequence 23, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-23

Query Match      100.0%; Score 47; DB 13; Length 383;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTNTGLYNL 9
Db 204 LTNTGLYNL 212

RESULT 14
US-10-899-771-23

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; Sequence 23, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 927262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeraic protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 18)
US-10-899-771-23
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Query Match 100.0%; Score 47; DB 17; Length 383;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 LNTGGLYNL 9
Db 204 LNTGGLYNL 212
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RESULT 15

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US-10-356-257-95
; Sequence 95, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 95
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-95
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Query Match 80.9%; Score 38; DB 15; Length 12;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Oy 1 LNTGGLYNL 9
Db 2 LNTGGLSNL 10
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Search completed: June 29, 2005, 04:19:21
Job time : 59.85 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-29
Perfect score: 47
Sequence: 1 LTNTGLYNL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	158	2	US-08-247-904B-10
2	47	100.0	158	3	US-08-767-942A-19
3	47	100.0	271	1	US-08-117-083-14
4	47	100.0	278	3	US-09-485-885-21
5	47	100.0	383	3	US-09-485-885-23
6	37	78.7	11	3	US-08-159-339A-1173
7	37	78.7	859	4	US-09-902-540-14220
8	35	74.5	209	4	US-09-248-796A-28163
9	35	74.5	329	4	US-09-902-540-11517
10	35	74.5	818	4	US-09-248-796A-18342
11	34	72.3	67	4	US-09-248-796A-19484
12	34	72.3	736	4	US-09-949-016-8076
13	34	72.3	773	4	US-09-078-030-215
14	34	72.3	785	4	US-09-079-030-216
15	33	70.2	245	4	US-09-949-016-7193
16	33	70.2	263	4	US-09-543-681A-5138
17	33	70.2	510	1	US-08-249-112-3
18	33	70.2	510	5	PCT-US95-06556-3
19	33	70.2	534	4	US-09-270-767-48833
20	33	70.2	567	2	US-08-841-483-2
21	33	70.2	567	3	US-09-382-911-2
22	33	70.2	632	4	US-09-949-016-6844
23	33	70.2	789	4	US-09-252-991A-27011
24	33	70.2	943	3	US-09-056-556-204
25	33	70.2	943	4	US-09-072-596-199
26	33	70.2	943	4	US-09-477-135A-131
27	33	70.2	943	4	US-09-072-967-204

28	33	70.2	1233	4	US-09-252-991A-23237	Sequence 23237, A
29	32	68.1	92	3	US-08-993-359-32	Sequence 32, Appl
30	32	68.1	92	4	US-09-482-558A-32	Sequence 32, Appl
31	32	68.1	157	4	US-09-270-767-38858	Sequence 38858, A
32	32	68.1	157	4	US-09-270-767-54075	Sequence 54075, A
33	32	68.1	194	4	US-09-902-540-10343	Sequence 10343, A
34	32	68.1	279	3	US-08-549-515-7	Sequence 7, Appl
35	32	68.1	304	4	US-10-101-464A-717	Sequence 717, Appl
36	32	68.1	512	3	US-09-015-296-3	Sequence 3, Appl
37	32	68.1	512	4	US-09-593-722-3	Sequence 3, Appl
38	32	68.1	631	4	US-09-248-796A-19403	Sequence 19403, A
39	32	68.1	728	4	US-09-747-259-18	Sequence 18, Appl
40	32	68.1	728	4	US-09-816-744-18	Sequence 18, Appl
41	32	68.1	802	4	US-09-661-322A-30	Sequence 30, Appl
42	32	68.1	1032	4	US-09-733-643B-16	Sequence 16, Appl
43	32	68.1	1156	3	US-09-001-982-10	Sequence 10, Appl
44	32	68.1	1156	3	US-09-002-285-70	Sequence 70, Appl
45	32	68.1	1156	4	US-09-589-477-70	Sequence 70, Appl

ALIGNMENTS

RESULT 1
US-08-247-904B-10
; Sequence 10, Application US/08247904B
; Patent No. 5981699
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Eckstein, Jens W.
; APPLICANT: Draetta, Giulio
; TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/247,904B
; FILING DATE: 23-MAY-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-247-904B-10

Query Match 100.0%; Score 47; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTNTGLYNL 9

Db 93 LTNTGLYNL 101

```
RESULT 2
US-08-767-942A-19
; Sequence 19, Application US/08767942A
; Patent No. 6068982
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Chiu, M. Isabel
; APPLICANT: Berlin, Vivian
; APPLICANT: Damagnez, Veronique
; APPLICANT: Draetta, Giulio
; APPLICANT: Guillaume, Cottarel
; TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,942A
; FILING DATE: 17-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-767-942A-19

Query Match 100.0%; Score 47; DB 3; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTNTGLYNL 9
Db 93 LTNTGLYNL 101

RESULT 3
US-08-117-083-14
; Sequence 14, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

US-08-117-083-14

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58783
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..271
OTHER INFORMATION: /note= "Xaa refers to stop codon in
the open reading frame."
US-08-117-083-14

Query Match 100.0%; Score 47; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTNTGLYNL 9
Db 94 LTNTGLYNL 102

RESULT 4
US-09-485-885-21
; Sequence 21, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-21

Query Match 100.0%; Score 47; DB 3; Length 278;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTNTGLYNL 9
Db 204 LTNTGLYNL 212

RESULT 5
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US-09-485-885-23
; Sequence 23, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-23

Query Match 100.0%; Score 47; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTNTGLYNL 9
Db 204 LTNTGLYNL 212

RESULT 6
US-09-159-339A-1173
; Sequence 1173, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1173:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1173

Query Match 78.7%; Score 37; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTNTGLY 7
Db 5 LTNTGLY 11

RESULT 7
US-09-902-540-14220
; Sequence 14220, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,893
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14220
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14220

Query Match 78.7%; Score 37; DB 4; Length 859;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LTNTGLYNL 9
Db 681 LTGTGFYNL 689

RESULT 8
US-09-248-796A-28163
; Sequence 28163, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Kelch Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 28163
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Candida albicans

US-09-248-796A-28163

Query Match 74.5%; Score 35; DB 4; Length 209;
Best Local Similarity 62.5%; Pred. No. 53;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTNGLYN 8
Db 137 MTNSGIYN 144

RESULT 9

US-09-540-540-11517
; Sequence 11517, Application US/09502540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11517
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-540-540-11517

Query Match 74.5%; Score 35; DB 4; Length 329;
Best Local Similarity 85.7%; Pred. No. 87;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NTGLYNL 9
Db 207 NTGLYV 213

RESULT 10

US-09-248-796A-18342
; Sequence 18342, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18342
; LENGTH: 818
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18342

Query Match 74.5%; Score 35; DB 4; Length 818;
Best Local Similarity 75.0%; Pred. No. 2,3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LTNGLYN 8
Db 294 LTNQGIYN 301

RESULT 11

US-09-248-796A-19484
; Sequence 19484, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19484
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19484

Query Match 72.3%; Score 34; DB 4; Length 67;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NTGLYNL 9
Db 38 NTGLFNL 44

RESULT 12

US-09-949-016-8076
; Sequence 8076, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8076
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8076

Query Match 72.3%; Score 34; DB 4; Length 736;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NTGLYNL 9
Db 593 NTGLFNL 599

RESULT 13

US-09-079-030-215
; Sequence 215, Application US/09079030
; Patent No. 6635623
; GENERAL INFORMATION:
; APPLICANT: Guevera, Jr., Juan G.
; APPLICANT: Hoogeveen, Ron C.
; APPLICANT: Moore, Paul J.

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OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds
(without alignments)
59.826 Million cell updates/sec

Title: US-08-170-344-28
Perfect score: 45
Sequence: 1 DTLEKLTNT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
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21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	27	17 US-10-751-845-153	Sequence 153, App
2	45	100.0	119	17 US-10-751-845-159	Sequence 159, App
3	45	100.0	178	16 US-10-800-023-27	Sequence 27, Appl
4	45	100.0	172	16 US-10-472-724-6	Sequence 6, Appl
5	45	100.0	236	17 US-10-751-845-157	Sequence 157, App
6	45	100.0	237	17 US-10-751-845-158	Sequence 158, App
7	45	100.0	261	17 US-10-751-845-160	Sequence 160, App
8	45	100.0	278	13 US-10-000-903-21	Sequence 21, Appl
9	45	100.0	278	17 US-10-899-771-21	Sequence 21, Appl
10	45	100.0	383	13 US-10-000-903-23	Sequence 23, Appl
11	45	100.0	383	17 US-10-899-771-23	Sequence 23, Appl

12	36	80.0	181	16	US-10-739-930-6845	Sequence 6845, App
13	35	77.8	115	9	US-09-824-787B-2	Sequence 2, Appl
14	35	77.8	115	15	US-10-435-696-93	Sequence 93, Appl
15	35	77.8	115	15	US-10-457-829-2	Sequence 2, Appl
16	35	77.8	115	17	US-10-887-230-2	Sequence 2, Appl
17	35	77.8	115	17	US-10-855-588-86	Sequence 86, Appl
18	35	77.8	117	10	US-09-833-203-34	Sequence 34, Appl
19	35	77.8	124	15	US-10-264-049-4187	Sequence 4187, App
20	35	77.8	131	9	US-09-925-301-966	Sequence 966, App
21	35	77.8	131	15	US-10-457-829-155	Sequence 155, App
22	35	77.8	206	14	US-10-177-293-480	Sequence 480, App
23	35	77.8	249	9	US-09-765-272-6	Sequence 6, Appl
24	35	77.8	250	9	US-09-765-272-226	Sequence 226, App
25	35	77.8	266	10	US-09-769-787-165	Sequence 165, App
26	35	77.8	271	17	US-10-472-928-1130	Sequence 1130, App
27	35	77.8	303	15	US-10-369-493-1100	Sequence 1100, App
28	35	77.8	463	17	US-10-732-923-20255	Sequence 20255, A
29	35	77.8	594	17	US-10-732-923-20254	Sequence 20254, A
30	35	77.8	603	17	US-10-732-923-20252	Sequence 20252, A
31	35	77.8	603	17	US-10-732-923-20253	Sequence 20253, A
32	35	77.8	982	15	US-10-369-493-10074	Sequence 10074, A
33	35	77.8	1211	15	US-10-282-122A-69274	Sequence 69274, A
34	35	77.8	1214	15	US-10-282-122A-67605	Sequence 67605, A
35	34	75.6	9	9	US-09-824-787B-117	Sequence 117, App
36	34	75.6	31	14	US-10-026-911-6	Sequence 6, Appl
37	34	75.6	80	16	US-10-799-514-6	Sequence 6, Appl
38	34	75.6	153	16	US-10-799-514-19	Sequence 19, Appl
39	34	75.6	153	16	US-10-799-514-21	Sequence 21, Appl
40	34	75.6	159	10	US-09-981-009B-1	Sequence 1, Appl
41	34	75.6	159	10	US-09-847-208-34	Sequence 34, Appl
42	34	75.6	159	10	US-09-847-208-36	Sequence 36, Appl
43	34	75.6	159	10	US-09-847-208-37	Sequence 37, Appl
44	34	75.6	159	10	US-09-847-208-38	Sequence 38, Appl
45	34	75.6	159	10	US-09-847-208-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-10-751-845-153
; Sequence 153, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman W.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-153

Query Match 100.0%; Score 45; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DTLEKLTNT 9
Db 5 DTLEKLTNT 13

RESULT 2
 US-10-751-845-159
 ; Sequence 159, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiccz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 159
 ; LENGTH: 119
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial fusion sequence
 US-10-751-845-159

Query Match 100.0%; Score 45; DB 17; Length 119;
 Best Local Similarity 100.0%; Pred. No. 0.57; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

QY 1 DTLEKLTNT 9
 |||||

Db 47 DTLEKLTNT 55

RESULT 3
 US-10-800-023-27
 ; Sequence 27, Application US/10800023
 ; Publication No. US20040258688A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Steinman, Ralph
 ; APPLICANT: Nussenzeig, Michel
 ; APPLICANT: Hawiger, Daniel
 ; APPLICANT: Bonifaz, Laura
 ; TITLE OF INVENTION: Enhanced Antigen Delivery and Modulation
 ; FILE REFERENCE: 600-1-081CONCIPI
 ; CURRENT APPLICATION NUMBER: US/10/800,023
 ; CURRENT FILING DATE: 2004-03-14
 ; PRIOR APPLICATION NUMBER: 09/925,284
 ; PRIOR FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: 09/586,704
 ; PRIOR FILING DATE: 2000-06-05
 ; PRIOR APPLICATION NUMBER: PCT/US96/01383
 ; PRIOR FILING DATE: 1996-01-31
 ; PRIOR APPLICATION NUMBER: 08/381,528
 ; PRIOR FILING DATE: 1995-01-31
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 158
 ; TYPE: PRT
 ; ORGANISM: human papilloma virus E6 protein
 US-10-800-023-27

Query Match 100.0%; Score 45; DB 16; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.78; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

QY 1 DTLEKLTNT 9

Db 88 DTLEKLTNT 96
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RESULT 4
 US-10-472-724-6
 ; Sequence 6, Application US/10472724
 ; Publication No. US20040171806A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cid-Arregui, Angel
 ; APPLICANT: Zur Hausen, Harald
 ; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
 ; FILE REFERENCE: 4121-154
 ; CURRENT APPLICATION NUMBER: US/10/472,724
 ; CURRENT FILING DATE: 2003-09-17
 ; PRIOR APPLICATION NUMBER: PCT/EP02/03271
 ; PRIOR FILING DATE: 2002-03-22
 ; PRIOR APPLICATION NUMBER: EP 01107271.7
 ; PRIOR FILING DATE: 2001-03-23
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 6
 ; LENGTH: 172
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Construct
 US-10-472-724-6

Query Match 100.0%; Score 45; DB 16; Length 172;
 Best Local Similarity 100.0%; Pred. No. 0.86; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

QY 1 DTLEKLTNT 9
 |||||

Db 94 DTLEKLTNT 102

RESULT 5
 US-10-751-845-157
 ; Sequence 157, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiccz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 157
 ; LENGTH: 236
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial fusion sequence
 US-10-751-845-157

Query Match 100.0%; Score 45; DB 17; Length 236;
 Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

QY 1 DTLEKLTNT 9
 |||||

Db 164 DTLEKLTNT 172


```
Db 189 DTLEKLTNT 197

RESULT 8
US-10-000-903-21
; Sequence 21, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-21

Query Match 100.0%; Score 45; DB 13; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTLEKLTNT 9
|||||
Db 199 DTLEKLTNT 207

RESULT 9
US-10-899-771-21
; Sequence 21, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 18)
US-10-899-771-21

Query Match 100.0%; Score 45; DB 17; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTLEKLTNT 9
|||||

Db 165 DTLEKLTNT 173

RESULT 7
US-10-751-845-160
; Sequence 160, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160

Query Match 100.0%; Score 45; DB 17; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTLEKLTNT 9
|||||

Db 165 DTLEKLTNT 173

RESULT 6
US-10-751-845-158
; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-158

Query Match 100.0%; Score 45; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTLEKLTNT 9
|||||
Db 165 DTLEKLTNT 173
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Db      199 DTLEKLTNT 207
|||||
RESULT 10
US-10-000-903-23
; Sequence 23, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-23
Query Match      100.0%; Score 45; DB 13; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.1; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy      1 DTLEKLTNT 9
|||||
Db      199 DTLEKLTNT 207
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RESULT 11
US-10-899-771-23
; Sequence 23, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 18)
US-10-899-771-23
Query Match      100.0%; Score 45; DB 17; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.1; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy      1 DTLEKLTNT 9
|||||
Db      199 DTLEKLTNT 207
|||||
RESULT 12
US-10-739-930-6845
; Sequence 6845, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 6845
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Brassica napus
; FEATURE:
; OTHER INFORMATION: Clone ID: BRANA-23APR03-C11583_1.p
US-10-739-930-6845
Query Match      80.0%; Score 36; DB 16; Length 181;
Best Local Similarity 77.8%; Pred. No. 53; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1;

Qy      1 DTLEKLTNT 9
|||||
Db      81 DTLEKLTNTS 89
|||||
RESULT 13
US-09-824-787B-2
; Sequence 2, Application US/09824787B
; Patent No. US20020155447A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Evans, Elizabeth E.
; APPLICANT: Borrello, Melinda A.
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and
; TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides
; FILE REFERENCE: 1821.0040001
; CURRENT APPLICATION NUMBER: US/09/824,787B
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/194,463
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-824-787B-2
Query Match      77.8%; Score 35; DB 9; Length 115;
Best Local Similarity 66.7%; Pred. No. 50; Mismatches 3; Indels 0; Gaps 0;
Matches 6; Conservative 3;

Qy      1 DTLEKLTNT 9
|||||
Db      100 ETLEKITNS 108
|||||
RESULT 14
US-10-435-696-93
; Sequence 93, Application US/10435696
; Publication No. US20040018525A1
; GENERAL INFORMATION:
; APPLICANT: Wirtz, Ralph
; APPLICANT: Munnes, Marc
```

; APPLICANT: Kallabis, Harald
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS
; FILE REFERENCE: Lea 36 108
; CURRENT APPLICATION NUMBER: US/10/435,696
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: EP03003112.4
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: EP02010291.9
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 93
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-435-696-93

Query Match 77.8%; Score 35; DB 15; Length 115;
Best Local Similarity 66.7%; Pred. No. 50;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTLEKLTNT 9
Db 100 ETEKITNS 108

RESULT 15
US-10-457-829-2
; Sequence 2, Application US/10457829
; Publication NO. US20040063907A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Evans, Elizabeth B.
; APPLICANT: Borrello, Melinda A.
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and
; FILE REFERENCE: 1821.0040005
; CURRENT APPLICATION NUMBER: US/10/457,829
; CURRENT FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/464,650
; PRIOR FILING DATE: 2003-04-23
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-457-829-2

Query Match 77.8%; Score 35; DB 15; Length 115;
Best Local Similarity 66.7%; Pred. No. 50;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTLEKLTNT 9
Db 100 ETEKITNS 108

Search completed: June 29, 2005, 04:19:19
Job time : 58.85 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-28
Perfect score: 45
Sequence: 1 DTLEKLTNT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	158	2	US-08-247-904B-10
2	45	100.0	158	3	US-08-767-942A-19
3	45	100.0	271	1	US-08-117-083-14
4	45	100.0	278	3	US-09-485-885-21
5	45	100.0	383	3	US-09-485-885-23
6	39	86.7	11	3	US-08-159-339A-1173
7	38	84.4	553	1	US-07-683-937B-3
8	35	77.8	180	4	US-09-107-433-4010
9	35	77.8	249	3	US-08-961-083-6
10	35	77.8	249	4	US-09-536-784-6
11	35	77.8	250	3	US-08-961-083-226
12	35	77.8	250	4	US-09-536-784-226
13	35	77.8	266	4	US-09-583-110-5299
14	35	77.8	316	4	US-09-543-681A-5023
15	34	75.6	32	1	US-08-466-285-4
16	34	75.6	32	3	US-08-164-768-4
17	34	75.6	160	1	US-07-847-010-23
18	34	75.6	328	4	US-09-270-767-62218
19	33	73.3	167	4	US-09-270-767-36082
20	33	73.3	167	4	US-09-270-767-51299
21	33	73.3	449	4	US-09-107-433-4132
22	33	73.3	454	4	US-09-583-110-3922
23	33	73.3	592	4	US-09-270-767-62306
24	33	73.3	852	4	US-09-270-767-45693
25	32	71.1	297	4	US-09-328-352-5769
26	32	71.1	469	4	US-09-107-532A-3672
27	32	71.1	625	4	US-09-248-796A-17352

28	31	68.9	121	4	US-09-248-796A-24131	Sequence 24131, A
29	31	68.9	200	4	US-09-543-681A-6662	Sequence 6662, Ap
30	31	68.9	233	2	US-08-928-692-31	Sequence 31, Appl
31	31	68.9	233	3	US-09-339-972-31	Sequence 31, Appl
32	31	68.9	236	4	US-09-248-796A-19850	Sequence 19850, A
33	31	68.9	271	4	US-09-328-352-7066	Sequence 7066, Ap
34	31	68.9	305	4	US-09-248-796A-18996	Sequence 18996, A
35	31	68.9	338	1	US-08-891-254-1	Sequence 1, Appli
36	31	68.9	338	2	US-08-484-358-2	Sequence 2, Appli
37	31	68.9	338	2	US-08-819-539-1	Sequence 1, Appli
38	31	68.9	338	2	US-09-030-270A-1	Sequence 1, Appli
39	31	68.9	338	3	US-09-118-959-2	Sequence 2, Appli
40	31	68.9	338	3	US-08-984-207-1	Sequence 1, Appli
41	31	68.9	338	3	US-09-013-587-1	Sequence 1, Appli
42	31	68.9	338	4	US-09-086-118-21	Sequence 21, Appl
43	31	68.9	338	4	US-09-431-614-1	Sequence 1, Appli
44	31	68.9	338	5	PCT-US96-08819-1	Sequence 1, Appli
45	31	68.9	339	4	US-09-107-532A-6947	Sequence 6947, Ap

ALIGNMENTS

RESULT 1
US-08-247-904B-10
; Sequence 10, Application US/08247904B
; Patent No. 5981699
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Eckstein, Jens W.
; APPLICANT: Draetta, Giulio
; TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/247,904B
; FILING DATE: 23-MAY-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-247-904B-10

Query Match 100.0%; Score 45; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTLEKLTNT 9
Db -88 DTLEKLTNT 96

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RESULT 2
US-08-767-942A-19
; Sequence 19, Application US/08767942A
; Patent No. 6068982
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Chiu, M. Isabel
; APPLICANT: Berlin, Vivian
; APPLICANT: Damagnez, Veronique
; APPLICANT: Draetta, Giulio
; APPLICANT: Guillaume, Cottarel
; TITLE OF INVENTION: UBQUITIN CONJUGATING ENZYMES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,942A
; FILING DATE: 17-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-767-942A-19

Query Match          100.0%; Score 45; DB 3; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTLEKLTNT 9
Db 88 DTLEKLTNT 96

RESULT 3
US-08-117-083-14
; Sequence 14, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Bournell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

US-08-170-344-28.ra1

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58783
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..271
OTHER INFORMATION: /note= "Xaa refers to stop codon in
the open reading frame."
US-08-117-083-14

Query Match          100.0%; Score 45; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTLEKLTNT 9
Db 89 DTLEKLTNT 97

RESULT 4
US-09-485-885-21
; Sequence 21, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-21

Query Match          100.0%; Score 45; DB 3; Length 278;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTLEKLTNT 9
Db 199 DTLEKLTNT 207

RESULT 5
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US-09-485-885-23
; Sequence 23, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-23

Query Match      100.0%; Score 45; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DTLEKLTNT 9
Db      199 DTLEKLTNT 207

RESULT 6
US-08-159-339A-1173
; Sequence 1173, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Eteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US

US-09-485-885-23
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1173:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1173

Query Match      86.7%; Score 39; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TLEKLTNT 9
Db      1 TLEKLTNT 8

RESULT 7
US-07-683-957B-3
; Sequence 3, Application US/07683957B
; Patent No. 5310880
; GENERAL INFORMATION:
; APPLICANT: Donahoe, Patricia K.
; APPLICANT: Ragin, Richard C.
; APPLICANT: MacLaughlin, David T.
; TITLE OF INVENTION: Purification of M llerian Inhibiting
; TITLE OF INVENTION: Substance
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/683,957B
; FILING DATE: 19910412
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0609.3060000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-683-957B-3

Query Match      84.4%; Score 38; DB 1; Length 553;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DTLEKLTNT 9
Db      23 DTVEELTNT 31
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RESULT 8
US-09-107-433-4010
; Sequence 4010, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNO
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: <unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4010:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...180
; SEQUENCE DESCRIPTION: SEQ ID NO: 4010:
US-09-107-433-4010
Query Match 77.8%; Score 35; DB 4; Length 180;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLEKLTNT 9
DB 159 TLEKLSNT 166

RESULT 9
US-08-961-083-6
; Sequence 6, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
```

```
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-083-6
Query Match 77.8%; Score 35; DB 3; Length 249;
Best Local Similarity 87.5%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLEKLTNT 9
DB 228 TLEKLSNT 235

RESULT 10
US-09-536-784-6
; Sequence 6, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
```


TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-536-784-6

Query Match 77.8%; Score 35; DB 4; Length 249;
Best Local Similarity 87.5%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLEKLTNT 9
DB 228 TLEKLSNT 235

RESULT 11
US-08-961-083-226
; Sequence 226, Application US/08961083
; Patent No. 6159469

; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 226:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-083-226

Query Match 77.8%; Score 35; DB 3; Length 250;
Best Local Similarity 87.5%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLEKLTNT 9
DB 229 TLEKLSNT 236

RESULT 12

US-09-536-784-226
; Sequence 226, Application US/09536784
; Patent No. 6573082

; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 226:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 226:
US-09-536-784-226

Query Match 77.8%; Score 35; DB 4; Length 250;
Best Local Similarity 87.5%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLEKLTNT 9
DB 229 TLEKLSNT 236

RESULT 13
US-09-583-110-5299

; Sequence 5299, Application US/09583110
; Patent No. 6699703

; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 5299
; LENGTH: 266
; TYPE: PRT

ORGANISM: Streptococcus pneumoniae
US-09-583-110-5299

Query Match 77.8%; Score 35; DB 4; Length 266;
Best Local Similarity 87.5%; Pred. No. 40;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DTLEKLTNT 9
Db 245 TLEKLSNT 252

RESULT 14

US-09-543-681A-5023
Sequence 5023, Application US/09543681A
Patent No. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BRTON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5023
LENGTH: 316
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-5023

Query Match 77.8%; Score 35; DB 4; Length 316;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTLEKLTNT 9
Db 241 EYLEQITNT 249

RESULT 15

US-08-466-285-4
Sequence 4, Application US/08466285
Patent No. 5753233

GENERAL INFORMATION:

APPLICANT: Bleul, Conrad
APPLICANT: Gissmann, Lutz
APPLICANT: Muller, Martin
TITLE OF INVENTION: Seroreactive Epitopes On Proteins Of
TITLE OF INVENTION: Human Papillomavirus (HPV)18
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSES: Finnegan, Henderson, Farabow, Garrett &
ADDRESSES: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,285
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,768
FILING DATE: 10-DEC-1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/947,992
FILING DATE: 21-SEP-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/696,953
FILING DATE: 08-MAY-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 40 15 044.5
FILING DATE: 10-MAY-1990
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Manspeizer, David A.
REGISTRATION NUMBER: 37,540
REFERENCE/DOCKET NUMBER: 05552.1075-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-466-285-4

Query Match 75.6%; Score 34; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTLEKLT 7
Db 26 DTLEKLT 32

Search completed: June 28, 2005, 21:33:24
Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds
(without alignments)
59.826 Million cell updates/sec

Title: US-08-170-344-27
Perfect score: 45
Sequence: 1 FAFKDLFVV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	158	16	US-10-800-023-27
2	45	100.0	172	16	US-10-472-724-6
3	45	100.0	278	17	US-10-000-903-21
4	45	100.0	278	17	US-10-899-771-21
5	45	100.0	383	13	US-10-000-903-23
6	45	100.0	383	17	US-10-899-771-23
7	38	84.4	1097	16	US-10-437-963-122842
8	35	77.8	1191	16	US-10-408-765A-12177
9	34	75.6	289	14	US-10-223-074-8
10	34	75.6	353	9	US-09-815-242-5109
11	34	75.6	353	15	US-10-282-122A-43553

12	75.6	669	9	US-09-862-027-27	Sequence 27, Appl
13	75.6	669	17	US-10-989-228-27	Sequence 27, Appl
14	75.6	685	16	US-10-437-963-181984	Sequence 181984,
15	75.6	1133	16	US-10-437-963-173023	Sequence 173023,
16	73.3	8	16	US-10-712-425-937	Sequence 937, App
17	73.3	8	17	US-10-773-032-937	Sequence 937, App
18	73.3	9	9	US-09-909-460-103	Sequence 103, App
19	73.3	9	11	US-09-872-836-103	Sequence 103, App
20	73.3	9	14	US-10-128-711-67	Sequence 67, Appl
21	73.3	9	14	US-10-133-210-281	Sequence 281, App
22	73.3	9	17	US-10-758-970-103	Sequence 103, App
23	73.3	9	17	US-10-751-845-57	Sequence 57, Appl
24	73.3	15	16	US-10-476-570-29	Sequence 29, Appl
25	73.3	22	17	US-10-858-384-6	Sequence 6, Appli
26	73.3	24	17	US-10-751-845-65	Sequence 65, Appl
27	73.3	62	16	US-10-425-115-302315	Sequence 302315,
28	73.3	81	15	US-10-424-599-275233	Sequence 275233,
29	73.3	117	17	US-10-751-845-126	Sequence 126, App
30	73.3	129	15	US-10-425-114-53781	Sequence 53781, A
31	73.3	129	16	US-10-425-115-198103	Sequence 198103,
32	73.3	151	14	US-10-177-390-6	Sequence 20, Appl
33	73.3	151	17	US-10-484-063-20	Sequence 27, Appl
34	73.3	151	17	US-10-484-063-27	Sequence 2, Appli
35	73.3	158	17	US-10-858-384-2	Sequence 16, Appl
36	73.3	158	17	US-10-367-057-16	Sequence 2, Appli
37	73.3	171	16	US-10-472-724-2	Sequence 157, App
38	73.3	236	17	US-10-751-845-157	Sequence 157, App
39	73.3	237	17	US-10-751-845-158	Sequence 158, App
40	73.3	261	17	US-10-751-845-160	Sequence 160, App
41	73.3	266	9	US-09-367-309A-1	Sequence 1, Appli
42	73.3	273	13	US-10-000-903-4	Sequence 4, Appli
43	73.3	273	17	US-10-899-771-4	Sequence 10, Appl
44	73.3	292	13	US-10-000-903-10	Sequence 10, Appl
45	73.3	292	17	US-10-899-771-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-800-023-27
; Sequence 27, Application US/108000023
; Publication No. US20040258688A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Ralph
; APPLICANT: Nussenzeig, Michel
; APPLICANT: Hawiger, Daniel
; APPLICANT: Bonifaz, Laura
; TITLE OF INVENTION: Enhanced Antigen Delivery and Modulation
; TITLE OF INVENTION: of the Immune Response Therefrom
; FILE REFERENCE: 600-1-081CONCIPI
; CURRENT APPLICATION NUMBER: US/10/800,023
; CURRENT FILING DATE: 2004-03-14
; PRIOR APPLICATION NUMBER: 09/925,284
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/586,704
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: PCT/US96/01383
; PRIOR FILING DATE: 1996-01-31
; PRIOR APPLICATION NUMBER: 08/381,528
; PRIOR FILING DATE: 1995-01-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 158
; TYPE: PRT
; ORGANISM: human papilloma virus E6 protein
US-10-800-023-27

Query Match 100.0%; Score 45; DB 16; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9
 |||||
 Db 47 FAFKDLFVV 55

RESULT 2

US-10-472-724-6
 ; Sequence 6, Application US/10472724
 ; Publication No. US20040171806A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cid-Arregui, Angel
 ; APPLICANT: Zur Hausen, Harald
 ; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
 ; FILE REFERENCE: 4121-154
 ; CURRENT APPLICATION NUMBER: US/10/472,724
 ; CURRENT FILING DATE: 2003-09-17
 ; PRIOR APPLICATION NUMBER: PCT/EP02/03271
 ; PRIOR FILING DATE: 2002-03-22
 ; PRIOR APPLICATION NUMBER: EP 01107271.7
 ; PRIOR FILING DATE: 2001-03-23
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 6
 ; LENGTH: 172
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Construct
 US-10-472-724-6

Query Match 100.0%; Score 45; DB 16; Length 172;
 Best Local Similarity 100.0%; Pred. No. 1.2; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

QY 1 FAFKDLFVV 9
 |||||
 Db 53 FAFKDLFVV 61

RESULT 3

US-10-000-903-21
 ; Sequence 21, Application US/10000903
 ; Publication No. US20020182221A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bruck, Claudine
 ; APPLICANT: Cabezon Silva, Teresa
 ; APPLICANT: Delisse, Anne-Marie Eva Fernande
 ; APPLICANT: Gerard, Catherine Marie Ghislaine
 ; APPLICANT: Lombardo-Bencheikh, Angela
 ; TITLE OF INVENTION: Vaccine
 ; FILE REFERENCE: B45107
 ; CURRENT APPLICATION NUMBER: US/10/000,903
 ; CURRENT FILING DATE: 2001-10-01
 ; PRIOR APPLICATION NUMBER: PCT/EP98/05285
 ; PRIOR FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: GB 9717953.5
 ; PRIOR FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 21
 ; LENGTH: 278
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-000-903-21

Query Match 100.0%; Score 45; DB 13; Length 278;
 Best Local Similarity 100.0%; Pred. No. 1.9; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

QY 1 FAFKDLFVV 9
 |||||
 Db 158 FAFKDLFVV 166

RESULT 4

US-10-899-771-21
 ; Sequence 21, Application US/10899771
 ; Publication No. US20050031638A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dalemans, Wilfried L.J.
 ; APPLICANT: Gerard, Catherine Marie Ghislaine
 ; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
 ; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
 ; FILE REFERENCE: B45124
 ; CURRENT APPLICATION NUMBER: US/10/899,771
 ; CURRENT FILING DATE: 2004-07-27
 ; PRIOR APPLICATION NUMBER: US/09/581,976
 ; PRIOR FILING DATE: 2000-06-20
 ; PRIOR APPLICATION NUMBER: PCT/EP98/08563
 ; PRIOR FILING DATE: 1998-12-18
 ; PRIOR APPLICATION NUMBER: GB 9727262.9
 ; PRIOR FILING DATE: 1997-12-24
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 21
 ; LENGTH: 278
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
 ; OTHER INFORMATION: Influenzae B and B6 from Human papilloma virus type
 ; OTHER INFORMATION: 18)
 US-10-899-771-21

Query Match 100.0%; Score 45; DB 17; Length 278;
 Best Local Similarity 100.0%; Pred. No. 1.9; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

QY 1 FAFKDLFVV 9
 |||||
 Db 158 FAFKDLFVV 166

RESULT 5

US-10-000-903-23
 ; Sequence 23, Application US/10000903
 ; Publication No. US20020182221A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bruck, Claudine
 ; APPLICANT: Cabezon Silva, Teresa
 ; APPLICANT: Delisse, Anne-Marie Eva Fernande
 ; APPLICANT: Gerard, Catherine Marie Ghislaine
 ; APPLICANT: Lombardo-Bencheikh, Angela
 ; TITLE OF INVENTION: Vaccine
 ; FILE REFERENCE: B45107
 ; CURRENT APPLICATION NUMBER: US/10/000,903
 ; CURRENT FILING DATE: 2001-10-01
 ; PRIOR APPLICATION NUMBER: PCT/EP98/05285
 ; PRIOR FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: GB 9717953.5
 ; PRIOR FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 383
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-000-903-23

Query Match 100.0%; Score 45; DB 13; Length 383;
 Best Local Similarity 100.0%; Pred. No. 2.7; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

QY 1 FAFKDLFVV 9
 |||||
 Db 158 FAFKDLFVV 166

RESULT 6

US-10-899-771-23
; Sequence 23, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 18)
US-10-899-771-23

Query Match 100.0%; Score 45; DB 17; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.7; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 FAFKDLFVV 9

DB 158 FAFKDLFVV 166

RESULT 7

US-10-437-963-122842
; Sequence 122842, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 122842
; LENGTH: 1097
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MNT4530_25734C.1.psp
US-10-437-963-122842

Query Match 84.4%; Score 38; DB 16; Length 1097;
Best Local Similarity 87.5%; Pred. No. 1.7e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 FAFKDLFV 8

DB 755 FAYKDLFV 762

RESULT 8

US-10-408-765A-2177
; Sequence 2177, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2177
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2177

Query Match 77.8%; Score 35; DB 16; Length 1191;
Best Local Similarity 77.8%; Pred. No. 6.7e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 FAFKDLFVV 9

DB 106 FLFNDLFVV 114

RESULT 9

US-10-223-074-8
; Sequence 8, Application US/10223074
; Publication No. US20030100094A1
; GENERAL INFORMATION:
; APPLICANT: Heiter, Daniel
; APPLICANT: Lunnen, Keith
; APPLICANT: Wilson, Geoffrey
; TITLE OF INVENTION: A Method For Engineering Strand-Specific, Sequence-Specific DNA N
; TITLE OF INVENTION: Enzymes
; FILE REFERENCE: NEB-178A-PCT
; CURRENT APPLICATION NUMBER: US/10/223,074
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/314,386
; PRIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Bacillus lentus
US-10-223-074-8

Query Match 75.6%; Score 34; DB 14; Length 289;
Best Local Similarity 85.7%; Pred. No. 2.4e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 2 AFKDLFV 8

DB 119 AFKDLFI 125

RESULT 10

US-09-815-242-5109
; Sequence 5109, Application US/09815242

```
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl U.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5109
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-5109

Query Match 75.6%; Score 34; DB 9; Length 353;
Best Local Similarity 81.8%; Pred. No. 2.9e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 FAF--KDLFVV 9
   ||| |||||
Db 302 FAFEAKDLFVV 312

RESULT 11
US-10-282-122A-43553
; Sequence 43553, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangseu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
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; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43553
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-43553

Query Match 75.6%; Score 34; DB 15; Length 353;
Best Local Similarity 81.8%; Pred. No. 2.9e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 FAF--KDLFVV 9
   ||| |||||
Db 302 FAFEAKDLFVV 312

RESULT 12
US-09-862-027-27
; Sequence 27, Application US/09862027
; Patent No. US20020142428A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: No. US20020142428A1el Kinases and Uses Thereof
; FILE REFERENCE: 35800/234862
; CURRENT APPLICATION NUMBER: US/09/862,027
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/345,473
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-862-027-27

Query Match 75.6%; Score 34; DB 9; Length 669;
Best Local Similarity 62.5%; Pred. No. 5.7e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFKDLFV 8
   ||:||||:
Db 332 FAYKDLVI 339

RESULT 13
US-10-989-228-27
; Sequence 27, Application US/10989228
; Publication No. US20050089917A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: Novel Kinases and Uses Thereof
; FILE REFERENCE: 35800/234862
; CURRENT APPLICATION NUMBER: US/10/989,228
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US/09/862,027
; PRIOR FILING DATE: 2001-05-21
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; PRIOR APPLICATION NUMBER: US 09/345,473
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-989-228-27

Query Match 75.6%; Score 34; DB 17; Length 669;
Best Local Similarity 62.5%; Pred No. 5.7e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAFKDLFV 8
||:||||:
DB 332 FAYKDLVI 339

RESULT 14

US-10-437-963-181984
; Sequence 181984, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 181984
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_79213C.1.pep
US-10-437-963-181984

Query Match 75.6%; Score 34; DB 16; Length 685;
Best Local Similarity 85.7%; Pred. No. 5.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAFKDLF 7
||:||||
DB 338 FAYKDLF 344

RESULT 15

US-10-437-963-173023
; Sequence 173023, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 173023
; LENGTH: 1133
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_71101C.1.pep
US-10-437-963-173023

Query Match 75.6%; Score 34; DB 16; Length 1133;
Best Local Similarity 85.7%; Pred No. 9.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAFKDLF 7
||:||||
DB 792 FAYKDLF 798

Search completed: June 29, 2005, 04:19:18
Job time : 57.85 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-27
Perfect score: 45
Sequence: 1 FAFKDLFVV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	158	2	US-08-247-904B-10
2	45	100.0	158	3	US-08-767-942A-19
3	45	100.0	271	1	US-08-117-083-14
4	45	100.0	278	3	US-09-485-885-21
5	45	100.0	383	3	US-09-485-885-23
6	35	77.8	329	4	US-09-328-352-6272
7	34	75.6	351	4	US-09-252-931A-32396
8	34	75.6	669	4	US-09-345-473E-27
9	33	73.3	9	1	US-08-787-547-103
10	33	73.3	9	4	US-08-197-484-67
11	33	73.3	9	5	PCT-US95-02121-67
12	33	73.3	22	4	US-09-980-523A-6
13	33	73.3	23	4	US-09-601-729-276
14	33	73.3	158	4	US-09-980-523A-2
15	33	73.3	162	1	US-08-316-239B-3
16	33	73.3	162	1	US-08-316-239B-4
17	33	73.3	172	3	US-08-860-165-14
18	33	73.3	172	3	US-09-359-382-14
19	33	73.3	266	3	US-08-860-165-10
20	33	73.3	266	3	US-09-359-382-10
21	33	73.3	266	4	US-09-367-309A-1
22	33	73.3	273	3	US-09-485-885-4
23	33	73.3	292	3	US-09-485-885-10
24	33	73.3	371	3	US-09-485-885-6
25	33	73.3	390	3	US-09-485-885-14
26	32	71.1	99	4	US-09-270-767-60100
27	32	71.1	175	4	US-09-248-796A-14111

28	71.1	182	1	US-08-117-083-10	Sequence 10, Appl
29	71.1	333	4	US-09-562-737-6	Sequence 6, Appl
30	71.1	333	4	US-09-562-737-9	Sequence 9, Appl
31	71.1	401	4	US-09-270-767-44648	Sequence 44648, A
32	71.1	502	4	US-09-328-352-6968	Sequence 6968, Ap
33	68.9	126	4	US-09-107-532A-7133	Sequence 7133, Ap
34	68.9	307	4	US-09-248-796A-17597	Sequence 17597, A
35	68.9	338	4	US-09-107-433-4666	Sequence 4666, Ap
36	68.9	370	4	US-09-270-767-45247	Sequence 45247, A
37	68.9	440	4	US-09-583-110-4693	Sequence 4693, Ap
38	68.9	560	4	US-09-902-540-15502	Sequence 15502, A
39	68.9	574	4	US-09-949-016-11325	Sequence 11325, A
40	66.7	62	1	US-08-464-531-114	Sequence 114, App
41	66.7	62	3	US-08-461-598-114	Sequence 114, App
42	66.7	67	4	US-08-322-137-114	Sequence 114, App
43	66.7	106	4	US-09-248-796A-25319	Sequence 25319, A
44	66.7	135	3	US-09-248-796A-15528	Sequence 15528, A
45	66.7			US-08-905-223-464	Sequence 464, App

ALIGNMENTS

RESULT 1
US-08-247-904B-10
; Sequence 10, Application US/08247904B
; Patent No. 5981699
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Eckstein, Jens W.
; APPLICANT: Draetta, Giulio
; TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/247,904B
; FILING DATE: 23-MAY-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-247-904B-10

Query Match 100.0%; Score 45; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFKDLFVV 9
| | | | |
Db 47 FAFKDLFVV 55

```
RESULT 2
US-08-767-942A-19
; Sequence 19, Application US/08767942A
; Patent No. 6068982
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Chiu, M. Isabel
; APPLICANT: Berlin, Vivian
; APPLICANT: Damagnez, Veronique
; APPLICANT: Draetta, Giulio
; APPLICANT: Guillaume, Cottarel
; TITLE OF INVENTION: UBQUITIN CONJUGATING ENZYMES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,942A
; FILING DATE: 17-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-767-942A-19

Query Match 100.0%; Score 45; DB 3; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9
DB 47 FAFKDLFVV 55

RESULT 3
US-08-117-083-14
; Sequence 14, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..271
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-14

Query Match 100.0%; Score 45; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9
DB 48 FAFKDLFVV 56

RESULT 4
US-09-485-885-21
; Sequence 21, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-21

Query Match 100.0%; Score 45; DB 3; Length 278;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9
DB 158 FAFKDLFVV 166

RESULT 5
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```

US-09-485-885-23
; Sequence 23, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernandez
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-23

Query Match      100.0%; Score 45; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FAFKDLFVV 9
Db      158 FAFKDLFVV 166

RESULT 6
US-09-328-352-6272
; Sequence 6272, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breston et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6272
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6272

Query Match      77.8%; Score 35; DB 4; Length 329;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FAFKDLF 7
Db      142 FAFKDLF 148

RESULT 7
US-09-252-991A-32396
; Sequence 32396, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fraser, Janis K.
;; REGISTRATION NUMBER: 34,819
;; REFERENCE/DOCKET NUMBER: 08191/003001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-542-5070
;; TELEFAX: 617-542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 103:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-787-547-103

Query Match 73.3%; Score 33; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FAFKDLFVV 9
Db 1 FAFRDLCLIV 9

RESULT 10
US-08-197-484-67
; Sequence 67, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 467-9600
;; TELEFAX: (206) 623-6793
;; INFORMATION FOR SEQ ID NO: 67:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-08-197-484-67

Query Match 73.3%; Score 33; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FAFKDLFVV 9
Db 1 FAFRDLCLIV 9

RESULT 11
PCT-US95-02121-67
; Sequence 67, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-67

Query Match 73.3%; Score 33; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 FAFKDLFVV 9
|||:|:|
Db 1 FAFRDLCLV 9

RESULT 12
US-09-980-523A-6
; Sequence 6, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/01 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-6

Query Match 73.3%; Score 33; DB 4; Length 22;
Best Local Similarity 66.7%; Pred. No. 5.1;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9
|||:|:|
Db 7 FAFRDLCLV 15

RESULT 13
US-09-601-729-276
; Sequence 276, Application US/09601729
; Patent No. 6683052
; GENERAL INFORMATION:
; APPLICANT: THIAM, KADER
; APPLICANT: AURIAULT, CLAUDE
; APPLICANT: GRAS-MASSE, HELENE
; APPLICANT: LOING, ESTELLE
; APPLICANT: VERWAERDE, CLAUDIE
; APPLICANT: GUILLET, JEAN GERARD
; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERPERON FRAGMENT AND USES
; TITLE OF INVENTION: THEROF IN PHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: USB-97-AU-IN
; CURRENT APPLICATION NUMBER: US/09/601,729
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: PCT/FR99/00259
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 98 01439
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 276
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-601-729-276
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Query Match 73.3%; Score 33; DB 4; Length 23;
Best Local Similarity 66.7%; Pred. No. 5.3;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9
|||:|:|
Db 8 FAFRDLCLV 16

RESULT 14
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: WO/01 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 73.3%; Score 33; DB 4; Length 158;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FAFKDLFVV 9
|||:|:|
Db 52 FAFRDLCLV 60

RESULT 15
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNWE-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
;
US-08-316-239B-3

Query Match 73.3%; Score 33; DB 1; Length 162;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FAFKDLFVW 9
Db 52 FAFRDLCLIV 60
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Search completed: June 28, 2005, 21:33:23
Job time : 17 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds
(without alignments)
59.826 Million cell updates/sec

Title: US-08-170-344-26

Perfect score: 44

Sequence: 1 ELTEVFPEFA 9

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Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	9	17 US-10-751-845-133	Sequence 133, App
2	44	100.0	42	17 US-10-751-845-152	Sequence 152, App
3	44	100.0	119	17 US-10-751-845-159	Sequence 159, App
4	44	100.0	158	16 US-10-800-023-27	Sequence 27, App
5	44	100.0	172	16 US-10-472-724-6	Sequence 6, Appl
6	44	100.0	236	17 US-10-751-845-157	Sequence 157, App
7	44	100.0	237	17 US-10-751-845-158	Sequence 158, App
8	44	100.0	261	17 US-10-751-845-160	Sequence 160, App
9	44	100.0	278	13 US-10-000-903-21	Sequence 21, App
10	44	100.0	278	17 US-10-899-771-21	Sequence 21, Appl
11	44	100.0	383	13 US-10-000-903-23	Sequence 23, Appl

44 100.0 383 17 US-10-899-771-23 Sequence 23, Appl
40 90.9 10 17 US-10-751-845-136 Sequence 136, App
39 88.6 10 17 US-10-751-845-127 Sequence 127, App
37 84.1 322 15 US-10-321-204-36 Sequence 36, Appl
35 79.5 244 15 US-10-282-122A-50681 Sequence 50681, A
34 77.3 336 9 US-09-815-242-13832 Sequence 13832, A
34 77.3 336 15 US-10-282-122A-74880 Sequence 74880, A
34 77.3 336 15 US-10-282-122A-76245 Sequence 76245, A
34 77.3 344 15 US-10-282-122A-73043 Sequence 73043, A
34 77.3 346 9 US-09-815-242-10162 Sequence 10162, A
34 77.3 346 15 US-10-369-493-833 Sequence 833, App
34 77.3 346 15 US-10-282-122A-56548 Sequence 56548, A
33 75.0 139 16 US-10-767-701-52361 Sequence 52361, A
33 75.0 180 16 US-10-425-115-192145 Sequence 192145, A
33 75.0 299 15 US-10-282-122A-71438 Sequence 71438, A
33 75.0 712 10 US-09-893-519A-35 Sequence 35, Appl
33 75.0 722 14 US-10-032-585-7153 Sequence 7153, Ap
32 72.7 104 16 US-10-425-115-229096 Sequence 229096, A
32 72.7 441 15 US-10-369-493-18771 Sequence 18771, A
32 72.7 454 16 US-10-767-701-41242 Sequence 41242, A
32 72.7 478 15 US-10-425-114-38072 Sequence 38072, A
32 72.7 496 14 US-10-193-896-11 Sequence 11, Appl
32 72.7 496 15 US-10-369-493-2914 Sequence 2914, Ap
32 72.7 504 15 US-10-425-114-64036 Sequence 64036, A
32 72.7 537 15 US-10-425-114-64000 Sequence 64000, A
32 72.7 550 15 US-10-425-114-41988 Sequence 41988, A
32 72.7 639 16 US-10-425-115-291636 Sequence 291636, A
32 72.7 683 16 US-10-425-115-265119 Sequence 265119, A
32 72.7 761 16 US-10-425-115-265128 Sequence 265128, A
32 72.7 787 16 US-10-437-963-126524 Sequence 126524, A
32 72.7 1053 16 US-10-437-963-126523 Sequence 126523, A
32 72.7 1347 16 US-10-437-963-164673 Sequence 164673, A
32 72.7 1555 14 US-10-128-714-3298 Sequence 3298, Ap
32 72.7 1832 14 US-10-128-714-8298 Sequence 8298, Ap

ALIGNMENTS

RESULT 1
US-10-751-845-133
; Sequence 133, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-133

Query Match 100.0%; Score 44; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELTEVFPEFA 9

Db 1 ELTEVFPEFA 9

RESULT 2

US-10-751-845-152
 ; Sequence 152, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiciz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 152
 ; LENGTH: 42
 ; TYPE: PRT
 ; ORGANISM: Human Papilloma virus
 ; ORGANISM: Human Papilloma virus

Query Match 100.0%; Score 44; DB 17; Length 42;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELTEVFEEFA 9
 Db 32 ELTEVFEEFA 40

RESULT 3

US-10-751-845-159
 ; Sequence 159, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiciz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 159
 ; LENGTH: 119
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial fusion sequence
 ; OTHER INFORMATION: Artificial fusion sequence

Query Match 100.0%; Score 44; DB 17; Length 119;
 Best Local Similarity 100.0%; Pred. No. 0.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELTEVFEEFA 9
 Db 32 ELTEVFEEFA 40

RESULT 4

US-10-800-023-27
 ; Sequence 27, Application US/10800023
 ; Publication No. US20040258688A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Steinman, Ralph
 ; APPLICANT: Nussenzweig, Michel
 ; APPLICANT: Hawiger, Daniel
 ; APPLICANT: Bonifaz, Laura
 ; TITLE OF INVENTION: Enhanced Antigen Delivery and Modulation
 ; FILE REFERENCE: 600-1-081CONCIP1
 ; CURRENT APPLICATION NUMBER: US/10/800,023
 ; CURRENT FILING DATE: 2004-03-14
 ; PRIOR APPLICATION NUMBER: 09/925,284
 ; PRIOR FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: 09/586,704
 ; PRIOR FILING DATE: 2000-06-05
 ; PRIOR APPLICATION NUMBER: PCT/US96/01383
 ; PRIOR FILING DATE: 1996-01-31
 ; PRIOR APPLICATION NUMBER: 08/381,528
 ; PRIOR FILING DATE: 1995-01-31
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 158
 ; TYPE: PRT
 ; ORGANISM: human papilloma virus E6 protein
 ; ORGANISM: human papilloma virus E6 protein

Query Match 100.0%; Score 44; DB 16; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELTEVFEEFA 9
 Db 40 ELTEVFEEFA 48

RESULT 5

US-10-472-724-6
 ; Sequence 6, Application US/10472724
 ; Publication No. US20040171806A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cid-Arregui, Angel
 ; APPLICANT: Zur Hausen, Harald
 ; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
 ; FILE REFERENCE: 4121-154
 ; CURRENT APPLICATION NUMBER: US/10/472,724
 ; CURRENT FILING DATE: 2003-09-17
 ; PRIOR APPLICATION NUMBER: PCT/EP02/03271
 ; PRIOR FILING DATE: 2002-03-22
 ; PRIOR APPLICATION NUMBER: EP 01107271.7
 ; PRIOR FILING DATE: 2001-03-23
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 6
 ; LENGTH: 172
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Construct
 ; OTHER INFORMATION: Synthetic Construct

Query Match 100.0%; Score 44; DB 16; Length 172;
 Best Local Similarity 100.0%; Pred. No. 0.88;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELTEVFEEFA 9
 Db 46 ELTEVFEEFA 54

RESULT 6

US-10-751-845-157
; Sequence 157, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-157

Query Match 100.0%; Score 44; DB 17; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 ELTEVFEEFA 9
Db 149 ELTEVFEEFA 157

RESULT 7

US-10-751-845-158
; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-158

Query Match 100.0%; Score 44; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 ELTEVFEEFA 9
Db 150 ELTEVFEEFA 158

RESULT 8

US-10-751-845-160
; Sequence 160, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160

Query Match 100.0%; Score 44; DB 17; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 ELTEVFEEFA 9
Db 174 ELTEVFEEFA 182

RESULT 9

US-10-000-903-21
; Sequence 21, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
; OTHER INFORMATION: Artificial fusion sequence
US-10-000-903-21

Query Match 100.0%; Score 44; DB 13; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 ELTEVFEEFA 9
Db 151 ELTEVFEEFA 159

RESULT 10
 US-10-899-771-21
 ; Sequence 21, Application US/10899771
 ; Publication No. US20050031638A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dalemans, Wilfried L.J.
 ; APPLICANT: Gerard, Catherine Marie Ghislaine
 ; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
 ; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
 ; FILE REFERENCE: B45124
 ; CURRENT APPLICATION NUMBER: US/10/899,771
 ; CURRENT FILING DATE: 2004-07-27
 ; PRIOR APPLICATION NUMBER: US/09/581,976
 ; PRIOR FILING DATE: 2000-06-20
 ; PRIOR APPLICATION NUMBER: PCT/EP98/08563
 ; PRIOR FILING DATE: 1998-12-18
 ; PRIOR APPLICATION NUMBER: GB 9727262.9
 ; PRIOR FILING DATE: 1997-12-24
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 21
 ; LENGTH: 278
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
 ; OTHER INFORMATION: Influenzae B and E6 from Human papilloma virus type
 ; OTHER INFORMATION: 18)
 US-10-899-771-21

Query Match 100.0%; Score 44; DB 17; Length 278;
 Best Local Similarity 100.0%; Pred. No. 1.5; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELTEVFEEFA 9
 Db 151 ELTEVFEEFA 159

RESULT 11
 US-10-000-903-23
 ; Sequence 23, Application US/10000903
 ; Publication No. US20020182221A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bruck, Claudine
 ; APPLICANT: Cabezon Silva, Teresa
 ; APPLICANT: Delisse, Anne-Marie Eva Fernande
 ; APPLICANT: Gerard, Catherine Marie Ghislaine
 ; APPLICANT: Lombardo-Bencheikh, Angela
 ; TITLE OF INVENTION: Vaccine
 ; FILE REFERENCE: B45107
 ; CURRENT APPLICATION NUMBER: US/10/000,903
 ; CURRENT FILING DATE: 2001-10-01
 ; PRIOR APPLICATION NUMBER: PCT/EP98/05285
 ; PRIOR FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: GB 9717953.5
 ; PRIOR FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 383
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-000-903-23

Query Match 100.0%; Score 44; DB 13; Length 383;
 Best Local Similarity 100.0%; Pred. No. 2; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELTEVFEEFA 9
 Db 151 ELTEVFEEFA 159

RESULT 12
 US-10-899-771-23
 ; Sequence 23, Application US/10899771
 ; Publication No. US20050031638A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dalemans, Wilfried L.J.
 ; APPLICANT: Gerard, Catherine Marie Ghislaine
 ; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
 ; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
 ; FILE REFERENCE: B45124
 ; CURRENT APPLICATION NUMBER: US/10/899,771
 ; CURRENT FILING DATE: 2004-07-27
 ; PRIOR APPLICATION NUMBER: US/09/581,976
 ; PRIOR FILING DATE: 2000-06-20
 ; PRIOR APPLICATION NUMBER: PCT/EP98/08563
 ; PRIOR FILING DATE: 1998-12-18
 ; PRIOR APPLICATION NUMBER: GB 9727262.9
 ; PRIOR FILING DATE: 1997-12-24
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 383
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
 ; OTHER INFORMATION: Influenzae B and E6E7 fusion from Human papilloma
 ; OTHER INFORMATION: virus type 18)
 US-10-899-771-23

Query Match 100.0%; Score 44; DB 17; Length 383;
 Best Local Similarity 100.0%; Pred. No. 2; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELTEVFEEFA 9
 Db 151 ELTEVFEEFA 159

RESULT 13
 US-10-751-845-136
 ; Sequence 136, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiciz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 136
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Human Papilloma virus
 US-10-751-845-136

Query Match 90.9%; Score 40; DB 17; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.27; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELTEVFEEF 8
 Db 3 ELTEVFEEF 10

RESULT 14
US-10-751-845-127
; Sequence 127, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-127

Query Match 88.6%; Score 39; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTVFEFA 9
Db 1 LTVFEFA 8

RESULT 15
US-10-321-204-36
; Sequence 36, Application US/10321204
; Publication No. US20030186871A1
; GENERAL INFORMATION:
; APPLICANT: Waters, Steve
; APPLICANT: Moodie, Shonna
; APPLICANT: Lavan, Brian
; APPLICANT: Gustafson, Thomas A.
; APPLICANT: Metabolex, Inc.
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating
; FILE REFERENCE: 016325-007310US
; CURRENT APPLICATION NUMBER: US/10/321,204
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/341,451
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-321-204-36

Query Match 84.1%; Score 37; DB 14; Length 322;
Best Local Similarity 87.5%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELTEVFEEF 8
Db 279 ELTQVFEEF 286

Search completed: June 29, 2005, 04:19:18
Job time : 58.85 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-26
Perfect score: 44
Sequence: 1 ELTVFPEFA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
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2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	15	US-08-159-339A-1174	Sequence 1174, Ap
2	44	100.0	158	US-08-247-904B-10	Sequence 10, Appl
3	44	100.0	158	US-08-767-942A-19	Sequence 19, Appl
4	44	100.0	271	US-08-117-083-14	Sequence 14, Appl
5	44	100.0	278	US-09-485-885-21	Sequence 21, Appl
6	44	100.0	383	US-09-485-885-23	Sequence 23, Appl
7	39	88.6	10	US-08-159-339A-87	Sequence 87, Appl
8	33	75.0	536	US-09-248-796A-19182	Sequence 19182, A
9	32	72.7	304	US-09-107-532A-4117	Sequence 4117, Ap
10	31	70.5	71	US-09-270-767-38165	Sequence 38165, A
11	31	70.5	71	US-09-270-767-53382	Sequence 53382, A
12	31	70.5	73	US-09-286-959B-16	Sequence 16, Appl
13	31	70.5	117	US-09-107-532A-5259	Sequence 6259, Ap
14	31	70.5	123	US-09-134-000C-4494	Sequence 4494, Ap
15	31	70.5	216	US-09-134-000C-5796	Sequence 5796, Ap
16	31	70.5	288	US-08-246-403A-3	Sequence 3, Appli
17	31	70.5	288	US-08-246-403A-6	Sequence 6, Appli
18	31	70.5	309	US-09-248-796A-25339	Sequence 25339, A
19	31	70.5	429	US-09-328-352-4643	Sequence 4643, Ap
20	30	68.2	8	US-08-159-339A-1177	Sequence 1177, Ap
21	30	68.2	109	US-09-663-600A-213	Sequence 213, App
22	30	68.2	137	US-09-270-767-33279	Sequence 33279, A
23	30	68.2	137	US-09-270-767-48496	Sequence 48496, A
24	30	68.2	141	US-08-187-186A-5	Sequence 5, Appli
25	30	68.2	141	US-08-442-497C-9	Sequence 9, Appli
26	30	68.2	141	US-09-333-033-9	Sequence 9, Appli
27	30	68.2	141	US-10-004-832-9	Sequence 9, Appli

28	30	68.2	142	2	US-08-187-186A-2	Sequence 2, Appli
29	30	68.2	142	2	US-08-442-497C-2	Sequence 2, Appli
30	30	68.2	142	3	US-09-333-033-2	Sequence 2, Appli
31	30	68.2	142	4	US-09-663-600A-229	Sequence 229, App
32	30	68.2	142	4	US-10-004-832-2	Sequence 2, Appli
33	30	68.2	142	5	PCT-US94-05186-2	Sequence 2, Appli
34	30	68.2	143	4	US-09-949-016-11009	Sequence 11009, A
35	30	68.2	157	4	US-09-949-016-7648	Sequence 7648, Ap
36	30	68.2	323	4	US-09-252-991A-17899	Sequence 17899, A
37	30	68.2	327	4	US-09-328-352-7138	Sequence 7138, Ap
38	30	68.2	355	4	US-09-134-000C-6752	Sequence 6752, Ap
39	30	68.2	365	4	US-09-902-540-13185	Sequence 13185, A
40	30	68.2	455	4	US-09-270-767-35242	Sequence 35242, A
41	30	68.2	455	4	US-09-270-767-50459	Sequence 50459, A
42	30	68.2	696	4	US-09-252-991A-16965	Sequence 16965, A
43	30	68.2	733	4	US-09-538-092-225	Sequence 225, App
44	30	68.2	764	4	US-09-585-858-15	Sequence 15, Appl
45	30	68.2	764	4	US-10-270-878-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-159-339A-1174
; Sequence 1174, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cellis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1174:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-1174

Query Match 100.0%; Score 44; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.008;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELTEVFEEFA 9
| | | | | | | | |
DB 5 ELTEVFEEFA 13

RESULT 2

US-08-247-904B-10
; Sequence 10, Application US/08247904B
; Patent No. 5981699

; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Eckstein, Jens W.
; APPLICANT: Draetta, Giulio
; TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/247.904B
; FILING DATE: 23-MAY-1994

; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.01

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-247-904B-10

Query Match 100.0%; Score 44; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELTEVFEEFA 9
| | | | | | | | |
DB 40 ELTEVFEEFA 48

RESULT 3

US-08-767-942A-19
; Sequence 19, Application US/08767942A
; Patent No. 6068982

; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Chiu, M. Isabel
; APPLICANT: Berlin, Vivian
; APPLICANT: Damagnez, Veronique
; APPLICANT: Draetta, Giulio
; APPLICANT: Guillaume, Cottarel
; TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES

; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/767,942A
; APPLICATION NUMBER: US/08/767,942A
; FILING DATE: 17-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-767-942A-19

Query Match 100.0%; Score 44; DB 3; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELTEVFEEFA 9
| | | | | | | | |
DB 40 ELTEVFEEFA 48

RESULT 4

US-08-117-083-14
; Sequence 14, Application US/08117083
; Patent No. 5719054

; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989

```

; TELEPAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..271
; OTHER INFORMATION: /note="Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
; US-08-117-083-14
;
; Query Match 100.0%; Score 44; DB 1; Length 271;
; Best Local Similarity 100.0%; Pred. No. 0.19;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 ELTEVFEEFA 9
; DB 41 ELTEVFEEFA 49
;
; RESULT 5
; US-09-485-885-21
; Sequence 21, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-21
;
; Query Match 100.0%; Score 44; DB 3; Length 278;
; Best Local Similarity 100.0%; Pred. No. 0.19;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 ELTEVFEEFA 9
; DB 151 ELTEVFEEFA 159
;
; RESULT 6
; US-09-485-885-23
; Sequence 23, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-21
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; Query Match 100.0%; Score 44; DB 3; Length 278;
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; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 ELTEVFEEFA 9
; DB 151 ELTEVFEEFA 159
;
; RESULT 7
; US-08-159-339A-87
; Sequence 87, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-87

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; TELEPAX: 415-398-3249
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; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
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; TOPOLOGY: linear
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; NAME/KEY: Protein
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; OTHER INFORMATION: the open reading frame."
; US-08-117-083-14
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; Query Match 100.0%; Score 44; DB 1; Length 271;
; Best Local Similarity 100.0%; Pred. No. 0.19;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 ELTEVFEEFA 9
; Db 41 ELTEVFEEFA 49
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; RESULT 5
; US-09-485-885-21
; Sequence 21, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-21
;
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; Db 151 ELTEVFEEFA 159
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; RESULT 6
; US-09-485-885-23
; Sequence 23, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
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; ORGANISM: Homo sapien
; US-09-485-885-21
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; Best Local Similarity 100.0%; Pred. No. 0.19;
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; QY 1 ELTEVFEEFA 9
; Db 151 ELTEVFEEFA 159
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; RESULT 7
; US-08-159-339A-87
; Sequence 87, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-87

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; TELEPAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..271
; OTHER INFORMATION: /note="Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
; US-08-117-083-14
;
; Query Match 100.0%; Score 44; DB 1; Length 271;
; Best Local Similarity 100.0%; Pred. No. 0.19;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 ELTEVFEEFA 9
; Db 41 ELTEVFEEFA 49
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; RESULT 5
; US-09-485-885-21
; Sequence 21, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-21
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; Query Match 100.0%; Score 44; DB 3; Length 278;
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; QY 1 ELTEVFEEFA 9
; Db 151 ELTEVFEEFA 159
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; RESULT 6
; US-09-485-885-23
; Sequence 23, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-21
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; Query Match 100.0%; Score 44; DB 3; Length 278;
; Best Local Similarity 100.0%; Pred. No. 0.19;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 ELTEVFEEFA 9
; Db 151 ELTEVFEEFA 159
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; RESULT 7
; US-08-159-339A-87
; Sequence 87, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-87

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; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-53382

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Qy 1 ELTEVFPEA 9
Db 50 QLSNVFEFA 58

RESULT 12
US-09-286-959B-16
; Sequence 16, Application US/09286959B
; Patent No. 6300131
; GENERAL INFORMATION:
; APPLICANT: Johns Hopkins University
; APPLICANT: Greider, Carol W.
; APPLICANT: Le, Siyuan
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157001
; CURRENT APPLICATION NUMBER: US/09/286,959B
; CURRENT FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,783
; PRIOR FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (0)...(0)
US-09-286-959B-16

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Qy 1 ELTEVFPEA 9
Db 5 ELSQVFPEIA 13

RESULT 13
US-09-107-532A-6259
; Sequence 6259, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
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; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6259:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
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; NAME/KEY: misc feature
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US-09-107-532A-6259

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Db 92 DLTEVFE 98

RESULT 14
US-09-134-000C-4494
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; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
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US-09-134-000C-4494

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Qy 1 ELTEVFE 7
Db 94 DLTEVFE 100

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; Sequence 5796, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
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; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
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; PRIOR FILING DATE: 1997-08-15
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; SEQ ID NO 5796
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; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5796
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Db      13 QLKEVFEEF 20
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Search completed: June 28, 2005, 21:33:23
Job time : 18 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2005, 19:19:47 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-25
Perfect score: 41
Sequence: 1 KTVLELTV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	57	2 Q90133	Q90133 human papil
2	41	100.0	158	1 V86 HPV18	P06463 human papil
3	41	100.0	158	2 Q90NP8	Q90NP8 human papil
4	36	87.8	1483	2 Q93332	Q93332 caenorhabdi
5	35	85.4	272	2 Q8JME9	Q8JME9 mamestra co
6	35	85.4	272	2 Q9QLN1	Q9QLN1 mamestra co
7	35	85.4	272	2 Q7IAK8	Q7IAK8 mamestra co
8	34	82.9	115	2 Q9RA93	Q9RA93 sinorhizobi
9	34	82.9	332	2 Q98GH0	Q98GH0 rhizobium 1
10	34	82.9	525	2 Q7AJ38	Q7AJ38 lactobacill
11	34	82.9	541	2 Q8AY32	Q8AY32 rattus norv
12	33	80.5	83	2 Q16304	Q16304 homo sapien
13	33	80.5	121	2 Q6FF91	Q6FF91 acinetobact
14	33	80.5	129	1 RL7 TREPA	Q83268 treponema p
15	33	80.5	129	2 Q73JJ6	Q73JJ6 treponema d
16	33	80.5	140	2 Q8LP93	Q8LP93 lycopersico
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18	33	80.5	362	2 Q6WAX1	Q6WAX1 toxoplasma
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26	33	80.5	481	2 Q8Y857	Q8Y857 listeria mo
27	33	80.5	492	2 Q73FL3	Q73FL3 wolbachia p
28	33	80.5	500	1 ICI HUMAN	P05155 homo sapien
29	33	80.5	504	1 ICI_MOUSE	P97290 mus musculu
30	33	80.5	504	2 Q6P734	Q6P734 rattus norv
31	32	78.0	276	2 Q846Y0	Q846Y0 streptomyce

32	32	78.0	298	2	Q20159	Q20159 caenorhabdi
33	32	78.0	367	2	Q6M035	Q6M035 methanococc
34	32	78.0	375	2	Q6DN68	Q6DN68 neisseria 1
35	32	78.0	380	2	Q9LXW1	Q9LXW1 arabidopsis
36	32	78.0	405	2	Q6M9K8	Q6M9K8 parachlamy
37	32	78.0	430	2	Q8ZQB0	Q8ZQB0 salmonella
38	32	78.0	446	2	Q8Z7Y8	Q8Z7Y8 salmonella
39	32	78.0	576	1	NAE2 THEME	Q9X0Y0 thermotoga
40	32	78.0	603	2	Q4Z967	Q4Z967 schizosacch
41	32	78.0	861	2	Q9NS19	Q9NS19 caenorhabdi
42	32	78.0	931	1	CAPP STRA3	Q8E647 streptococc
43	32	78.0	931	1	CAPP STRA5	Q8E0H2 streptococc
44	32	78.0	997	2	Q9UUY0	Q9UUY0 neurospora
45	32	78.0	1412	2	Q8MUF5	Q8MUF5 hydra atten

ALIGNMENTS

RESULT 1
Q90133 PRELIMINARY; PRT; 57 AA.
AC Q90133;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Protein E6.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88188247; PubMed=2833614;
RA Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M.,
RA Sugimura T.;
RT "Nucleotide sequences of cDNAs for human papillomavirus type 18
RT transcripts in HeLa cells.";
RL J. Virol. 62:1640-1646(1988).
DR EMBL; M20324; AAA99512.1; -.
DR PIR; I56705; I56705.
SQ SEQUENCE 57 AA; 6531 MW; 31CF1A5B3740D2C CRC64;

Query Match 100.0%; Score 41; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9
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Db 36 KTVLELTV 44

RESULT 2
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ID VE6 HPV18
AC P06463;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87283882; PubMed=3039146;
RA Cole S.T., Danos O.;
RT "Nucleotide sequence and comparative analysis of the human
RT papillomavirus type 18 genome. Phylogeny of papillomaviruses and
RT repeated structure of the E6 and E7 gene products.";
RL J. Mol. Biol. 193:599-608(1987).

RN [2]
RP SEQUENCE FROM N.A. PubMed=3018129;
RX MEDLINE=8630665; PubMed=3018129;
RA Matlashewski G., Banks L., Wu-Liao J., Spence P., Pim D., Crawford L.;
RT "The expression of human papillomavirus type 18 E6 protein in bacteria
and the production of anti-E6 antibodies.";
RL J. Gen. Virol. 67:1909-1916(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88189247; PubMed=2833614;
RA Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M.,
RA Sugimura T.;
RT "Nucleotide sequences of cDNAs for human papillomavirus type 18
transcripts in HeLa cells.";
RL J. Virol. 62:1640-1646(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=87053870; PubMed=3023067;
RA Schneider-Gaedcke A., Schwarz E.;
RT "Different human cervical carcinoma cell lines show similar
transcription patterns of human papillomavirus type 18 early genes.";
RL EMBO J. 5:2285-2292(1986).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=87218459; PubMed=3034571;
RA Seedorf K., Oltersdorf T., Kraemer G., Roewekamp W.;
RT "Identification of early proteins of the human papilloma viruses type
16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells.";
RL EMBO J. 6:139-144(1987).
RN [6]
RP ZINC-BINDING.
RX MEDLINE=89385606; PubMed=2550872;
RA Grossman S.R., Laimins L.A.;
RT "E6 protein of human papillomavirus type 18 binds zinc.";
RL Oncogene 4:1089-1093(1989).
RN [7]
RP INTERACTION WITH FBLN1, AND INHIBITION OF E6-MEDIATED TRANSFORMATION.
RX MEDLINE=22189366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;
RA Du M., Fan X., Hong E., Chen J.J.;
RT "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";
RL Biochem. Biophys. Res. Commun. 296:962-969(2002).
CC -!- FUNCTION: This protein has transforming activity in vitro.
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double
stranded DNA (in vitro). FBLN1.
CC -!- SUBUNIT: Interacts with FBLN1.
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X04354; CAA27879.1; -;
DR EMBL; X05015; CAA28664.1; -;
DR EMBL; M20325; AAA99514.1; -;
DR EMBL; M26798; AAA46946.1; -;
DR EMBL; X04773; CAA28466.1; -;
DR EMBL; A06324; CAA00539.1; -;
DR EMBL; A06328; CAA00542.1; -;
DR FIR; A26165; W6WL18.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW DNA-binding; Early protein; Nuclear protein; Oncogene; Zinc-finger.
FT ZN_FING 32 68
FT ZN_FING 105 141
FT ZN_FING 22 22 N -> S (in Ref. 4).
FT CONFLICT 22 22
SQ SEQUENCE 158 AA; 18871 MW; 5BCF13CF43D157FA CRC64;
Query Match 100.0%; Score 41; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KTVLELTV 9
Db 36 KTVLELTV 44
RESULT 3
Q9QNP8 PRELIMINARY; PRT; 159 AA.
ID Q9QNP8;
AC Q9QNP8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
SEQUENCE FROM N.A.
RA Laassri M., Gul'ko L., Vinokurova S., Kissel'jova N., Veiko V.,
RA Kissel'jev F.;
RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
Transformation Potential of E7 Gene and its Mutants.";
RL Virus Genes 182:139-149(1999).
RN [2]
SEQUENCE FROM N.A.
RA Veiko V.P.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y18491; CAB53096.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 18886 MW; 5BCF13CF43D407AF CRC64;
Query Match 100.0%; Score 41; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KTVLELTV 9
Db 36 KTVLELTV 44
RESULT 4
Q93332 PRELIMINARY; PRT; 1483 AA.
ID Q93332;
AC Q93332;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein C35C5.2.
GN ORFNames=C35C5.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA White S.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z78417; CAB01688.1; -;

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DR PIR: T19751; T19751.
DR WormBase; WBGene00007954; C35C5.2.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR003137; PA.
DR InterPro; IPR007484; Peptidase_M28.
DR InterPro; IPR007365; Transferrin_dmr.
DR Pfam; PF02225; PA; 2.
DR Pfam; PF04389; Peptidase_M28; 2.
DR Pfam; PF04253; TFR dimer; 2.
KW Hypothetical protein.
SQ SEQUENCE 1483 AA; 168163 MW; AE07537AD8E8E8F8C CRC64;

Query Match      87.8%; Score 36; DB 2; Length 1483;
Best Local Similarity 77.8%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTVLELTV 9
DB 665 KTVLELSBI 673

RESULT 5
QBQJME9
ID QBQJME9 PRELIMINARY; PRT; 272 AA.
AC QBQJME9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein pkl.
GN Name=pkl;
OS Mamestra configurata nucleopolyhedrovirus B.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=204440;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22080411; PubMed=12083822; DOI=10.1006/viro.2002.1411;
RA Li L., Donly C., Li Q., Willis L.G., Keddle B.A., Erlandson M.A.,
RA Theilmann D.A.;
RT "Identification and genomic analysis of a second species of
RT nucleopolyhedrovirus isolated from Mamestra configurata.";
RL Virology 297:226-244 (2002).
DR EMBL; AY126275; AAM9490.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR008271; Ser Thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 272 AA; 32157 MW; 134383C0C826A699 CRC64;

Query Match      85.4%; Score 35; DB 2; Length 272;
Best Local Similarity 87.5%; Pred. No. 61;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTVLELTE 8
DB 11 KTVIELTE 18

RESULT 6
QBQJLN1
ID QBQJLN1 PRELIMINARY; PRT; 272 AA.
AC QBQJLN1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

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DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Protein kinase 1.
GN Name=pkl;
OS Mamestra configurata nucleopolyhedrovirus (MaconPv).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=191492;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=90/2;
RA MEDLINE=97163493; PubMed=9010313;
RA Li S., Erlandson M., Moody D., Gillett C.;
RT "A physical map of the Mamestra configurata nucleopolyhedrovirus
RT genome and sequence analysis of the polyhedrin gene.";
RL J. Gen. Virol. 78:265-271 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=90/2;
RX MEDLINE=21884635; PubMed=1186270; DOI=10.1006/viro.2001.1313;
RA Li Q., Donly C., Li L., Willis L.G., Theilmann D.A., Erlandson M.;
RT "Sequence and organization of the Mamestra configurata
RT nucleopolyhedrovirus genome.";
RL Virology 294:106-121 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=90/2;
RA Li Q., Donly C., Li L., Willis L.G., Theilmann D.A., Erlandson M.A.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59461; AAM09111.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser Thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW Kinase.
SQ SEQUENCE 272 AA; 32172 MW; 4C3588F879856847 CRC64;

Query Match      85.4%; Score 35; DB 2; Length 272;
Best Local Similarity 87.5%; Pred. No. 61;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTVLELTE 8
DB 11 KTVIELTE 18

RESULT 7
QBQJAK8
ID QBQJAK8 PRELIMINARY; PRT; 272 AA.
AC QBQJAK8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein pkl.
GN Name=pkl;
OS Mamestra configurata nucleopolyhedrovirus A.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=207830;
RN [1]
RP SEQUENCE FROM N.A.
RA Li L., Li Q., Willis L.G., Erlandson M., Theilmann D.A., Donly C.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF539999; AAQ11023.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

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DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot Kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR ProDom; PD000001; Prot_Kinase; 1.
 DR SMART; SM00220; S_TK; 1.
 DR SMART; SM00219; TyRK; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 272 AA; 32172 MW; 4C3588F879856847 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 272;
 Best Local Similarity 87.5%; Pred. No. 61;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTE 8
 |||:||||
 Db 11 KTVLELTE 18

RESULT 8
 Q9RA93 PRELIMINARY; PRT; 115 AA.
 AC Q9RA93;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Arsr.
 OS Sinorhizobium sp. As4.
 GN Sinorhizobium sp. As4.
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
 OX NCBI_TaxID=102286;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=As4;
 RA Xu Z.Q., Zhang R.;
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Contains 1 HTH arsr-type DNA-binding domain.
 DR EMBL; AF178758; AAD51845.1; -.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003700; E:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001845; HTH_Arsr.
 DR Pfam; PF01022; HTH 5; 1.
 DR PRINTS; PR00778; HTHARSR.
 DR SMART; SM00418; HTH_Arsr; 1.
 KW DNA-binding; Transcription; Transcription regulation.
 SQ SEQUENCE 115 AA; 13304 MW; B63B3D6E41EB3F46 CRC64;

Query Match 82.9%; Score 34; DB 2; Length 115;
 Best Local Similarity 77.8%; Pred. No. 42;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTVLELTEV 9
 |||:||||
 Db 3 KTVLELTRV 11

RESULT 9
 Q98GH0 PRELIMINARY; PRT; 332 AA.
 AC Q98GH0;
 DT 01-OCT-2001 (TRENBLrel. 18, Created)
 DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Oxidoreductase; D-threo-aldoase 1-dehydrogenase (EC 1.1.1.122).
 GN OrderedLocustNames=mlr3332;
 OS Rhizobium loti (Mesorhizobium loti).
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP003001; BAB50246.1; -.
 DR HSRF; P10499; IEXB.
 DR GO; GO:0047834; F:D-threo-aldoase 1-dehydrogenase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro; IPR001395; Aldo/ket_red.
 DR Pfam; PF00248; Aldo_ket_red; 1.
 DR ProDom; PD000288; Aldo/Ket_red; 1.
 KW Complete proteome; Oxidoreductase.
 SQ SEQUENCE 332 AA; 36737 MW; ADBFA22E2983C3ED CRC64;

Query Match 82.9%; Score 34; DB 2; Length 332;
 Best Local Similarity 77.8%; Pred. No. 1.2e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTVLELTEV 9
 |||:||||
 Db 8 KTALEVTev 16

RESULT 10
 Q74J38 PRELIMINARY; PRT; 525 AA.
 AC Q74J38;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DE Phosphoenolpyruvate carboxylase.
 GN OrderedLocustNames=LJ1272;
 OS Lactobacillus johnsonii.
 CC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 CC Lactobacillus.
 OX NCBI_TaxID=33959;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCC 533;
 RX PubMed=14966310;
 RA Pridmore R.D., Berger B., Desiere F., Villanova D., Barretto C.,
 RA Pittet A.-C., Zwaalen M.-C., Rouvet M., Altermann E., Barrangou R.,
 RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
 RT "The genome sequence of the probiotic intestinal bacterium
 Lactobacillus johnsonii NCC 533";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
 CC -!- FUNCTION: Forms oxaloacetate, a four-carbon dicarboxylic acid
 source for the tricarboxylic acid cycle (By similarity).
 CC -!- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
 phosphoenolpyruvate + CO(2).
 CC -!- PATHWAY: Tricarboxylic acid cycle.
 CC -!- SIMILARITY: Belongs to the PEPCase family.
 DR EMBL; AE017203; AAS09093.1; -.
 DR GO; GO:0008964; F:phosphoenolpyruvate carboxylase activity; IEA.
 DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.
 DR InterPro; IPR001449; PEPCase.
 DR PRINTS; PR00150; PEPCARBLASE.
 DR PROSITE; PS00781; PEPCASE 1; 1.
 KW Carbon dioxide fixation; Complete proteome; Lyase; Pyruvate;
 SQ Tricarboxylic acid cycle.
 SQ SEQUENCE 525 AA; 59846 MW; 7740A95B589D211C CRC64;

Query Match 82.9%; Score 34; DB 2; Length 525;

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Best Local Similarity 87.5%; Pred. No. 1.9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 1;

QY 1 KTVLELITE 8
Db 145 KTVLELTD 152

RESULT 11
Q6AY32 PRELIMINARY; PRT; 541 AA.
AC Q6AY32;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettenan M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC079213; AAH79213.1; -.
KW Hypothetical protein.
SQ SEQUENCE 541 AA; 63035 MW; 0E0BAF2614AC7F19 CRC64;

Query Match 82.9%; Score 34; DB 2; Length 541;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTVLELITE 8
Db 441 KTVLELITE 448

RESULT 12
Q16304 PRELIMINARY; PRT; 83 AA.
AC Q16304;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE C1-inhibitor (Fragment).
GN Name=C1-INH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=951114132; PubMed=7814636;
RA Verpy E., Couture-Tosi E., Eldering E., Lopez-Trascasa M., Spath P.,
RA Meo T., Tosi M.;
RT "Crucial residues in the carboxy-terminal end of C1 inhibitor revealed
RT by pathogenic mutants impaired in secretion or function.";
RL J. Clin. Invest. 95:350-359(1995).
DR EMBL; S76944; AAB33044.2; -.
DR HSSP; P01009; IQMB.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR00215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
FT NON TER 1
SQ SEQUENCE 83 AA; 9455 MW; F6325A899AC7C8CB CRC64;

Query Match 80.5%; Score 33; DB 2; Length 83;
Best Local Similarity 87.5%; Pred. No. 49;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTVLELITE 8
Db 27 KTVLELITE 34

RESULT 13
Q6FF91 PRELIMINARY; PRT; 121 AA.
AC Q6FF91;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE 50S ribosomal protein L7/L12.
GN Name=rplL; OrderedLocustNames=ACIAD0306;
OS Acinetobacter sp. (strain ADP1).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=62977;
RN [1]
RP SEQUENCE FROM N.A.
RA Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S.,
RA Labarre L., Cruveillier S., Robert C., Duprat S., Wincker P.,
RA Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;
RT "Unique features revealed by the genome sequence of Acinetobacter sp.
RT ADP1, a versatile and naturally transformation competent bacterium.";
RL Nucleic Acids Res. 0:0-0(2004).
DR EMBL; CR543861; CAG67266.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR00206; Ribosomal L12.
DR InterPro; IPR008932; Ribosomal L12/7.
DR Pfam; PF00542; Ribosomal L12; 1.
DR ProDom; PD001326; Ribosomal L12; 1.
DR TIGRFAMs; TIGR00855; L12; 1.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 121 AA; 12667 MW; 966E122249272112 CRC64;

Query Match 80.5%; Score 33; DB 2; Length 121;
Best Local Similarity 77.8%; Pred. No. 71;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTVLELITE 9
Db 15 KTVLELITE 23

RESULT 14
RL7_TREPA
ID - RL7_TREPA STANDARD; PRT; 129 AA.

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AC O83268;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L7/L12.
GN Name=rplL; OrderedLocusNames=TF0240;
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=9832770; PubMed=9665876; DOI=10.1126/science.281.5375.375;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R.J., Winn M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,
RA Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,
RA Utterback T.R., McDonald L.A., Artach P., Bowman C., Cotton M.D.,
RA Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,
RA Weidman J.F., Smith H.O., Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RL Science 281:375-388(1998).
CC -!- FUNCTION: Seems to be the binding site for several of the factors
CC involved in protein synthesis and appears to be essential for
CC accurate translation.
CC -!- SIMILARITY: Belongs to the ribosomal protein L12P family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE001205; AAC65228.1; -
DR PIR; B71350; B71350.
DR HSP; F02392; ICTF.
DR TIGR; TP0240; -.
DR HAMAP; MF_00368; -.
DR InterPro; IPR000206; Ribosomal_L12.
DR InterPro; IPR008932; Ribosomal_L12/7.
DR Pfam; PF00542; Ribosomal_L12; 1.
DR ProDom; PD001326; Ribosomal_L12; 1.
DR TIGRFAMs; TIGR00855; L12; 1.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 129 AA; 13338 MW; AF2A0E7454B2F322 CRC64;

Query Match 80.5%; Score 33; DB 1; Length 129;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9
Db 16 KTVLELSEL 24

RESULT 15
Q73JJ6 PRELIMINARY; .PRT; 129 AA.
AC Q73JJ6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Ribosomal protein L7/L12.
GN Name=rplL; OrderedLocusNames=TDE2422;
OS Treponema denticola.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35405 / DSM 14222;
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RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA Durkin S.A., Dougherty S.C., Shetty J., Shvartsbeyn A.,
RA Gebregorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
RA Shatsman S., McLeod M.P., Smajls D., Howell J.K., Pal S., Amin A.,
RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT "Comparison of the genome of the oral pathogen Treponema denticola
RT with other spirochete genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
DR EMBL; AE017254; AAS12940.1; -.
DR TIGR; TDE2422; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR000206; Ribosomal_L12.
DR InterPro; IPR008932; Ribosomal_L12/7.
DR Pfam; PF00542; Ribosomal_L12; 1.
DR ProDom; PD001326; Ribosomal_L12; 1.
DR TIGRFAMs; TIGR00855; L12; 1.
KW Complete proteome.
SQ SEQUENCE 129 AA; 13223 MW; FA211F6DDB17CDC5 CRC64;

Query Match 80.5%; Score 33; DB 2; Length 129;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9
Db 16 KTVLELSEL 24

Search completed: June 28, 2005, 21:23:52
Job time : 57.1 secs
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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds
(without alignments)
59.826 Million cell updates/sec

Title: US-08-170-344-25

Perfect score: 41

Sequence: 1 KTVLELTV 9

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	9	17 US-10-751-845-132	Sequence 132, App
2	41	100.0	42	17 US-10-751-845-152	Sequence 152, App
3	41	100.0	119	17 US-10-751-845-159	Sequence 159, App
4	41	100.0	158	16 US-10-800-023-27	Sequence 27, App
5	41	100.0	172	16 US-10-472-724-6	Sequence 6, Appli
6	41	100.0	236	17 US-10-751-845-157	Sequence 157, App
7	41	100.0	237	17 US-10-751-845-158	Sequence 158, App
8	41	100.0	261	17 US-10-751-845-160	Sequence 160, App
9	41	100.0	278	13 US-10-000-903-21	Sequence 21, Appl
10	41	100.0	278	17 US-10-899-771-21	Sequence 21, Appl
11	41	100.0	383	13 US-10-000-903-23	Sequence 23, Appl

12	41	100.0	383	17	US-10-899-771-23	Sequence 23, Appl
13	33	80.5	74	15	US-10-236-392-88	Sequence 88, Appl
14	33	80.5	86	15	US-10-282-122A-45170	Sequence 45170, A
15	33	80.5	128	16	US-10-425-115-340269	Sequence 340269, A
16	33	80.5	129	15	US-10-282-122A-76448	Sequence 76448, A
17	33	80.5	145	15	US-10-236-392-84	Sequence 84, Appl
18	33	80.5	145	15	US-10-236-392-86	Sequence 86, Appl
19	33	80.5	161	15	US-10-236-392-90	Sequence 90, Appl
20	33	80.5	327	9	US-09-945-301-862	Sequence 862, App
21	33	80.5	346	15	US-10-282-122A-71775	Sequence 71775, A
22	33	80.5	500	14	US-10-005-956-22	Sequence 22, Appl
23	33	80.5	500	14	US-10-005-956-24	Sequence 24, Appl
24	33	80.5	500	14	US-10-005-956-26	Sequence 26, Appl
25	33	80.5	500	14	US-10-005-956-28	Sequence 28, Appl
26	33	80.5	500	14	US-10-005-956-30	Sequence 30, Appl
27	33	80.5	500	14	US-10-005-956-294	Sequence 294, App
28	33	80.5	522	15	US-10-264-049-2645	Sequence 2645, Ap
29	33	80.5	778	15	US-10-424-599-183425	Sequence 183425, A
30	32	78.0	46	15	US-10-424-599-238328	Sequence 238328, A
31	32	78.0	267	16	US-10-425-115-186757	Sequence 186757, A
32	32	78.0	276	11	US-09-980-217-15	Sequence 15, Appl
33	32	78.0	398	9	US-09-864-761-37735	Sequence 37735, A
34	32	78.0	1046	15	US-10-369-493-3073	Sequence 3073, Ap
35	31	75.6	10	17	US-10-751-845-136	Sequence 136, App
36	31	75.6	52	9	US-09-764-869-1229	Sequence 1229, Ap
37	31	75.6	52	14	US-10-091-504-1229	Sequence 1229, Ap
38	31	75.6	52	15	US-10-227-577-1229	Sequence 1229, Ap
39	31	75.6	118	16	US-10-437-963-204256	Sequence 204256, A
40	31	75.6	291	14	US-10-043-487-360	Sequence 360, App
41	31	75.6	343	15	US-10-369-493-5584	Sequence 5584, App
42	31	75.6	388	15	US-10-424-599-177645	Sequence 177645, A
43	31	75.6	496	14	US-10-097-559-40	Sequence 40, Appl
44	31	75.6	496	17	US-10-732-923-1085	Sequence 1085, Ap
45	31	75.6	538	15	US-10-094-749-2659	Sequence 2659, Ap

ALIGNMENTS

RESULT 1
US-10-751-845-132
; Sequence 132, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751.845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-132

Query Match 100.0%; Score 41; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9

Db 1 KTVLELTV 9

RESULT 2

US-10-751-845-152
; Sequence 152, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-152

Query Match 100.0%; Score 41; DB 17; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9
Db 28 KTVLELTV 36

RESULT 3

US-10-751-845-159
; Sequence 159, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-159

Query Match 100.0%; Score 41; DB 17; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9
Db 28 KTVLELTV 36

RESULT 4

US-10-800-023-27
; Sequence 27, Application US/10800023
; Publication No. US20040258688A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Ralph
; APPLICANT: Nussenzweig, Michel
; APPLICANT: Hawiger, Daniel
; APPLICANT: Bonifaz, Laura
; TITLE OF INVENTION: Enhanced Antigen Delivery and Modulation
; FILE REFERENCE: 600-1-081CONCIP1
; CURRENT APPLICATION NUMBER: US/10/800,023
; CURRENT FILING DATE: 2004-03-14
; PRIOR APPLICATION NUMBER: 09/925,284
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/586,704
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: PCT/US96/01383
; PRIOR FILING DATE: 1996-01-31
; PRIOR APPLICATION NUMBER: 08/381,528
; PRIOR FILING DATE: 1995-01-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 158
; TYPE: PRT
; ORGANISM: human papilloma virus E6 protein
US-10-800-023-27

Query Match 100.0%; Score 41; DB 16; Length 158;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9
Db 36 KTVLELTV 44

RESULT 5

US-10-472-724-6
; Sequence 6, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-6

Query Match 100.0%; Score 41; DB 16; Length 172;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9
Db 42 KTVLELTV 50

RESULT 6
US-10-751-845-157
; Sequence 157, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-157

Query Match 100.0%; Score 41; DB 17; Length 236;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9
| | | | | | | | | |
Db 145 KTVLELTV 153

RESULT 7
US-10-751-845-158
; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-158

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Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9
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Db 146 KTVLELTV 154

RESULT 8
US-10-751-845-160
; Sequence 160, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160

Query Match 100.0%; Score 41; DB 17; Length 261;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9
| | | | | | | | | |
Db 170 KTVLELTV 178

RESULT 9
US-10-000-903-21
; Sequence 21, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-21

Query Match 100.0%; Score 41; DB 13; Length 278;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9
| | | | | | | | | |
Db 147 KTVLELTV 155

RESULT 10
US-10-899-771-21
; Sequence 21, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 18)
US-10-899-771-21

Query Match 100.0%; Score 41; DB 17; Length 278;
Best Local Similarity 100.0%; Pred. No. 5.7; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9
|||||
Db 147 KTVLELTV 155

RESULT 11
US-10-000-903-23
; Sequence 23, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-23

Query Match 100.0%; Score 41; DB 13; Length 383;
Best Local Similarity 100.0%; Pred. No. 8.1; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9
|||||
Db 147 KTVLELTV 155

RESULT 12
US-10-899-771-23
; Sequence 23, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and E6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 18)
US-10-899-771-23

Query Match 100.0%; Score 41; DB 17; Length 383;
Best Local Similarity 100.0%; Pred. No. 8.1; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9
|||||
Db 147 KTVLELTV 155

RESULT 13
US-10-236-392-88
; Sequence 88, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladamir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRochelle, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh

```
; APPLICANT: Shinkets, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 88
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-392-88

Query Match      80.5%; Score 33; DB 15; Length 74;
Best Local Similarity 87.5%; Pred. No. 51;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KTVLELTE 8
Db      17 QTVLELTE 24

RESULT 14
US-10-282-122A-45170
; Sequence 45170, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
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; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45170
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-10-282-122A-45170

Query Match      80.5%; Score 33; DB 15; Length 86;
Best Local Similarity 77.8%; Pred. No. 61;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KTVLELTEV 9
Db      15 KTVLELVEL 23

RESULT 15
US-10-425-115-340269
; Sequence 340269, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 340269
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_73495C.1.pep
US-10-425-115-340269

Query Match      80.5%; Score 33; DB 16; Length 128;
Best Local Similarity 87.5%; Pred. No. 95;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KTVLELTE 8
Db      100 QTVLELTE 107

Search completed: June 29, 2005, 04:19:17
Job time : 58.85 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-25
Perfect score: 41
Sequence: 1 KTVLELFEV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	15	US-08-159-339A-1174	Sequence 1174, Ap
2	41	100.0	158	US-08-247-904B-10	Sequence 10, Appl
3	41	100.0	158	US-08-767-942A-19	Sequence 19, Appl
4	41	100.0	271	US-08-117-083-14	Sequence 14, Appl
5	41	100.0	278	US-09-485-885-21	Sequence 21, Appl
6	41	100.0	383	US-09-485-885-23	Sequence 23, Appl
7	35	85.4	270	US-09-107-532A-5220	Sequence 5220, Ap
8	33	80.5	77	US-09-621-976-5771	Sequence 5771, Ap
9	33	80.5	84	US-08-605-163-22	Sequence 22, Appl
10	33	80.5	500	US-07-755-573C-8	Sequence 8, Appl
11	33	80.5	500	US-09-519-878-2	Sequence 2, Appl
12	33	80.5	504	US-09-519-878-4	Sequence 4, Appl
13	33	80.5	520	US-09-943-016-10586	Sequence 10586, A
14	31	75.6	386	US-09-902-540-11825	Sequence 11825, A
15	31	75.6	489	US-09-902-540-16694	Sequence 16694, A
16	31	75.6	496	US-08-881-784-1	Sequence 1, Appl
17	31	75.6	496	US-09-292-768-2	Sequence 2, Appl
18	31	75.6	496	US-09-292-768-64	Sequence 64, Appl
19	31	75.6	496	US-09-292-768-66	Sequence 66, Appl
20	31	75.6	496	US-09-172-339-6	Sequence 6, Appl
21	31	75.6	575	US-09-107-532A-5733	Sequence 5733, Ap
22	31	75.6	1128	US-09-328-352-4973	Sequence 4973, Ap
23	30	73.2	166	US-09-107-532A-5004	Sequence 5004, Ap
24	30	73.2	180	US-09-270-767-58131	Sequence 58131, A
25	30	73.2	202	US-09-540-236-2012	Sequence 2012, Ap
26	30	73.2	230	US-09-248-796A-18704	Sequence 18704, A
27	30	73.2	302	US-09-710-279-3062	Sequence 3062, Ap

28 30 73.2 315 3 US-09-134-001C-4521 Sequence 4521, Ap
29 30 73.2 423 4 US-09-270-767-42815 Sequence 42815, A
30 30 73.2 519 4 US-09-198-452A-561 Sequence 561, App
31 30 73.2 521 4 US-09-438-185A-523 Sequence 523, App
32 30 73.2 561 3 US-09-233-989-5 Sequence 5, Appl
33 30 73.2 738 4 US-09-107-532A-5096 Sequence 5096, Ap
34 30 73.2 742 1 US-07-921-807B-2 Sequence 2, Appl
35 30 73.2 742 1 US-08-441-944A-2 Sequence 2, Appl
36 30 73.2 1501 2 US-08-447-464-3 Sequence 3, Appl
37 30 73.2 1501 2 US-08-716-679-3 Sequence 3, Appl
38 30 73.2 1911 1 US-08-348-006B-5 Sequence 5, Appl
39 30 73.2 1911 2 US-08-800-825A-5 Sequence 5, Appl
40 30 73.2 1911 3 US-09-158-657-5 Sequence 5, Appl
41 30 73.2 1911 5 PCT-US94-10166-5 Sequence 5, Appl
42 29 70.7 62 4 US-09-513-999C-4219 Sequence 5, Appl
43 29 70.7 72 4 US-09-513-999C-4220 Sequence 4220, Ap
44 29 70.7 94 4 US-09-902-540-11096 Sequence 11096, A
45 29 70.7 121 4 US-09-248-796A-14182 Sequence 14182, A

ALIGNMENTS

RESULT 1
US-08-159-339A-1174
; Sequence 1174, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cellis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1174:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-1174

Query Match 100.0%; Score 41; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTVLELTV 9
|||||
Db 1 KTVLELTV 9

RESULT 2

US-08-247-904B-10
; Sequence 10, Application US/08247904B
; Patent No. 5981699
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Eckstein, Jens W.
; APPLICANT: Draetta, Giulio
; TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICANT: US/08/247.904B
FILING DATE: 23-MAY-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-029.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-247-904B-10

Query Match 100.0%; Score 41; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTVLELTV 9
|||||
Db 36 KTVLELTV 44

RESULT 3

US-08-767-942A-19
; Sequence 19, Application US/08767942A
; Patent No. 6068982
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Chiu, M. Isabel
; APPLICANT: Berlin, Vivian
; APPLICANT: Damagnez, Veronique
; APPLICANT: Draetta, Giulio
; APPLICANT: Guillaume, Cottarel
; TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES

NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: US/08/767,942A
FILING DATE: 17-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-029.04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-767-942A-19

Query Match 100.0%; Score 41; DB 3; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTVLELTV 9
|||||
Db 36 KTVLELTV 44

RESULT 4

US-08-117-083-14
; Sequence 14, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58783
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989


```
;
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..271
; OTHER INFORMATION: /note= "xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-14

Query Match 100.0%; Score 41; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9
Db 37 KTVLELTV 45

RESULT 5
US-09-485-885-21
; Sequence 21, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-21

Query Match 100.0%; Score 41; DB 3; Length 278;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9
Db 147 KTVLELTV 155

RESULT 6
US-09-485-885-23
; Sequence 23, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885

;
; TELEFAX: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-23

Query Match 100.0%; Score 41; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTV 9
Db 147 KTVLELTV 155

RESULT 7
US-09-107-532A-5220
; Sequence 5220, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...270
; SEQUENCE DESCRIPTION: SEQ ID NO: 5220:
US-09-107-532A-5220
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Query Match      85.4%; Score 35; DB 4; Length 270;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTE 8
Db 190 KTVMELTE 197

RESULT 8
US-09-621-976-5771
; Sequence 5771, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2006-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5771
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21...-1
US-09-621-976-5771

Query Match      80.5%; Score 33; DB 4; Length 77;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TVLELTEV 9
Db 33 TVVELTEV 40

RESULT 9
US-08-605-163-22
; Sequence 22, Application US/08605163
; Patent No. 5879886
; GENERAL INFORMATION:
; APPLICANT: Neo, Tommaso
; APPLICANT: Tosi, Mario
; APPLICANT: Verpy, Elisabeth
; APPLICANT: Biasotto, Michel
; TITLE OF INVENTION: Method for Detecting Molecules
; TITLE OF INVENTION: Containing Nucleotide Mismatches and the Location of These
; TITLE OF INVENTION: Mismatches, and Application to the Detection of Base
; TITLE OF INVENTION: Substitutions or Deletions in Nucleotide Sequences.
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,163
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
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; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05986.0005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 57
; OTHER INFORMATION: /note= "Xaa = Val or Met"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 58
; OTHER INFORMATION: /note= "Xaa = Gln or Glu"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 61
; OTHER INFORMATION: /note= "Xaa = Phe or Ser"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 64
; OTHER INFORMATION: /note= "Xaa = Val or Met"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 65
; OTHER INFORMATION: /note= "Xaa = Leu or Pro or Arg"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 73
; OTHER INFORMATION: /note= "Xaa = Pro or Arg"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 78
; OTHER INFORMATION: /note= "Xaa = Arg or Stop"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 82
; OTHER INFORMATION: /note= "Xaa = Pro or Ser"
; US-08-605-163-22

Query Match      80.5%; Score 33; DB 2; Length 84;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTE 8
Db 28 QTVLELTE 35

RESULT 10
US-07-755-573C-8
; Sequence 8, Application US/07755573C
; Patent No. 5622930
; GENERAL INFORMATION:
; APPLICANT: Eldering, Eric
; APPLICANT: Arden, Lucien
; TITLE OF INVENTION: C1 Esterase Inhibitor Muteins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,573C
FILING DATE: 05-SEP-1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Pochopien, Donald J.
REGISTRATION NUMBER: 32,167
REFERENCE/DOCKET NUMBER: 28687/32920
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-755-573C-8

Query Match 80.5%; Score 33; DB 1; Length 500;
Best Local Similarity 87.5%; Pred. No. 81;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTE 8
Db 444 QTVLELTE 451

RESULT 11
US-09-519-878-2
Sequence 2, Application US/09519878
Patent No. 6500929
GENERAL INFORMATION:
APPLICANT: MIYAGAWA, Shuji
TITLE OF INVENTION: MEMBRANE-BOUND C1 INHIBITOR
FILE REFERENCE: 10797-0001-0
CURRENT APPLICATION NUMBER: US/09/519,878
CURRENT FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: JP 11-206535
PRIOR FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 500
TYPE: PRT
ORGANISM: Homo sapiens
US-09-519-878-2

Query Match 80.5%; Score 33; DB 4; Length 500;
Best Local Similarity 87.5%; Pred. No. 81;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTE 8
Db 444 QTVLELTE 451

RESULT 12
US-09-519-878-4
Sequence 4, Application US/09519878
Patent No. 6500929
GENERAL INFORMATION:
APPLICANT: MIYAGAWA, Shuji
TITLE OF INVENTION: MEMBRANE-BOUND C1 INHIBITOR
FILE REFERENCE: 10797-0001-0
CURRENT APPLICATION NUMBER: US/09/519,878
CURRENT FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: JP 11-206535

PRIOR FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 504
TYPE: PRT
ORGANISM: Mus musculus
US-09-519-878-4

Query Match 80.5%; Score 33; DB 4; Length 504;
Best Local Similarity 87.5%; Pred. No. 82;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTE 8
Db 448 QTVLELTE 455

RESULT 13
US-09-949-016-10586
Sequence 10586, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10586
LENGTH: 520
TYPE: PRT
ORGANISM: Human
US-09-949-016-10586

Query Match 80.5%; Score 33; DB 4; Length 520;
Best Local Similarity 87.5%; Pred. No. 84;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTVLELTE 8
Db 464 QTVLELTE 471

RESULT 14
US-09-902-540-11825
Sequence 11825, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 11825
LENGTH: 386
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-11825

Query Match 75.6%; Score 31; DB 4; Length 386;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTVLELTE 8
|:|:|:|:
Db 56 KTILELAE 63

RESULT 15
US-09-902-540-16694
; Sequence 16694, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16694
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16694

Query Match 75.6%; Score 31; DB 4; Length 489;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVLELTEV 9
|:|:|:|:
Db 71 TILDLEI 78

Search completed: June 28, 2005, 21:33:22
Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds
(without alignments)
59.826 Million cell updates/sec

Title: US-08-170-344-24

Perfect score: 53

Sequence: 1 EITCVYCKT 9

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Minimum DB seq length: 0

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13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	42	17	US-10-751-845-152
2	53	100.0	119	17	US-10-751-845-159
3	53	100.0	158	16	US-10-800-023-27
4	53	100.0	172	16	US-10-472-724-6
5	53	100.0	236	17	US-10-751-845-157
6	53	100.0	237	17	US-10-751-845-158
7	53	100.0	261	17	US-10-751-845-160
8	53	100.0	278	13	US-10-000-903-21
9	53	100.0	278	17	US-10-899-771-21
10	53	100.0	383	13	US-10-000-903-23
11	53	100.0	383	17	US-10-899-771-23

12	45	84.9	625	16	US-10-408-765A-2049	Sequence 2049, Ap
13	45	84.9	734	16	US-10-408-765A-324	Sequence 324, App
14	45	84.9	734	16	US-10-723-860-297	Sequence 297, App
15	45	84.9	735	16	US-10-408-765A-2050	Sequence 2050, Ap
16	41	77.4	314	10	US-09-949-029-78	Sequence 78, Appl
17	40	75.5	727	15	US-10-108-260A-3060	Sequence 3060, Ap
18	40	75.5	3572	16	US-10-471-450-16	Sequence 16, Appl
19	39	73.6	10	17	US-10-751-845-139	Sequence 139, App
20	39	73.6	290	9	US-09-815-242-13432	Sequence 13432, A
21	39	73.6	290	9	US-09-815-242-13659	Sequence 13659, A
22	39	73.6	290	10	US-09-769-787-153	Sequence 153, App
23	39	73.6	290	15	US-10-282-122A-74226	Sequence 74226, A
24	39	73.6	290	17	US-10-472-928-4594	Sequence 4594, Ap
25	38	71.7	95	16	US-10-425-115-276810	Sequence 276810, App
26	38	71.7	123	16	US-10-425-115-276807	Sequence 276807, App
27	37	69.8	45	15	US-10-424-599-200471	Sequence 200471, App
28	37	69.8	52	15	US-10-424-599-193040	Sequence 193040, A
29	37	69.8	55	15	US-10-425-114-44730	Sequence 44730, A
30	37	69.8	55	16	US-10-425-115-191172	Sequence 191172, App
31	37	69.8	64	16	US-10-437-963-139053	Sequence 139053, App
32	37	69.8	70	15	US-10-424-599-249892	Sequence 249892, App
33	37	69.8	137	16	US-10-437-963-124482	Sequence 124482, App
34	37	69.8	147	15	US-10-369-493-11069	Sequence 11069, A
35	37	69.8	183	9	US-09-895-913A-330	Sequence 330, App
36	37	69.8	328	9	US-09-815-242-11324	Sequence 11324, A
37	37	69.8	328	15	US-10-282-122A-58706	Sequence 58706, A
38	37	69.8	328	15	US-10-335-977-6995	Sequence 6995, Ap
39	37	69.8	330	15	US-10-282-122A-54453	Sequence 54453, A
40	37	69.8	331	15	US-10-335-977-6996	Sequence 6996, Ap
41	36	67.9	68	15	US-10-424-599-239799	Sequence 239799, App
42	36	67.9	116	13	US-10-114-893-170	Sequence 170, App
43	36	67.9	130	16	US-10-437-963-103599	Sequence 103599, App
44	36	67.9	222	16	US-10-425-115-317438	Sequence 317438, App
45	36	67.9	405	9	US-09-768-781-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

; Sequence 152, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751.845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-152

Query Match 100.0%; Score 53; DB 17; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9

Db 21 EITCVYCKT 29

RESULT 2
US-10-751-845-159
; Sequence 159, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-159

Query Match 100.0%; Score 53; DB 17; Length 119;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9
Db 21 EITCVYCKT 29

RESULT 3
US-10-800-023-27
; Sequence 27, Application US/10800023
; Publication No. US20040258688A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Ralph
; APPLICANT: Nussenzweig, Michel
; APPLICANT: Hawiger, Daniel
; APPLICANT: Bonifaz, Laura
; TITLE OF INVENTION: Enhanced Antigen Delivery and Modulation
; FILE REFERENCE: 600-1-081CONCIPI
; CURRENT APPLICATION NUMBER: US/10/800,023
; CURRENT FILING DATE: 2004-03-14
; PRIOR APPLICATION NUMBER: 09/925,284
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/586,704
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: PCT/US96/01383
; PRIOR FILING DATE: 1996-01-31
; PRIOR APPLICATION NUMBER: 08/381,528
; PRIOR FILING DATE: 1995-01-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 158
; TYPE: PRT
; ORGANISM: human papilloma virus E6 protein
US-10-800-023-27

Query Match 100.0%; Score 53; DB 16; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9

Db 29 EITCVYCKT 37
RESULT 4
US-10-472-724-6
; Sequence 6, Application US/10472724
; Publication No. US20040171808A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-6

Query Match 100.0%; Score 53; DB 16; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9
Db 35 EITCVYCKT 43

RESULT 5
US-10-751-845-157
; Sequence 157, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-157

Query Match 100.0%; Score 53; DB 17; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9
Db 138 EITCVYCKT 146

```
Db 163 EITCVYCKT 171

RESULT 8
US-10-000-903-21
; Sequence 21, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-21

Query Match 100.0%; Score 53; DB 13; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9
Db 140 EITCVYCKT 148

RESULT 9
US-10-899-771-21
; Sequence 21, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 18)
US-10-899-771-21

Query Match 100.0%; Score 53; DB 17; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9

Db 139 EITCVYCKT 147

RESULT 7
US-10-751-845-160
; Sequence 160, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160

Query Match 100.0%; Score 53; DB 17; Length 261;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9

Db 139 EITCVYCKT 147

RESULT 7
US-10-751-845-160
; Sequence 160, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160

Query Match 100.0%; Score 53; DB 17; Length 261;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9
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Db 140 EITCVYCKT 148
|||||

RESULT 10

US-10-000-903-23
; Sequence 23, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-23

Query Match 100.0%; Score 53; DB 13; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9
|||||

Db 140 EITCVYCKT 148
|||||

RESULT 11

US-10-899-771-23
; Sequence 23, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and E6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 18)
US-10-899-771-23

Query Match 100.0%; Score 53; DB 17; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9
|||||

Db 140 EITCVYCKT 148
|||||

RESULT 12

US-10-408-765A-2049
; Sequence 2049, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2049
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376,
; LOCATION: 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388,
; LOCATION: 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400,
; LOCATION: 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423,
; LOCATION: 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435,
; LOCATION: 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447,
; LOCATION: 448, 449
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-408-765A-2049

Query Match 84.9%; Score 45; DB 16; Length 625;
Best Local Similarity 77.8%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EITCVYCKT 9
|||||

Db 464 EITCVYCKT 472
|||||

RESULT 13

US-10-408-765A-324
; Sequence 324, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 324

; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-324

Query Match 84.9%; Score 45; DB 16; Length 734;
Best Local Similarity 77.8%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1. EITCVYCKT 9
Db 581 EFTCAYCKT 589

RESULT 14

US-10-723-860-297
; Sequence 297, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:

; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 297
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-297

Query Match 84.9%; Score 45; DB 16; Length 734;
Best Local Similarity 77.8%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1. EITCVYCKT 9
Db 581 EFTCAYCKT 589

RESULT 15

US-10-408-765A-2050
; Sequence 2050, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:

; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2050
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486,
; LOCATION: 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498,

; LOCATION: 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510,
; LOCATION: 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533,
; LOCATION: 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545,
; LOCATION: 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557,
; LOCATION: 558, 559
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-408-765A-2050

Query Match 84.9%; Score 45; DB 16; Length 735;
Best Local Similarity 77.8%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1. EITCVYCKT 9
Db 574 EFTCAYCKT 582

Search completed: June 29, 2005, 04:19:16
Job time : 59.85 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-24

Perfect score: 53

Sequence: 1 EITCVYCKT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	32	1	US-08-466-285-2
2	53	100.0	32	3	US-08-164-788-2
3	53	100.0	158	2	US-08-247-904B-10
4	53	100.0	158	3	US-08-767-942A-19
5	53	100.0	271	1	US-08-117-083-14
6	53	100.0	278	3	US-09-485-885-21
7	53	100.0	383	3	US-09-485-885-23
8	48	90.6	15	3	US-08-159-339A-1176
9	40	75.5	134	4	US-09-248-796A-19660
10	39	73.6	290	4	US-09-583-110-4329
11	39	73.6	305	4	US-09-107-433-2649
12	37	69.8	598	4	US-09-270-767-61572
13	36	67.9	368	3	US-09-000-094-20
14	36	67.9	368	4	US-10-011-749-20
15	36	67.9	375	3	US-09-000-094-22
16	36	67.9	375	4	US-10-011-749-22
17	36	67.9	465	3	US-09-000-094-24
18	36	67.9	465	4	US-10-011-749-24
19	36	67.9	1587	3	US-09-000-094-46
20	36	67.9	1587	4	US-10-011-749-46
21	36	67.9	3730	4	US-09-949-016-9908
22	35	66.0	9	3	US-08-159-339A-570
23	35	66.0	10	3	US-08-159-339A-573
24	35	66.0	20	2	US-08-934-915-160
25	35	66.0	30	4	US-09-980-523A-4
26	35	66.0	158	4	US-09-980-523A-2
27	35	66.0	162	1	US-08-316-239B-3

28	35	66.0	162	1	US-08-316-239B-4
29	35	66.0	172	3	US-08-860-165-14
30	35	66.0	172	3	US-09-359-382-14
31	35	66.0	182	1	US-08-117-083-10
32	35	66.0	189	4	US-09-270-767-58555
33	35	66.0	262	4	US-09-270-767-32820
34	35	66.0	266	3	US-08-860-165-10
35	35	66.0	266	3	US-09-359-382-10
36	35	66.0	266	4	US-09-367-309A-1
37	35	66.0	273	3	US-09-485-885-4
38	35	66.0	273	4	US-09-270-767-40146
39	35	66.0	273	4	US-09-270-767-55362
40	35	66.0	292	3	US-09-485-885-10
41	35	66.0	352	4	US-09-270-767-43213
42	35	66.0	371	3	US-09-485-885-6
43	35	66.0	390	3	US-09-485-885-14
44	35	66.0	1112	4	US-09-717-364A-27
45	34	64.2	10	3	US-08-159-339A-86

ALIGNMENTS

RESULT 1

US-08-466-285-2
; Sequence 2, Application US/08466285
; Patent No. 5753233
; GENERAL INFORMATION:
; APPLICANT: Bleul, Conrad
; APPLICANT: Gissmann, Lutz
; APPLICANT: Muller, Martin
; TITLE OF INVENTION: Seroreactive Epitopes On Proteins Of
; TITLE OF INVENTION: Human Papillomavirus (HPV)18
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,285
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/164,768
; FILING DATE: 10-DEC-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/947,992
; FILING DATE: 21-SEP-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/696,953
; FILING DATE: 08-MAY-1991
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P 40 15 044.5
; FILING DATE: 10-MAY-1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Manspeizer, David A.
; REGISTRATION NUMBER: 37,540
; REFERENCE/DOCKET NUMBER: 05552.1075-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)408-4000

TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-466-285-2

Query Match 100.0%; Score 53; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BITCVYCKT 9
 DB 24 BITCVYCKT 32

RESULT 2

US-08-164-768-2
 Sequence 2, Application US/08164768
 Patent No. 6322794

GENERAL INFORMATION:
 APPLICANT: BLEUL, Conrad
 APPLICANT: GISSMANN, Lutz
 APPLICANT: MULLER, Martin
 TITLE OF INVENTION: SEORREACTIVE EPITOPES ON PROTEINS OF
 TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS (HPV) 18
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
 ADDRESSEE: DUNNER, L.L.P.
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/164,768
 FILING DATE: 10-DEC-1993
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Forman, David S.
 REGISTRATION NUMBER: 33,694
 REFERENCE/DOCKET NUMBER: 05552.1075-02000

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4000
 TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-164-768-2

Query Match 100.0%; Score 53; DB 3; Length 32;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BITCVYCKT 9
 DB 24 BITCVYCKT 32

RESULT 3

US-08-247-904B-10
 Sequence 10, Application US/08247904B
 Patent No. 5981699

GENERAL INFORMATION:
 APPLICANT: Rolfe, Mark
 APPLICANT: Eckstein, Jens W.
 APPLICANT: Draetta, Giulio
 TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
 NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley, Hoag & Eliot
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA

COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII(text)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/247,904B
 FILING DATE: 23-MAY-1994

CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: MIV-029.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 832-1000
 TELEFAX: (617) 832-7000
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 158 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-247-904B-10

Query Match 100.0%; Score 53; DB 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BITCVYCKT 9
 DB 29 BITCVYCKT 37

RESULT 4

US-08-767-942A-19
 Sequence 19, Application US/08767942A
 Patent No. 6068982

GENERAL INFORMATION:
 APPLICANT: Rolfe, Mark
 APPLICANT: Chiu, M. Isabel
 APPLICANT: Berlin, Vivian
 APPLICANT: Damagnez, Veronique
 APPLICANT: Draetta, Giulio
 APPLICANT: Guillaume, Cottarel
 TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA

COUNTRY: USA
 ZIP: 02109-2170

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,942A
; FILING DATE: 17-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-767-942A-19

Query Match 100.0%; Score 53; DB 3; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EITCVYCKT 9
DB 29 EITCVYCKT 37

RESULT 5
US-08-117-083-14
; Sequence 14, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Bournell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..271
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; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
; US-08-117-083-14

Query Match 100.0%; Score 53; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EITCVYCKT 9
DB 30 EITCVYCKT 38

RESULT 6
US-09-485-885-21
; Sequence 21, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-21

Query Match 100.0%; Score 53; DB 3; Length 278;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EITCVYCKT 9
DB 140 EITCVYCKT 148

RESULT 7
US-09-485-885-23
; Sequence 23, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-23
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Query Match 100.0%; Score 53; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.41; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EITCVYCKT 9
|||||
DB 140 EITCVYCKT 148
RESULT 8
US-08-159-339A-1176
; Sequence 1176, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Eteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-0050300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1176:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1176
Query Match 90.6%; Score 48; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EITCVYCK 8
|||||
DB 8 EITCVYCK 15
RESULT 9
US-09-248-796A-19660

; Sequence 19660, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19660
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19660
Query Match 75.5%; Score 40; DB 4; Length 134;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 EITCVYCK 8
|||||
DB 49 EITCVYCK 56
RESULT 10
US-09-583-110-4329
; Sequence 4329, Application US/09583110
; Patent No. 6899703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4329
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4329
Query Match 73.6%; Score 39; DB 4; Length 290;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EITCVYCKT 9
|||||
DB 265 EITCQFCQT 273
RESULT 11
US-09-107-433-2649
; Sequence 2649, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2649:
SEQUENCE CHARACTERISTICS:
LENGTH: 305 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...305
SEQUENCE DESCRIPTION: SEQ ID NO: 2649:
US-09-107-433-2649

Query Match 73.6%; Score 39; DB 4; Length 305;
Best Local Similarity 66.7%; Pred. No. 56;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EITCVYCKT 9
Db 280 EITCQFCQT 288

RESULT 12
US-09-270-767-61572
; Sequence 61572, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61572
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-61572

Query Match 69.8%; Score 37; DB 4; Length 598;
Best Local Similarity 62.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EITCVYCK 8
Db 121 KLTCFYCK 128

RESULT 13
US-09-000-094-20
; Sequence 20, Application US/09000094
; Patent No. 6365160
; GENERAL INFORMATION:
; APPLICANT: WEBB, Elizabeth Ann
; MARGETTS, Mary Brigid
; COX, John Cooper
; FRAZER, Ian
; MCMILLAN, Nigel Alan John
; WILLIAMS, Mark Philip
; MOLONEY, Margaret Bridget
; Holland
; EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-000-094-20

Query Match 67.9%; Score 36; DB 3; Length 368;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EITCVYCK 8
Db 28 QINCVPCK 35

RESULT 14
US-10-011-749-20
; Sequence 20, Application US/10011749
; Patent No. 6726912
; GENERAL INFORMATION:

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;
; APPLICANT: WEBB, Elizabeth Ann
; MARGETTS, Mary Brigid
; COX, John Cooper
; FRAZER, Ian
; MCMILLAN, Nigel Alan John
; WILLIAMS, Mark Philip
; MOLONEY, Margaret Bridget
; Holland
; EDWARDS, Stirling John
;
; TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
;
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,749
; FILING DATE: 11-Dec-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/000,094
; FILING DATE: 21-Apr-1998
; APPLICATION NUMBER: WO PCT/AU96/00473
; FILING DATE: 26-JUL-1996
; APPLICATION NUMBER: AU PN 4439/95
; FILING DATE: 26-JUL-1996
; APPLICATION NUMBER: AU PN 4439/95
; FILING DATE: 27-JUL-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 017227/0137
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
;
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 368 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-011-749-20

Query Match 67.9%; Score 36; DB 4; Length 368;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 BITCVYCK 8
Db 28 QINCVFCK 35

RESULT 15
US-09-000-094-22
; Sequence 22, Application US/09000094
; Patent No. 6365160
;
; GENERAL INFORMATION:
; APPLICANT: WEBB, Elizabeth Ann
; MARGETTS, Mary Brigid
; COX, John Cooper
; FRAZER, Ian
; MCMILLAN, Nigel Alan John
; WILLIAMS, Mark Philip
; MOLONEY, Margaret Bridget
; Holland
; EDWARDS, Stirling John

```

```

;
; TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
;
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/000,094
; FILING DATE: 21-Apr-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/AU96/00473
; FILING DATE: 26-JUL-1996
; APPLICATION NUMBER: AU PN 4439/95
; FILING DATE: 27-JUL-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 017227/0137
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
;
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-000-094-22

Query Match 67.9%; Score 36; DB 3; Length 375;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 BITCVYCK 8
Db 28 QINCVFCK 35

Search completed: June 28, 2005, 21:33:21
Job time : 17 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds
(without alignments)

59.826 Million cell updates/sec

Title: US-08-170-344-23

Perfect score: 46

Sequence: 1 LQDIEITCV 9

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	46	100.0	9	17 US-10-751-845-131
2	46	100.0	10	17 US-10-751-845-130
3	46	100.0	42	17 US-10-751-845-152
4	46	100.0	119	17 US-10-751-845-159
5	46	100.0	158	16 US-10-800-023-27
6	46	100.0	172	16 US-10-472-724-6
7	46	100.0	236	17 US-10-751-845-157
8	46	100.0	237	17 US-10-751-845-158
9	46	100.0	261	17 US-10-751-845-160
10	46	100.0	278	13 US-10-000-903-21
11	46	100.0	278	17 US-10-899-771-21

12	46	100.0	383	13	US-10-000-903-23	Sequence 23, Appl
13	46	100.0	383	17	US-10-899-771-23	Sequence 23, Appl
14	42	91.3	9	17	US-10-751-845-129	Sequence 129, App
15	40	87.0	99	15	US-10-389-647-605	Sequence 605, App
16	37	80.4	873	8	US-08-911-824-61	Sequence 61, Appl
17	36	78.3	162	16	US-10-767-701-58324	Sequence 58324, A
18	36	78.3	274	15	US-10-369-493-1669	Sequence 1669, Ap
19	36	78.3	282	15	US-10-243-552-539	Sequence 539, App
20	36	78.3	454	16	US-10-437-963-184385	Sequence 184385,
21	36	78.3	462	16	US-10-425-115-227314	Sequence 227314,
22	35	76.1	1070	14	US-10-032-585-7389	Sequence 7389, Ap
23	35	76.1	2478	16	US-10-437-963-131742	Sequence 131742,
24	34	73.9	30	15	US-10-296-734-1354	Sequence 1354, Ap
25	34	73.9	67	16	US-10-767-701-31617	Sequence 31617, A
26	34	73.9	131	17	US-10-732-180-228	Sequence 228, App
27	34	73.9	140	15	US-10-316-194-9	Sequence 9, Appli
28	34	73.9	140	15	US-10-316-194-37	Sequence 37, Appli
29	34	73.9	140	17	US-10-732-180-9	Sequence 9, Appli
30	34	73.9	140	17	US-10-732-180-37	Sequence 37, Appl
31	34	73.9	179	16	US-10-425-115-246840	Sequence 246840,
32	34	73.9	344	15	US-10-382-122A-47485	Sequence 47485, A
33	34	73.9	369	14	US-10-328-675A-74	Sequence 74, Appl
34	34	73.9	390	17	US-10-732-923-20210	Sequence 20210, A
35	34	73.9	400	9	US-03-804-357-6	Sequence 6, Appli
36	34	73.9	400	9	US-09-804-006-6	Sequence 6, Appli
37	34	73.9	509	14	US-10-097-340-254	Sequence 254, App
38	34	73.9	509	14	US-10-157-031-44	Sequence 44, Appl
39	34	73.9	509	15	US-10-170-385-87	Sequence 87, Appl
40	34	73.9	509	15	US-10-117-937-77	Sequence 77, Appl
41	34	73.9	509	15	US-10-173-999-2	Sequence 2, Appli
42	34	73.9	509	15	US-10-058-270A-110	Sequence 110, App
43	34	73.9	509	15	US-10-296-734-830	Sequence 830, App
44	34	73.9	509	16	US-10-657-022-77	Sequence 77, Appl
45	34	73.9	509	16	US-10-643-795A-92	Sequence 92, Appl

ALIGNMENTS

RESULT 1
US-10-751-845-131
; Sequence 131, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751.845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-131

Query Match 100.0%; Score 46; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9

Db 1 LQDIEITCV 9

```

RESULT 2
US-10-751-845-130
; Sequence 130, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiccz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-130

```

```

Query Match      100.0%; Score 46; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LQDIEITCV 9
Db 2 LQDIEITCV 10

```

```

RESULT 3
US-10-751-845-152
; Sequence 152, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiccz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-152

```

```

Query Match      100.0%; Score 46; DB 17; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LQDIEITCV 9
Db 17 LQDIEITCV 25

```

```

RESULT 4
US-10-751-845-159

```

```

; Sequence 159, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiccz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-159

```

```

Query Match      100.0%; Score 46; DB 17; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LQDIEITCV 9
Db 17 LQDIEITCV 25

```

```

RESULT 5
US-10-800-023-27
; Sequence 27, Application US/10800023
; Publication No. US20040258688A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Ralph
; APPLICANT: Nussenzweig, Michel
; APPLICANT: Hawiger, Daniel
; APPLICANT: Bonifaz, Laura
; TITLE OF INVENTION: Enhanced Antigen Delivery and Modulation
; FILE REFERENCE: 600-1-081CONCIPI
; CURRENT APPLICATION NUMBER: US/10/800,023
; CURRENT FILING DATE: 2004-03-14
; PRIOR APPLICATION NUMBER: 09/925,284
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/586,704
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: PCT/US96/01383
; PRIOR FILING DATE: 1996-01-31
; PRIOR APPLICATION NUMBER: 08/381,528
; PRIOR FILING DATE: 1995-01-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 158
; TYPE: PRT
; ORGANISM: human papilloma virus E6 protein
US-10-800-023-27

```

```

Query Match      100.0%; Score 46; DB 16; Length 158;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LQDIEITCV 9
Db 25 LQDIEITCV 33

```

RESULT 6
 US-10-472-724-6
 ; Sequence 6, Application US/10472724
 ; Publication No. US20040171806A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cid-Arregui, Angel
 ; APPLICANT: Zur Hausen, Harald
 ; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
 ; FILE REFERENCE: 4121-154
 ; CURRENT APPLICATION NUMBER: US/10/472,724
 ; CURRENT FILING DATE: 2003-09-17
 ; PRIOR APPLICATION NUMBER: PCT/EP02/03271
 ; PRIOR FILING DATE: 2002-03-22
 ; PRIOR APPLICATION NUMBER: EP 01107271.7
 ; PRIOR FILING DATE: 2001-03-23
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 6
 ; LENGTH: 172
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Construct
 US-10-472-724-6

Query Match 100.0%; Score 46; DB 16; Length 172;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
 |||||
 Db 31 LQDIEITCV 39

RESULT 7
 US-10-751-845-157
 ; Sequence 157, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiciz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 157
 ; LENGTH: 236
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial fusion sequence
 US-10-751-845-157

Query Match 100.0%; Score 46; DB 17; Length 236;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
 |||||
 Db 134 LQDIEITCV 142

RESULT 8

US-10-751-845-158
 ; Sequence 158, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiciz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 158
 ; LENGTH: 237
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial fusion sequence
 US-10-751-845-158

Query Match 100.0%; Score 46; DB 17; Length 237;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
 |||||
 Db 135 LQDIEITCV 143

RESULT 9
 US-10-751-845-160
 ; Sequence 160, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiciz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 160
 ; LENGTH: 261
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial fusion sequence
 US-10-751-845-160

Query Match 100.0%; Score 46; DB 17; Length 261;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
 |||||
 Db 159 LQDIEITCV 167

```
RESULT 10
US-10-000-903-21
; Sequence 21, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-21

Query Match      100.0%; Score 46; DB 13; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
Db 136 LQDIEITCV 144

RESULT 11
US-10-899-771-21
; Sequence 21, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 18)
US-10-899-771-21

Query Match      100.0%; Score 46; DB 17; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
Db 136 LQDIEITCV 144

RESULT 12
US-10-000-903-23
; Sequence 23, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-23

Query Match      100.0%; Score 46; DB 13; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
Db 136 LQDIEITCV 144

RESULT 13
US-10-899-771-23
; Sequence 23, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 18)
US-10-899-771-23

Query Match      100.0%; Score 46; DB 17; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
Db 136 LQDIEITCV 144
```

RESULT 14
US-10-751-845-129
; Sequence 129, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 129
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-129

Query Match 91.3%; Score 42; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LQDIEITC 8
Db 2 LQDIEITC 9
|||||

RESULT 15
US-10-389-647-605
; Sequence 605, Application US/10389647
; Publication No. US20040033549A1
; GENERAL INFORMATION:
; APPLICANT: GREENBERG, E. Peter
; APPLICANT: SCHUSTER, Martin
; APPLICANT: LOSTROH, Candi
; TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
; FILE REFERENCE: UI2-038CP
; CURRENT APPLICATION NUMBER: US/10/389,647
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 09/653730
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/153022
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 710
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 605
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-389-647-605

Query Match 87.0%; Score 40; DB 15; Length 99;
Best Local Similarity 77.8%; Pred. No. 8.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LQDIEITCV 9
Db 4 LNDIEITCV 12
|||||

Search completed: June 29, 2005, 04:19:14
Job time : 57.85 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-23

Perfect score: 46

Sequence: 1 LQDIEITCV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	100.0	10	3	US-08-159-339A-86
2	46	100.0	15	3	US-08-159-339A-1176
3	46	100.0	32	1	US-08-466-285-2
4	46	100.0	32	3	US-08-164-768-2
5	46	100.0	158	2	US-08-247-904B-10
6	46	100.0	158	3	US-08-767-942A-19
7	46	100.0	271	1	US-08-117-083-14
8	46	100.0	278	3	US-09-485-885-21
9	46	100.0	383	3	US-09-485-885-23
10	40	87.0	127	4	US-09-252-991A-28397
11	37	80.4	873	2	US-08-912-129A-61
12	35	76.1	724	4	US-09-248-796A-19040
13	34	73.9	369	4	US-09-519-232-74
14	34	73.9	509	3	US-08-809-999D-17
15	34	73.9	509	3	US-09-069-637-17
16	34	73.9	509	3	US-09-322-360-17
17	34	73.9	509	3	US-09-131-831B-17
18	34	73.9	528	4	US-09-949-016-11233
19	34	73.9	3135	1	US-08-323-170B-2
20	34	73.9	3135	3	US-08-954-441-2
21	33	71.7	519	4	US-09-720-655B-1
22	33	71.7	520	3	US-08-964-127-2
23	33	71.7	520	3	US-09-496-692-2
24	33	71.7	520	4	US-10-000-273-2
25	33	71.7	839	4	US-09-949-016-10846
26	32	69.6	53	4	US-09-270-767-61394
27	32	69.6	303	4	US-09-270-767-45862

28	32	69.6	402	4	US-09-270-767-46012	Sequence 46012, A
29	31	67.4	205	3	US-09-134-001C-4786	Sequence 4786, Ap
30	31	67.4	374	4	US-09-638-937-2	Sequence 2, Appli
31	31	67.4	826	4	US-09-248-796A-14387	Sequence 14387, A
32	31	67.4	852	4	US-09-585-858-19	Sequence 19, Appl
33	31	67.4	852	4	US-10-270-878-19	Sequence 19, Appl
34	31	67.4	1039	4	US-09-501-136-2	Sequence 2, Appli
35	31	67.4	1194	2	US-08-680-326-35	Sequence 35, Appl
36	31	67.4	4968	4	US-09-424-783-5	Sequence 5, Appli
37	30	65.2	10	3	US-09-051-529-1	Sequence 1, Appli
38	30	65.2	55	4	US-09-621-976-6262	Sequence 6262, Ap
39	30	65.2	72	4	US-09-621-976-6737	Sequence 6737, Ap
40	30	65.2	126	4	US-09-489-039A-8230	Sequence 8230, Ap
41	30	65.2	281	4	US-09-949-016-6831	Sequence 6831, Ap
42	30	65.2	324	4	US-09-949-016-7870	Sequence 7870, Ap
43	30	65.2	363	4	US-09-328-352-7018	Sequence 7018, Ap
44	30	65.2	455	4	US-09-949-016-6949	Sequence 6949, Ap
45	30	65.2	455	4	US-09-949-016-11026	Sequence 11026, A

ALIGNMENTS

RESULT 1
US-08-159-339A-86
; Sequence 86, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-86

Query Match 100.0%; Score 46; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
Db 1 LQDIEITCV 9

RESULT 2

US-08-159-339A-1176
; Sequence 1176, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Eteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1176:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-1176

Query Match 100.0%; Score 46; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
Db 4 LQDIEITCV 12

RESULT 3

US-08-466-285-2

; Sequence 2, Application US/08466285
; Patent No. 5753233
; GENERAL INFORMATION:
; APPLICANT: Bleul, Conrad
; APPLICANT: Gissmann, Lutz
; APPLICANT: Muller, Martin
; TITLE OF INVENTION: Seroreactive Epitopes On Proteins Of
; TITLE OF INVENTION: Human Papillomavirus (HPV)18
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,285
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/164,768
; FILING DATE: 10-DEC-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/947,992
; FILING DATE: 21-SEP-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/696,953
; FILING DATE: 08-MAY-1991
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P 40 15 044.5
; FILING DATE: 10-MAY-1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Manspeizer, David A.
; REGISTRATION NUMBER: 37,540
; REFERENCE/DOCKET NUMBER: 05552.1075-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)408-4000
; TELEFAX: (202)408-4400
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-466-285-2

Query Match 100.0%; Score 46; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
Db 20 LQDIEITCV 28

RESULT 4

US-08-164-768-2
; Sequence 2, Application US/08164768
; Patent No. 6322794
; GENERAL INFORMATION:

APPLICANT: BLEUL, Conrad
APPLICANT: GISSMANN, Lucz
APPLICANT: MULLER, Martin
TITLE OF INVENTION: SEROREACTIVE EPITOPES ON PROTEINS OF
HUMAN PAPILLOMA VIRUS (HPV) 18
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
ADDRESSEE: DUNNER, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,768
FILING DATE: 10-DEC-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05552.1075-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-164-768-2

Query Match 100.0%; Score 46; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
Db 20 LQDIEITCV 28

RESULT 5
US-08-247-904B-10
Sequence 10, Application US/08247904B
Patent No. 5981699
GENERAL INFORMATION:
APPLICANT: Rolfe, Mark
APPLICANT: Eckstein, Jens W.
APPLICANT: Draetta, Giulio
TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/247,904B
FILING DATE: 23-MAY-1994

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-029.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-247-904B-10

Query Match 100.0%; Score 46; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9
Db 25 LQDIEITCV 33

RESULT 6
US-08-767-942A-19
Sequence 19, Application US/08767942A
Patent No. 6068982
GENERAL INFORMATION:
APPLICANT: Rolfe, Mark
APPLICANT: Chiu, M. Isabel
APPLICANT: Berlin, Vivian
APPLICANT: Damagnez, Veronique
APPLICANT: Draetta, Giulio
APPLICANT: Guillaume, Cottarel
TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,942A
FILING DATE: 17-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-029.04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-767-942A-19

Query Match 100.0%; Score 46; DB 3; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITCV 9

```
Db      25 LQDIEITCV 33
|||||
RESULT 7
US-08-117-083-14
; Sequence 14, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Bourneil, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESS: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..271
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; the open reading frame."
US-08-117-083-14
Query Match      100.0%; Score 46; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LQDIEITCV 9
|||||
Db      26 LQDIEITCV 34
|||||
RESULT 8
US-09-485-885-21
; Sequence 21, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-23
Query Match      100.0%; Score 46; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LQDIEITCV 9
|||||
Db      136 LQDIEITCV 144
|||||
RESULT 10
US-09-252-991A-28397
; Sequence 28397, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
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;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 28397
;; LENGTH: 127
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28397

Query Match 87.0%; Score 40; DB 4; Length 127;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LODIEITCV 9
Db 32 LNDIEITCV 40

RESULT 11
US-08-912-129A-61
; Sequence 61, Application US/08912129A
; Patent No. 5922533
; GENERAL INFORMATION:
; APPLICANT: VALLARI, ANADRUZELA S.
; APPLICANT: HACKETT, JOHN JR.
; APPLICANT: HICKMAN, ROBERT K.
; APPLICANT: VARITEK, VINCENT A. JR.
; APPLICANT: NECKLAWS, ELIZABETH A.
; APPLICANT: GOLDEN, ALAN M.
; APPLICANT: BRENNAN, CATHERINE A.
; APPLICANT: DEVARE, SUSHIL G.
; TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS (Windows 95)
; SOFTWARE: Microsoft Word (ASCII format output)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,129A
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dancigers, Andreas M.
; REGISTRATION NUMBER: 32,652
; REFERENCE/DOCKET NUMBER: 6109.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-9803
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 873 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-912-129A-61

Query Match 80.4%; Score 37; DB 2; Length 873;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DIEITCV 9

Db 293 DIEITCV 299

RESULT 12
US-09-248-796A-19040
; Sequence 19040, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19040
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19040

Query Match 76.1%; Score 35; DB 4; Length 724;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QDIEITC 8
Db 488 EDIEITC 494

RESULT 13
US-09-519-232-74
; Sequence 74, Application US/09519232
; Patent No. 6528702
; GENERAL INFORMATION:
; APPLICANT: Salmeron, John
; APPLICANT: Weislo, Laura
; APPLICANT: Willits, Michael
; APPLICANT: Mengiste, Tesfaye
; TITLE OF INVENTION: NOVEL PLANT GENES AND USES THEREOF
; FILE REFERENCE: S-30857A/RTP2095
; CURRENT APPLICATION NUMBER: US/09/519,232
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-519-232-74

Query Match 73.9%; Score 34; DB 4; Length 369;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DIEITCV 9
Db 227 DLEITCI 233

RESULT 14
US-08-809-999D-17
; Sequence 17, Application US/08809999D
; Patent No. 6013765
; GENERAL INFORMATION:
; APPLICANT: Coullie, Pierre; Ikeda, Hideyuki;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules

;; TITLE OF INVENTION: Coding For Tumor Rejection Antigen Precursors DAGE and

;; TITLE OF INVENTION: Uses Thereof

;; NUMBER OF SEQUENCES: 18

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Fulbright & Jaworski, L.L.P.

;; STREET: 666 Fifth Avenue

;; CITY: New York City

;; STATE: New York

;; COUNTRY: USA

;; ZIP: 10103

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage

;; COMPUTER: IBM PS/2

;; OPERATING SYSTEM: PC-DOS

;; SOFTWARE: Wordperfect

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/809,999D

;; FILING DATE: 9-April-1997

;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/316,231

;; FILING DATE: 30-September-1994

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Hanson, No. 6013765man D.

;; REGISTRATION NUMBER: 30,946

;; REFERENCE/DOCKET NUMBER: LUD 5386.1

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (212) 318-3000

;; TELEFAX: (212) 752-5958

;; INFORMATION FOR SEQ ID NO: 17:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 509 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; FEATURE:

;; NAME/KEY: DAGE amino acid sequence

;; NAME/KEY: corresponding to SEQ ID NO:2

US-08-809-999D-17

Query Match

Best Local Similarity 73.9%; Score 34; DB 3; Length 509;

Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDIEITC 8

Db 235 IEDLEVTC 242

RESULT 15

US-09-069-637-17

; Sequence 17, Application US/09069637

; Patent No. 6022692

; GENERAL INFORMATION:

; APPLICANT: Coullie, Pierre; Ikeda, Hideyuki;

; APPLICANT: Boon-Palleur, Thierry

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; COUNTRY: USA

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/069,637

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds
(without alignments)
59.826 Million cell updates/sec

Title: US-08-170-344-22
Perfect score: 46
Sequence: 1 SLQDIETIC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/ECT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	9	17 US-10-751-845-129	Sequence 129, App
2	46	100.0	10	17 US-10-751-845-130	Sequence 130, App
3	46	100.0	42	17 US-10-751-845-152	Sequence 152, App
4	46	100.0	119	17 US-10-751-845-159	Sequence 159, App
5	46	100.0	158	16 US-10-800-023-27	Sequence 27, Appl
6	46	100.0	172	16 US-10-472-724-6	Sequence 6, Appli
7	46	100.0	236	17 US-10-751-845-157	Sequence 157, App
8	46	100.0	237	17 US-10-751-845-158	Sequence 158, App
9	46	100.0	261	17 US-10-751-845-160	Sequence 160, App
10	46	100.0	278	13 US-10-000-903-21	Sequence 21, Appl
11	46	100.0	278	17 US-10-899-771-21	Sequence 21, Appl

12	46	100.0	383	13	US-10-000-903-23	Sequence 23, Appl
13	46	100.0	383	17	US-10-899-771-23	Sequence 23, Appl
14	42	91.3	9	17	US-10-751-845-131	Sequence 131, App
15	39	84.8	282	15	US-10-243-552-539	Sequence 539, App
16	38	82.6	30	15	US-10-296-734-1354	Sequence 1354, App
17	38	82.6	509	14	US-10-037-340-254	Sequence 254, App
18	38	82.6	509	14	US-10-157-031-44	Sequence 44, Appl
19	38	82.6	509	15	US-10-170-385-87	Sequence 87, Appl
20	38	82.6	509	15	US-10-117-937-77	Sequence 77, Appl
21	38	82.6	509	15	US-10-173-999-2	Sequence 2, Appli
22	38	82.6	509	15	US-10-058-270A-110	Sequence 110, App
23	38	82.6	509	15	US-10-296-734-830	Sequence 830, App
24	38	82.6	509	16	US-10-657-022-77	Sequence 77, Appl
25	38	82.6	509	16	US-10-643-795A-92	Sequence 92, Appl
26	38	82.6	509	16	US-10-723-860-4358	Sequence 4358, App
27	38	82.6	509	17	US-10-482-029-136	Sequence 136, App
28	38	82.6	509	17	US-10-948-518-92	Sequence 92, Appl
29	38	82.6	509	17	US-10-794-514A-451	Sequence 451, App
30	38	82.6	509	17	US-10-871-708-8	Sequence 8, Appli
31	38	82.6	3541	15	US-10-296-734-1454	Sequence 1454, App
32	36	78.3	99	15	US-10-389-647-605	Sequence 605, App
33	36	78.3	162	16	US-10-767-701-58324	Sequence 58324, A
34	36	78.3	454	16	US-10-437-963-184385	Sequence 184385
35	36	78.3	462	16	US-10-425-115-227314	Sequence 227314, A
36	35	76.1	67	16	US-10-767-701-31617	Sequence 31617, A
37	35	76.1	179	16	US-10-425-115-246840	Sequence 246840,
38	35	76.1	195	15	US-10-424-599-205020	Sequence 205020,
39	35	76.1	1070	14	US-10-032-585-7389	Sequence 7389, App
40	35	76.1	2478	16	US-10-437-963-131742	Sequence 131742,
41	34	73.9	131	17	US-10-732-180-228	Sequence 228, App
42	34	73.9	140	15	US-10-316-194-9	Sequence 9, Appli
43	34	73.9	140	15	US-10-316-194-37	Sequence 37, Appl
44	34	73.9	140	17	US-10-732-180-9	Sequence 9, Appli
45	34	73.9	140	17	US-10-732-180-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-10-751-845-129
; Sequence 129, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiccz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 129
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-129

Query Match 100.0%; Score 46; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLQDIETIC 9

DB 1 SLQDIETIC 9

RESULT 2
 US-10-751-845-130
 ; Sequence 130, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiciz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 130
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Human Papilloma virus
 US-10-751-845-130

Query Match 100.0%; Score 46; DB 17; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.036;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLQDIEITC 9
 DB 1 SLQDIEITC 9

RESULT 3
 US-10-751-845-152
 ; Sequence 152, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiciz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 152
 ; LENGTH: 42
 ; TYPE: PRT
 ; ORGANISM: Human Papilloma virus
 US-10-751-845-152

Query Match 100.0%; Score 46; DB 17; Length 42;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLQDIEITC 9
 DB 16 SLQDIEITC 24

RESULT 4
 US-10-751-845-159

; Sequence 159, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiciz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 159
 ; LENGTH: 119
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial fusion sequence
 US-10-751-845-159

Query Match 100.0%; Score 46; DB 17; Length 119;
 Best Local Similarity 100.0%; Pred. No. 0.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLQDIEITC 9
 DB 16 SLQDIEITC 24

RESULT 5
 US-10-800-023-27
 ; Sequence 27, Application US/10800023
 ; Publication No. US20040258688A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Steinman, Ralph
 ; APPLICANT: Nussenzweig, Michel
 ; APPLICANT: Hawiger, Daniel
 ; APPLICANT: Bonifaz, Laura
 ; TITLE OF INVENTION: Enhanced Antigen Delivery and Modulation
 ; FILE REFERENCE: 600-1-081CONCIP1
 ; CURRENT APPLICATION NUMBER: US/10/800,023
 ; CURRENT FILING DATE: 2004-03-14
 ; PRIOR APPLICATION NUMBER: 09/925,284
 ; PRIOR FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: 09/586,704
 ; PRIOR FILING DATE: 2000-06-05
 ; PRIOR APPLICATION NUMBER: PCT/US96/01383
 ; PRIOR FILING DATE: 1996-01-31
 ; PRIOR APPLICATION NUMBER: 08/381,528
 ; PRIOR FILING DATE: 1995-01-31
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 158
 ; TYPE: PRT
 ; ORGANISM: human papilloma virus E6 protein
 US-10-800-023-27

Query Match 100.0%; Score 46; DB 16; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.67;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLQDIEITC 9
 DB 24 SLQDIEITC 32

RESULT 6
US-10-472-724-6
; Sequence 6, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-6

Query Match 100.0%; Score 46; DB 16; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.74; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLQDIEITC 9
Db 30 SLQDIEITC 38
|||||

RESULT 7
US-10-751-845-157
; Sequence 157, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-157

Query Match 100.0%; Score 46; DB 17; Length 236;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLQDIEITC 9
Db 133 SLQDIEITC 141
|||||

RESULT 8

US-10-751-845-158
; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-158

Query Match 100.0%; Score 46; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLQDIEITC 9
Db 134 SLQDIEITC 142
|||||

RESULT 9
US-10-751-845-160
; Sequence 160, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160

Query Match 100.0%; Score 46; DB 17; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLQDIEITC 9
Db 158 SLQDIEITC 166
|||||

```
RESULT 10
US-10-000-903-21
; Sequence 21, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-21

Query Match      100.0%; Score 46; DB 13; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLQDIEITC 9
Db 135 SLQDIEITC 143

RESULT 11
US-10-899-771-21
; Sequence 21, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 18)
US-10-899-771-21

Query Match      100.0%; Score 46; DB 17; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLQDIEITC 9
Db 135 SLQDIEITC 143

RESULT 12
US-10-000-903-23
; Sequence 23, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-23

Query Match      100.0%; Score 46; DB 13; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLQDIEITC 9
Db 135 SLQDIEITC 143

RESULT 13
US-10-899-771-23
; Sequence 23, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 18)
US-10-899-771-23

Query Match      100.0%; Score 46; DB 17; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLQDIEITC 9
Db 135 SLQDIEITC 143
```



```
RESULT 14
US-10-751-845-131
; Sequence 131, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-131

Query Match      91.3%; Score 42; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LQDIEITC 9
Db      1 LQDIEITC 8

RESULT 15
US-10-243-552-539
; Sequence 539, Application US/10243552
; Publication No. US20030224379A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Ma, Yunqing
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 807A
; CURRENT APPLICATION NUMBER: US/10/243,552
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/322,511
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/04927
; PRIOR FILING DATE: 2001-02-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 998
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 539
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-243-552-539

Query Match      84.8%; Score 39; DB 15; Length 282;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLQDIEITC 9
Db      116 SLQDLDLTC 124

Search completed: June 29, 2005, 04:19:14
Job time : 58.85 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-22

Perfect score: 46

Sequence: 1 SLQDIETC 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	100.0	15	3	US-08-159-339A-1176
2	46	100.0	32	1	Sequence 1176, Ap
3	46	100.0	32	1	Sequence 2, Appli
4	46	100.0	32	3	US-08-164-768-2
5	46	100.0	158	2	US-08-247-904B-10
6	46	100.0	158	3	US-08-767-942A-19
7	46	100.0	271	1	US-08-117-083-14
8	46	100.0	278	3	US-09-485-885-21
9	42	91.3	383	3	US-09-485-885-23
10	38	82.6	509	3	US-08-159-339A-86
11	38	82.6	509	3	US-09-069-637-17
12	38	82.6	509	3	US-09-322-360-17
13	38	82.6	509	3	US-09-131-831B-17
14	38	82.6	528	4	US-09-949-016-11233
15	36	78.3	127	4	US-09-252-991A-28397
16	35	76.1	724	4	US-09-248-796A-19040
17	34	73.9	519	4	US-09-720-655B-1
18	34	73.9	520	3	US-08-964-127-2
19	34	73.9	520	3	US-09-496-692-2
20	34	73.9	520	4	US-10-000-273-2
21	34	73.9	3135	1	US-08-323-170B-2
22	34	73.9	3135	3	US-08-954-441-2
23	33	71.7	286	4	US-09-328-352-7626
24	33	71.7	839	4	US-09-949-016-10846
25	33	71.7	873	2	US-08-912-129A-61
26	32	69.6	53	4	US-09-270-767-61394
27	32	69.6	303	4	US-09-270-767-45862

28	32	69.6	402	4	US-09-270-767-46012	Sequence 46012, A
29	32	69.6	873	4	US-09-543-681A-6927	Sequence 6927, Ap
30	31	67.4	123	4	US-09-543-681A-4522	Sequence 4522, Ap
31	31	67.4	126	4	US-09-489-039A-8230	Sequence 8230, Ap
32	31	67.4	205	3	US-09-134-001C-4766	Sequence 4766, Ap
33	31	67.4	369	4	US-09-519-232-74	Sequence 74, Appli
34	31	67.4	592	4	US-08-248-796A-17389	Sequence 17389, A
35	31	67.4	733	4	US-09-270-767-41626	Sequence 41626, A
36	31	67.4	826	4	US-09-248-796A-14387	Sequence 14387, A
37	31	67.4	852	4	US-09-585-858-19	Sequence 19, Appli
38	31	67.4	852	4	US-10-270-878-19	Sequence 19, Appli
39	31	67.4	1194	2	US-08-680-326-35	Sequence 35, Appli
40	31	67.4	4968	4	US-09-424-783-5	Sequence 5, Appli
41	30	65.2	10	3	US-09-051-529-1	Sequence 1, Appli
42	30	65.2	281	4	US-09-949-016-6831	Sequence 6831, Ap
43	30	65.2	322	3	US-08-964-127-6	Sequence 6, Appli
44	30	65.2	322	3	US-09-496-692-6	Sequence 6, Appli
45	30	65.2	322	4	US-10-000-273-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-08-159-339A-1176
; Sequence 1176, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1176:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-1176

Query Match 100.0%; Score 46; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.02; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLQDIEITC 9
| | | | |
Db 3 SLQDIEITC 11
| | | | |

RESULT 2

US-08-466-285-2
; Sequence 2, Application US/08466285
; Patent No. 5753233
; GENERAL INFORMATION:
; APPLICANT: Bleul, Conrad
; APPLICANT: Gissmann, Lutz
; APPLICANT: Muller, Martin
; TITLE OF INVENTION: Seroreactive Epitopes On Proteins Of
; TITLE OF INVENTION: Human Papillomavirus (HPV)18
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,285
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/164,768
; FILING DATE: 10-DEC-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/947,992
; FILING DATE: 21-SEP-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/696,953
; FILING DATE: 08-MAY-1991
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P 40 15 044.5
; FILING DATE: 10-MAY-1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Manspeizer, David A.
; REGISTRATION NUMBER: 37,540
; REFERENCE/DOCKET NUMBER: 05552.1075-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-466-285-2

Query Match 100.0%; Score 46; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.044;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLQDIEITC 9
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Db 19 SLQDIEITC 27
| | | | |

RESULT 3

US-08-164-768-2
; Sequence 2, Application US/08164768
; Patent No. 6322794
; GENERAL INFORMATION:
; APPLICANT: BLEUL, Conrad
; APPLICANT: GISSMANN, Lutz
; APPLICANT: MULLER, Martin
; TITLE OF INVENTION: SEROREACTIVE EPITOPES ON PROTEINS OF
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS (HPV) 18
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; ADDRESSEE: DUNNER, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,768
; FILING DATE: 10-DEC-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortman, David S.
; REGISTRATION NUMBER: 33,694
; REFERENCE/DOCKET NUMBER: 05552.1075-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-164-768-2

Query Match 100.0%; Score 46; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLQDIEITC 9
| | | | |
Db 19 SLQDIEITC 27
| | | | |

RESULT 4

US-08-247-904B-10
; Sequence 10, Application US/08247904B
; Patent No. 5981899
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Eckstein, Jens W.
; APPLICANT: Draetta, Giulio
; TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square

```
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/247,904B
; FILING DATE: 23-MAY-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-247-904B-10

Query Match 100.0%; Score 46; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLQDIEITC 9
DB 24 SLQDIEITC 32

RESULT 5
US-08-767-942A-19
; Sequence 19, Application US/08767942A
; Patent No. 6068982
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Chiu, M. Isabel
; APPLICANT: Berlin, Vivian
; APPLICANT: Damagnez, Veronique
; APPLICANT: Draetta, Giulio
; APPLICANT: Guillaume, Cottarel
; TITLE OF INVENTION: UBQUITIN CONJUGATING ENZYMES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,942A
; FILING DATE: 17-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 19:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-767-942A-19

Query Match 100.0%; Score 46; DB 3; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLQDIEITC 9
DB 24 SLQDIEITC 32

RESULT 6
US-08-117-083-14
; Sequence 14, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Bourneil, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..271
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; the open reading frame."
; US-08-117-083-14

Query Match 100.0%; Score 46; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLQDIEITC 9
DB 25 SLQDIEITC 33
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RESULT 7
US-09-485-885-21
; Sequence 21, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-21

Query Match      100.0%; Score 46; DB 3; Length 278;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLQDIEITC 9
Db      135 SLQDIEITC 143

RESULT 8
US-09-485-885-23
; Sequence 23, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-23

Query Match      100.0%; Score 46; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLQDIEITC 9
Db      135 SLQDIEITC 143

RESULT 9
US-08-159-339A-86
; Sequence 86, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-86

Query Match      91.3%; Score 42; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LQDIEITC 9
Db      1 LQDIEITC 8

RESULT 10
US-08-809-999D-17
; Sequence 17, Application US/08809999D
; Patent No. 6013765
; GENERAL INFORMATION:
; APPLICANT: Coulie, Pierre; Ikeda, Hideyuki;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules
; TITLE OF INVENTION: Coding For Tumor Rejection Antigen Precursors DAGE and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
```

; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,999D
; FILING DATE: 9-April-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/316,231
; FILING DATE: 30-September-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No 6013765man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5386.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: DAGE amino acid sequence
; NAME/KEY: corresponding to SEQ ID NO:2
US-08-809-999D-17

Query Match 82.6%; Score 38; DB 3; Length 509;
Best Local Similarity 55.6%; Pred. No. 27;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLQDIEITC 9
|:|:|:|:
Db 234 SIEDLEVTC 242

RESULT 11
US-09-069-637-17
; Sequence 17, Application US/09069637
; Patent No. 6022692
; GENERAL INFORMATION:
; APPLICANT: Coullie, Pierre, Ikeda, Hideyuki;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules
; TITLE OF INVENTION: Coding For Tumor Rejection Antigen Precursors DAGE and Uses Th
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,637
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,999
; FILING DATE: 9-April-1997
; APPLICATION NUMBER: 08/316,231

; FILING DATE: 30-September-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6022692man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5386.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: DAGE amino acid sequence
; NAME/KEY: corresponding to SEQ ID NO:2
US-09-069-637-17

Query Match 82.6%; Score 38; DB 3; Length 509;
Best Local Similarity 55.6%; Pred. No. 27;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLQDIEITC 9
|:|:|:|:
Db 234 SIEDLEVTC 242

RESULT 12
US-09-322-360-17
; Sequence 17, Application US/09322360
; Patent No. 6297050
; GENERAL INFORMATION:
; APPLICANT: Coullie, Pierre, Ikeda, Hideyuki;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules
; TITLE OF INVENTION: Coding For Tumor Rejection Antigen Precursors DAGE and
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/322,360
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,999
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6297050man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5386.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: DAGE amino acid sequence

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; NAME/KEY: corresponding to SEQ ID NO:2
US-09-322-360-17

Query Match      82.6%; Score 38; DB 3; Length 509;
Best Local Similarity 55.6%; Pred. No. 27;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLQDIEITC 9
Db      234 SIEDLEVTC 242

RESULT 13
US-09-131-831B-17
; GENERAL INFORMATION:
; APPLICANT: Coullie, Pierre; Ikeda, Hideyuki; Boon-
;           Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules
;           Coding For Tumor Rejection Antigen Precursors DAGE and
;           Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/131,831B
; FILING DATE: 11-Aug-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,999
; FILING DATE: 9-April-1997
; APPLICATION NUMBER: 08/316,231
; FILING DATE: 30-September-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6339149man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5386.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3100
; TELEFAX: (212) 318-3400
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-131-831B-17

Query Match      82.6%; Score 38; DB 3; Length 509;
Best Local Similarity 55.6%; Pred. No. 27;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLQDIEITC 9
Db      234 SIEDLEVTC 242

RESULT 14
US-09-949-016-11233
; Sequence 11233, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;           WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11233
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11233

Query Match      82.6%; Score 38; DB 4; Length 528;
Best Local Similarity 55.6%; Pred. No. 28;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLQDIEITC 9
Db      253 SIEDLEVTC 261

RESULT 15
US-09-252-991A-28397
; Sequence 28397, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;           AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28397
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28397

Query Match      78.3%; Score 36; DB 4; Length 127;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LQDIEITC 9
Db      32 LNDIEVTC 39

Search completed: June 28, 2005, 21:33:20
Job time : 17 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 03:24:20 ; Search time 57.85 Seconds
(without alignments)
59.826 Million cell updates/sec

Title: US-08-170-344-21

Perfect score: 49

Sequence: 1 KLPDLCTEL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/FCT_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
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21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	16	US-10-472-661-1
2	49	100.0	9	17	US-10-751-845-124
3	49	100.0	42	17	US-10-751-845-152
4	49	100.0	119	17	US-10-751-845-159
5	49	100.0	158	16	US-10-800-023-27
6	49	100.0	172	16	US-10-472-724-6
7	49	100.0	236	17	US-10-751-845-157
8	49	100.0	237	17	US-10-751-845-158
9	49	100.0	261	17	US-10-751-845-160
10	49	100.0	278	13	US-10-000-903-21
11	49	100.0	278	17	US-10-899-771-21
					Sequence 1, Appli
					Sequence 124, App
					Sequence 152, App
					Sequence 159, App
					Sequence 27, Appli
					Sequence 6, Appli
					Sequence 157, App
					Sequence 158, App
					Sequence 160, App
					Sequence 21, Appli

12	49	100.0	383	13	US-10-000-903-23	Sequence 23, Appli
13	49	100.0	383	17	US-10-899-771-23	Sequence 23, Appli
14	43	87.8	9	9	US-09-909-460-101	Sequence 101, App
15	43	87.8	9	11	US-09-872-836-101	Sequence 101, App
16	43	87.8	9	14	US-10-133-210-278	Sequence 278, App
17	43	87.8	9	16	US-10-777-053-546	Sequence 546, App
18	43	87.8	9	16	US-10-837-217-546	Sequence 546, App
19	43	87.8	9	17	US-10-758-970-101	Sequence 101, App
20	43	87.8	9	17	US-10-484-063-1	Sequence 1, Appli
21	43	87.8	9	17	US-10-751-845-55	Sequence 55, Appli
22	43	87.8	15	16	US-10-476-570-20	Sequence 20, Appli
23	43	87.8	20	17	US-10-751-845-64	Sequence 64, Appli
24	43	87.8	21	16	US-10-476-570-8	Sequence 8, Appli
25	43	87.8	30	16	US-10-476-570-53	Sequence 53, Appli
26	43	87.8	30	17	US-10-858-384-4	Sequence 4, Appli
27	43	87.8	32	16	US-10-476-570-9	Sequence 9, Appli
28	43	87.8	33	16	US-10-476-570-19	Sequence 19, Appli
29	43	87.8	117	17	US-10-751-845-126	Sequence 126, App
30	43	87.8	151	14	US-10-177-390-6	Sequence 6, Appli
31	43	87.8	151	17	US-10-484-063-20	Sequence 20, Appli
32	43	87.8	151	17	US-10-484-063-27	Sequence 27, Appli
33	43	87.8	158	17	US-10-858-384-2	Sequence 2, Appli
34	43	87.8	158	17	US-10-367-057-16	Sequence 16, Appli
35	43	87.8	171	16	US-10-472-724-2	Sequence 2, Appli
36	43	87.8	266	9	US-09-367-309A-1	Sequence 1, Appli
37	43	87.8	273	13	US-10-000-903-4	Sequence 4, Appli
38	43	87.8	273	17	US-10-899-771-4	Sequence 4, Appli
39	43	87.8	292	13	US-10-000-903-10	Sequence 10, Appli
40	43	87.8	292	17	US-10-899-771-10	Sequence 10, Appli
41	43	87.8	371	13	US-10-000-903-6	Sequence 6, Appli
42	43	87.8	371	17	US-10-899-771-6	Sequence 6, Appli
43	43	87.8	390	13	US-10-000-903-14	Sequence 14, Appli
44	43	87.8	390	17	US-10-899-771-14	Sequence 14, Appli
45	43	87.8	536	15	US-10-367-095-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-10-472-661-1
; Sequence 1, Application US/10472661
; Publication No. US20040106551A1
; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS IMMUNOREACTIVE
; FILE REFERENCE: 14014.0406U2
; CURRENT FILING DATE: 2003-09-22
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: PCT/US02/09261
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/278,520
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note =
; OTHER INFORMATION: synthetic construct
US-10-472-661-1

Query Match 100.0%; Score 49; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KLPDLCTEL 9
Db 1 KLPDLCTEL 9

RESULT 2

US-10-751-845-124
 ; Sequence 124, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiciz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 124
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Human Papilloma virus
 US-10-751-845-124

Query Match 100.0%; Score 49; DB 17; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLPDLCTEL 9
 |||||
 Db 1 KLPDLCTEL 9

RESULT 3

US-10-751-845-152
 ; Sequence 152, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiciz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 152
 ; LENGTH: 42
 ; TYPE: PRT
 ; ORGANISM: Human Papilloma virus
 US-10-751-845-152

Query Match 100.0%; Score 49; DB 17; Length 42;
 Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLPDLCTEL 9
 |||||
 Db 5 KLPDLCTEL 13

RESULT 4

US-10-751-845-159
 ; Sequence 159, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiciz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 159
 ; LENGTH: 119
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial fusion sequence
 US-10-751-845-159

Query Match 100.0%; Score 49; DB 17; Length 119;
 Best Local Similarity 100.0%; Pred. No. 0.3; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLPDLCTEL 9
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 Db 5 KLPDLCTEL 13

RESULT 5

US-10-800-023-27
 ; Sequence 27, Application US/10800023
 ; Publication No. US20040258688A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Steinman, Ralph
 ; APPLICANT: Nussenzweig, Michel
 ; APPLICANT: Hawiger, Daniel
 ; APPLICANT: Bonifaz, Laura
 ; TITLE OF INVENTION: Enhanced Antigen Delivery and Modulation
 ; FILE REFERENCE: 600-1-081CONCIPI
 ; CURRENT APPLICATION NUMBER: US/10/800,023
 ; CURRENT FILING DATE: 2004-03-14
 ; PRIOR APPLICATION NUMBER: 09/925,284
 ; PRIOR FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: 09/586,704
 ; PRIOR FILING DATE: 2000-06-05
 ; PRIOR APPLICATION NUMBER: PCT/US96/01383
 ; PRIOR FILING DATE: 1996-01-31
 ; PRIOR APPLICATION NUMBER: 08/381,528
 ; PRIOR FILING DATE: 1995-01-31
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 158
 ; TYPE: PRT
 ; ORGANISM: human papilloma virus E6 protein
 US-10-800-023-27

Query Match 100.0%; Score 49; DB 16; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.4; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLPDLCTEL 9
 |||||
 Db 13 KLPDLCTEL 21

RESULT 6
US-10-472-724-6
; Sequence 6, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-6

Query Match 100.0%; Score 49; DB 16; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.44; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0

QY 1 KLPDLCTEL 9
| | | | | | | |
DB 19 KLPDLCTEL 27

RESULT 7
US-10-751-845-157
; Sequence 157, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-157

Query Match 100.0%; Score 49; DB 17; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.6; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0

QY 1 KLPDLCTEL 9
| | | | | | | |
DB 122 KLPDLCTEL 130

RESULT 8
US-10-751-845-158
; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-158

Query Match 100.0%; Score 49; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.6; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0

QY 1 KLPDLCTEL 9
| | | | | | | |
DB 123 KLPDLCTEL 131

RESULT 9
US-10-751-845-160
; Sequence 160, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160

Query Match 100.0%; Score 49; DB 17; Length 261;
Best Local Similarity 100.0%; Pred. No. 0.66; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0

QY 1 KLPDLCTEL 9
| | | | | | | |
DB 147 KLPDLCTEL 155

```

RESULT 10
US-10-000-903-21
; Sequence 21, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-21

Query Match      100.0%; Score 49; DB 13; Length 278;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
Db 124 KLPDLCTEL 132

RESULT 11
US-10-899-771-21
; Sequence 21, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 18)
US-10-899-771-21

Query Match      100.0%; Score 49; DB 17; Length 278;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
Db 124 KLPDLCTEL 132

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```

RESULT 12
US-10-000-903-23
; Sequence 23, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-23

Query Match      100.0%; Score 49; DB 13; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
Db 124 KLPDLCTEL 132

RESULT 13
US-10-899-771-23
; Sequence 23, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and B6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 18)
US-10-899-771-23

Query Match      100.0%; Score 49; DB 17; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
Db 124 KLPDLCTEL 132

```

Db 124 KLPDLCTEL 132

RESULT 14

US-09-909-460-101
; Sequence 101, Application US/09909460
; Publication No. US20020182258A1
; GENERAL INFORMATION:
; APPLICANT: Lunsford, Lynn B.
; APPLICANT: Putnam, David
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
; TITLE OF INVENTION: ACID
; FILE REFERENCE: 08191/014001
; CURRENT APPLICATION NUMBER: US/09/909,460
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-909-460-101

Query Match 87.8%; Score 43; DB 9; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KLPDLCTEL 9

Db 1 KLPDLCTEL 9

RESULT 15

US-09-872-836-101
; Sequence 101, Application US/09872836
; Publication No. US20040142475A1
; GENERAL INFORMATION:
; APPLICANT: Barman, Shikha P.
; APPLICANT: McKeever, Una
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 08191-018001
; CURRENT APPLICATION NUMBER: US/09/872,836
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,830
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-836-101

Query Match 87.8%; Score 43; DB 11; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KLPDLCTEL 9

Db 1 KLPDLCTEL 9

Search completed: June 29, 2005, 04:19:13
Job time : 59.85 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 19:29:22 ; Search time 16.95 Seconds
(without alignments)
39.637 Million cell updates/sec

Title: US-08-170-344-21
Perfect score: 49
Sequence: 1 KLPDLCTEL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	32	1	US-08-466-285-2
2	49	100.0	32	3	US-08-164-788-2
3	49	100.0	158	2	US-08-247-904B-10
4	49	100.0	158	3	US-08-767-942A-19
5	49	100.0	271	1	US-08-117-083-14
6	49	100.0	278	3	US-09-485-885-21
7	49	100.0	383	3	US-09-485-885-23
8	43	87.8	9	1	US-08-787-547-101
9	43	87.8	9	4	US-09-601-729-274
10	43	87.8	20	2	US-08-934-915-159
11	43	87.8	30	1	US-08-363-586-4
12	43	87.8	30	4	US-09-980-523A-4
13	43	87.8	158	4	US-09-980-523A-2
14	43	87.8	162	1	US-08-316-239B-3
15	43	87.8	162	1	US-08-316-239B-4
16	43	87.8	172	3	US-08-860-165-14
17	43	87.8	172	3	US-09-359-382-14
18	43	87.8	182	1	US-08-117-083-10
19	43	87.8	266	3	US-08-860-165-10
20	43	87.8	266	3	US-09-359-382-10
21	43	87.8	266	4	US-09-367-309A-1
22	43	87.8	273	3	US-09-485-885-4
23	43	87.8	292	3	US-09-485-885-10
24	43	87.8	371	3	US-09-485-885-6
25	43	87.8	390	3	US-09-485-885-14
26	40	81.6	504	4	US-09-198-452A-1036
27	40	81.6	504	4	US-09-438-185A-966

28	36	73.5	89	4	US-09-543-681A-7711	Sequence 7711, Ap
29	36	73.5	108	4	US-09-328-352-4646	Sequence 4646, Ap
30	36	73.5	117	4	US-09-540-236-3305	Sequence 3305, Ap
31	36	73.5	410	4	US-09-489-039A-10689	Sequence 10689, A
32	35	71.4	148	4	US-09-270-767-38382	Sequence 38382, A
33	35	71.4	148	4	US-09-270-767-53599	Sequence 53599, A
34	34	69.4	161	4	US-09-673-395A-248	Sequence 248, App
35	34	69.4	199	4	US-09-902-540-10941	Sequence 10941, A
36	34	69.4	307	4	US-09-198-452A-10941	Sequence 10941, A
37	34	69.4	341	3	US-08-481-968A-11	Sequence 11, Appl
38	34	69.4	341	3	US-08-154-712B-11	Sequence 11, Appl
39	34	69.4	341	4	US-09-947-925A-11	Sequence 11, Appl
40	34	69.4	453	4	US-09-686-583B-12	Sequence 12, Appl
41	34	69.4	530	4	US-09-585-174-6	Sequence 6, Appl
42	34	69.4	611	4	US-09-438-185A-970	Sequence 970, App
43	33	67.3	53	4	US-09-513-999C-7763	Sequence 7763, Ap
44	33	67.3	73	4	US-09-270-767-62327	Sequence 62327, A
45	33	67.3	138	2	US-08-609-049A-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-466-285-2
; Sequence 2, Application US/08466285
; Patent No. 5753233
; GENERAL INFORMATION:
; APPLICANT: Bleul, Conrad
; APPLICANT: Gissmann, Lutz
; TITLE OF INVENTION: Seroreactive Epitopes On Proteins Of
; TITLE OF INVENTION: Human Papillomavirus (HPV)18
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,285
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/164,768
; FILING DATE: 10-DEC-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/947,992
; FILING DATE: 21-SEP-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/696,953
; FILING DATE: 08-MAY-1991
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P 40 15 044.5
; FILING DATE: 10-MAY-1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Manepeizer, David A.
; REGISTRATION NUMBER: 37,540
; REFERENCE/DOCKET NUMBER: 05552.1075-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)408-4000

TELEFAX: (202)408-4400
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 32 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-466-285-2

Query Match 100.0%; Score 49; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
 Db 8 KLPDLCTEL 16

RESULT 2

US-08-164-768-2
 ; Sequence 2, Application US/08164768
 ; Patent No. 6322794
 ; GENERAL INFORMATION:

APPLICANT: BLEUL, Conrad
 APPLICANT: GISSMANN, Lutz
 APPLICANT: MULLER, Martin
 ; TITLE OF INVENTION: SPOROACTIVE EPITOPES ON PROTEINS OF
 ; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS (HPV) 18
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
 ADDRESSEE: DUNNER, L.L.P.
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/164,768

FILING DATE: 10-DEC-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Forman, David S.

REGISTRATION NUMBER: 33,694

REFERENCE/DOCKET NUMBER: 05552.1075-02000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-164-768-2

Query Match 100.0%; Score 49; DB 3; Length 32;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
 Db 8 KLPDLCTEL 16

RESULT 3

US-08-247-904B-10
 ; Sequence 10, Application US/08247904B
 ; Patent No. 5981699
 ; GENERAL INFORMATION:

APPLICANT: Rolfe, Mark

APPLICANT: Eckstein, Jens W.

APPLICANT: Draetta, Giulio

TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, Hoag & Eliot

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/247,904B

FILING DATE: 23-MAY-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MIV-029.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 832-1000

TELEFAX: (617) 832-7000

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 158 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-247-904B-10

Query Match 100.0%; Score 49; DB 2; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9

Db 13 KLPDLCTEL 21

RESULT 4

US-08-767-942A-19

; Sequence 19, Application US/08767942A

; Patent No. 6068982

; GENERAL INFORMATION:

APPLICANT: Rolfe, Mark

APPLICANT: Chiu, M. Isabel

APPLICANT: Berlin, Vivian

APPLICANT: Damagnez, Veronique

APPLICANT: Draetta, Giulio

APPLICANT: Guillaume, Cottarel

TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS


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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,942A
; FILING DATE: 17-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-767-942A-19

Query Match      100.0%; Score 49; DB 3; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLPDLCTEL 9
DB      13 KLPDLCTEL 21

RESULT 5
US-08-117-083-14
; Sequence 14, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Bournelli, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-56783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..271
```

```
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
; US-08-117-083-14

Query Match      100.0%; Score 49; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLPDLCTEL 9
DB      14 KLPDLCTEL 22

RESULT 6
US-09-485-885-21
; Sequence 21, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-21

Query Match      100.0%; Score 49; DB 3; Length 278;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLPDLCTEL 9
DB      124 KLPDLCTEL 132

RESULT 7
US-09-485-885-23
; Sequence 23, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-23
```

Query Match 100.0%; Score 49; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLPDLCTEL 9
DB 124 KLPDLCTEL 132

RESULT 8

US-08-787-547-101
; Sequence 101, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Curley, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-787-547-101

Query Match 87.8%; Score 43; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLPDLCTEL 9
DB 1 KLPDLCTEL 9

RESULT 9

US-09-601-729-274
; Sequence 274, Application US/09601729
; Patent No. 6683052
; GENERAL INFORMATION:
; APPLICANT: THIAM, KADER
; APPLICANT: AURIAULT, CLAUDE
; APPLICANT: GRAS-MASSE, HELENE

; APPLICANT: LOING, ESTELLE
; APPLICANT: VERWAERDE, CLAUDE
; APPLICANT: GUILLET, JEAN GERARD
; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
; TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: USB-97-AU-IN
; CURRENT APPLICATION NUMBER: US/09/601,729
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: PCT/FR99/00259
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 98 01439
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 274
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-601-729-274

Query Match 87.8%; Score 43; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLPDLCTEL 9
DB 1 KLPDLCTEL 9

RESULT 10

US-08-934-915-159
; Sequence 159, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 159:

SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-934-915-159

Query Match 87.8%; Score 43; DB 2; Length 20;
 Best Local Similarity 88.9%; Pred. No. 0.17;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
 ||| |||||
 Db 2 KLPQLCTEL 10

RESULT 11

US-08-363-586-4
 ; Sequence 4, Application US/08363586
 ; Patent No. 5629161

GENERAL INFORMATION:

APPLICANT: Mueller, Martin
 APPLICANT: Gissmann, Lutz
 TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ADDRESS: Dunner
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/363,586
 FILING DATE: 23-DEC-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/909,296

FILING DATE: 09-JUL-1992

APPLICATION NUMBER: EP 9111720.8

FILING DATE: 13-JUL-1991

ATTORNEY/AGENT INFORMATION:

NAME: Wadler, Linda A.

REGISTRATION NUMBER: 33,218

REFERENCE/DOCKET NUMBER: 02481-1195-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-363-586-4

Query Match 87.8%; Score 43; DB 1; Length 30;
 Best Local Similarity 88.9%; Pred. No. 0.26;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
 ||| |||||
 Db 11 KLPQLCTEL 19

RESULT 12

US-09-980-523A-4
 ; Sequence 4, Application US/09980523A
 ; Patent No. 6783763

GENERAL INFORMATION:

APPLICANT: CHOPPIN, JEANNINE
 APPLICANT: BOURGAULT VILLADA, ISABELLE
 APPLICANT: GUILLET, JEAN-GERARD
 APPLICANT: CONNAN, FRANCINE
 APPLICANT: FERRIES, ESTELLE
 TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
 TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
 TITLE OF INVENTION: PARTICULARLY IN VACCINATION

FILE REFERENCE: WO/01 AO INS

CURRENT APPLICATION NUMBER: US/09/980,523A

CURRENT FILING DATE: 2002-04-29

PRIOR APPLICATION NUMBER: PCT/FR00/01513

PRIOR FILING DATE: 2000-05-31

PRIOR APPLICATION NUMBER: FR 99/07012

PRIOR FILING DATE: 1999-06-03

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 30

TYPE: PRT

ORGANISM: Human Papillomavirus

US-09-980-523A-4

Query Match 87.8%; Score 43; DB 4; Length 30;

Best Local Similarity 88.9%; Pred. No. 0.26;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
 ||| |||||
 Db 4 KLPQLCTEL 12

RESULT 13

US-09-980-523A-2

; Sequence 2, Application US/09980523A

; Patent No. 6783763

GENERAL INFORMATION:

APPLICANT: CHOPPIN, JEANNINE

APPLICANT: BOURGAULT VILLADA, ISABELLE

APPLICANT: GUILLET, JEAN-GERARD

APPLICANT: CONNAN, FRANCINE

APPLICANT: FERRIES, ESTELLE

TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7

TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE

TITLE OF INVENTION: PARTICULARLY IN VACCINATION

FILE REFERENCE: WO/01 AO INS

CURRENT APPLICATION NUMBER: US/09/980,523A

CURRENT FILING DATE: 2002-04-29

PRIOR APPLICATION NUMBER: PCT/FR00/01513

PRIOR FILING DATE: 2000-05-31

PRIOR APPLICATION NUMBER: FR 99/07012

PRIOR FILING DATE: 1999-06-03

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 158

TYPE: PRT

ORGANISM: Human Papillomavirus

US-09-980-523A-2

Query Match 87.8%; Score 43; DB 4; Length 158;

Best Local Similarity 88.9%; Pred. No. 1.5;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
 ||| |||||
 Db 18 KLPQLCTEL 26

```
RESULT 14
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316.239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 87.8%; Score 43; DB 1; Length 162;
Best Local Similarity 88.9%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
Db 18 KLPQLCTEL 26

Search completed: June 28, 2005, 21:33:20
Job time : 18 secs

RESULT 15
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316.239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 87.8%; Score 43; DB 1; Length 162;
Best Local Similarity 88.9%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
Db 18 KLPQLCTEL 26

Search completed: June 28, 2005, 21:33:20
Job time : 18 secs
```

```
;
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316.239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 87.8%; Score 43; DB 1; Length 162;
Best Local Similarity 88.9%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLPDLCTEL 9
Db 18 KLPQLCTEL 26

Search completed: June 28, 2005, 21:33:20
Job time : 18 secs
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RESULT 1
 US-09-759-960-2
 ; Sequence 2, Application US/09759960
 ; Patent No. US2001000639A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiczo, Roman M.
 ; APPLICANT: Collins, Edward J.
 ; APPLICANT: Hedley, Mary Lynn
 ; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
 ; TITLE OF INVENTION: PROTEIN
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: Fish & Franklin, P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/759,960
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/169,425
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fraser, Janis K.
 ; REGISTRATION NUMBER: 34,819
 ; REFERENCE/DOCKET NUMBER: 08191/004002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070
TELEFAX: 617-543-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-09-759-960-2

Query Match 91.5%; Score 43; DB 9; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9

Db 1 TLGIVCPIC 9

RESULT 2

US-09-909-460-111

Sequence 111, Application US/09909460
Publication No. US20020182258A1

GENERAL INFORMATION:

APPLICANT: Lunsford, Lynn B.
APPLICANT: Putnam, David
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
FILE REFERENCE: 08191/014001
CURRENT APPLICATION NUMBER: US/09/909,460
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 111
LENGTH: 9
TYPE: PRT
ORGANISM: Human papilloma virus

US-09-909-460-111

Query Match 91.5%; Score 43; DB 9; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9

Db 1 TLGIVCPIC 9

RESULT 3

US-09-872-836-115

Sequence 115, Application US/09872836
Publication No. US20040142475A1

GENERAL INFORMATION:

APPLICANT: Barman, Shikha P.
APPLICANT: McKeever, Una
APPLICANT: Hedley, Mary Lynne
TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
FILE REFERENCE: 08191-018001
CURRENT APPLICATION NUMBER: US/09/872,836
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/208,830
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 120
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 115
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens

US-09-872-836-115

Query Match 91.5%; Score 43; DB 11; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9

Db 1 TLGIVCPIC 9

RESULT 4

US-10-128-711-68

Sequence 68, Application US/10128711
Publication No. US20030099634A1

GENERAL INFORMATION:

APPLICANT: VITIELLO, Maria A.
CHESTNUT, Robert W.
SETTE, Alessandro D.
CELIS, Esteban
GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
CTL IMMUNITY
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/128,711
FILING DATE: 22-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-10-128-711-68

Query Match 91.5%; Score 43; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9

```
Db          1 TLGIVCPIC 9
||||| |||
RESULT 5
US-10-472-661-5
; Sequence 5, Application US/10472661
; Publication No. US20040106551A1
; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Berzofsky, Jay A.
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS IMMUNOREACTIVE
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 14014.040602
; CURRENT APPLICATION NUMBER: US/10/472,661
; PRIOR FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: PCT/US02/09261
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/278,520
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note =
; OTHER INFORMATION: synthetic construct
US-10-472-661-5
Query Match          91.5%; Score 43; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1 TLGIVAPIC 9
||||| |||
Db          1 TLGIVCPIC 9
||||| |||
RESULT 6
US-10-472-661-6
; Sequence 6, Application US/10472661
; Publication No. US20040106551A1
; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Berzofsky, Jay A.
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS IMMUNOREACTIVE
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 14014.040602
; CURRENT APPLICATION NUMBER: US/10/472,661
; PRIOR FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: PCT/US02/09261
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/278,520
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note =
; OTHER INFORMATION: synthetic construct
US-10-472-661-6
Query Match          91.5%; Score 43; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1 TLGIVAPIC 9
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Db          1 TLGIVCPIC 9
||||| |||
RESULT 7
US-10-777-053-326
; Sequence 326, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANNK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 326
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papillomavirus 16
US-10-777-053-326
Query Match          91.5%; Score 43; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1 TLGIVAPIC 9
||||| |||
Db          1 TLGIVCPIC 9
||||| |||
RESULT 8
US-10-777-053-490
; Sequence 490, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANNK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 490
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Himetobi P Virus (HiPV)
US-10-777-053-490
Query Match          91.5%; Score 43; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1 TLGIVAPIC 9
||||| |||
Db          1 TLGIVCPIC 9
||||| |||
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RESULT 9
US-10-837-217-326
; Sequence 326, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANNK.022C2
; CURRENT APPLICATION NUMBER: US/10/837,217
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 326
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papillomavirus 16
US-10-837-217-326

Query Match          91.5%; Score 43; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLGIVAPIC 9
   |||||
Db 1 TLGIVCPIC 9

RESULT 10
US-10-837-217-490
; Sequence 490, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANNK.022C2
; CURRENT APPLICATION NUMBER: US/10/837,217
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 490
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Himetobi P Virus (HiPV)
US-10-837-217-490

Query Match          91.5%; Score 43; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLGIVAPIC 9
   |||||
Db 1 TLGIVCPIC 9

RESULT 11
US-10-603-062-2
; Sequence 2, Application US/10603062
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; Publication No. US20040229809A1
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/603,062
; FILING DATE: 24-Jun-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,425C
; FILING DATE: 09-OCT-1998
; APPLICATION NUMBER: 60/061,657
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-603-062-2

Query Match          91.5%; Score 43; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLGIVAPIC 9
   |||||
Db 1 TLGIVCPIC 9

RESULT 12
US-10-751-845-102
; Sequence 102, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
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; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-102

Query Match      91.5%; Score 43; DB 17; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 TLGIVAPIC 9
Db 1 TLGIVCPIC 9

RESULT 13
US-09-888-721-8
; Sequence 8, Application US/09888721
; Patent No. US20020132990A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scherman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-09-888-721-8

Query Match      91.5%; Score 43; DB 9; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.23;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 TLGIVAPIC 9
Db 2 TLGIVCPIC 10

RESULT 14
US-10-668-400-10
; Sequence 10, Application US/10668400
; Publication No. US20040058859A1
; GENERAL INFORMATION:
; APPLICANT: Bay, Sylvie
; APPLICANT: Cantacuzene, Daniele
; APPLICANT: Leclerc, Claude
; APPLICANT: Lo-Man, Richard
; TITLE OF INVENTION: MULTIPLE ANTIGEN GLYCOPEPTIDE CARBOHYDRATE,
; FILE REFERENCE: 102.166A-1
; CURRENT APPLICATION NUMBER: US/10/668,400
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 09/049,847
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/041,726
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10

; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: HPV16 E7 PEPTIDE
US-10-668-400-10

Query Match      91.5%; Score 43; DB 15; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.23;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 TLGIVAPIC 9
Db 2 TLGIVCPIC 10

RESULT 15
US-10-484-063-18
; Sequence 18, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-18

Query Match      91.5%; Score 43; DB 17; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.23;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 TLGIVAPIC 9
Db 2 TLGIVCPIC 10

Search completed: June 29, 2005, 03:24:12
Job time : 57.55 secs
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)
39.174 Million cell updates/sec

Title: US-08-170-344-20
Perfect score: 47
Sequence: 1 TLGIVAPIC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	91.5	9	3	US-08-948-378A-2
2	43	91.5	9	3	US-09-169-425C-2
3	43	91.5	9	4	US-08-197-484-68
4	43	91.5	9	4	US-09-759-960-2
5	43	91.5	9	5	PCT-US95-02121-68
6	43	91.5	10	4	US-09-000-003A-9
7	43	91.5	10	4	US-09-408-986A-10
8	43	91.5	11	3	US-09-169-425C-31
9	43	91.5	11	3	US-09-169-425C-33
10	43	91.5	11	4	US-09-759-960-31
11	43	91.5	11	4	US-09-759-960-33
12	43	91.5	12	3	US-08-948-378A-16
13	43	91.5	12	3	US-09-169-425C-16
14	43	91.5	12	4	US-09-759-960-16
15	43	91.5	13	3	US-08-948-378A-3
16	43	91.5	13	3	US-08-948-378A-4
17	43	91.5	13	3	US-08-948-378A-19
18	43	91.5	13	3	US-08-159-339A-1167
19	43	91.5	13	3	US-09-169-425C-3
20	43	91.5	13	3	US-09-169-425C-4
21	43	91.5	13	3	US-09-169-425C-19
22	43	91.5	13	4	US-09-759-960-3
23	43	91.5	13	4	US-09-759-960-4
24	43	91.5	13	4	US-09-759-960-19
25	43	91.5	14	3	US-09-169-425C-32
26	43	91.5	14	4	US-09-759-960-32
27	43	91.5	15	3	US-08-159-339A-1168

28	43	91.5	16	3	US-09-169-425C-25
29	43	91.5	16	4	US-09-759-960-25
30	43	91.5	19	4	US-09-980-523A-18
31	43	91.5	20	3	US-08-075-541D-50
32	43	91.5	21	2	US-08-934-915-50
33	43	91.5	21	2	US-08-934-915-157
34	43	91.5	21	4	US-09-980-177A-76
35	43	91.5	26	3	US-08-075-541D-40
36	43	91.5	28	4	US-09-486-394-5
37	43	91.5	30	2	US-08-934-915-54
38	43	91.5	38	3	US-08-948-378A-6
39	43	91.5	38	3	US-09-169-425C-6
40	43	91.5	38	4	US-09-759-960-6
41	43	91.5	98	1	US-08-076-248-6
42	43	91.5	98	3	US-08-075-541D-42
43	43	91.5	98	3	US-09-382-616A-1
44	43	91.5	98	3	US-08-944-368A-4
45	43	91.5	98	3	US-09-820-764-4

ALIGNMENTS

RESULT 1
US-08-948-378A-2
; Sequence 2, Application US/08948378A
; Patent No. 6013258
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM
; TITLE OF INVENTION: THE HPV E7 PROTEIN
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,378A
; FILING DATE: 09-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-948-378A-2

Query Match 91.5%; Score 43; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 TLGIVAPIC 9
Db 1 TLGIVCPIC 9

RESULT 2
US-09-169-425C-2
; Sequence 2, Application US/09169425C
; Patent No. 6183746
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,425C
; FILING DATE: 09-OCT-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/061,657
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-169-425C-2

Query Match 91.5%; Score 43; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
Db 1 TLGIVCPIC 9

RESULT 3
US-08-197-484-68
; Sequence 68, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Eteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-197-484-68

Query Match 91.5%; Score 43; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
Db 1 TLGIVCPIC 9

RESULT 4
US-09-759-960-2
; Sequence 2, Application US/09759960
; Patent No. 6582704
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,960
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/169,425
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/004002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-543-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-759-960-2

Query Match 91.5%; Score 43; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
Db 1 TLGIVCPIC 9

RESULT 5
PCT-US95-02121-68
Sequence 68, Application PC/TUS9502121
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02121
FILING DATE: 16-FEB-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,484
FILING DATE: 16-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600

TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-02121-68

Query Match 91.5%; Score 43; DB 5; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
Db 1 TLGIVCPIC 9

RESULT 6
US-09-000-003A-9
Sequence 9, Application US/09000003A
Patent No. 6652850
GENERAL INFORMATION:
APPLICANT: Philip, Ramila
Lebkowski, Jane S.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRAL LIPOSOMES AND
THEIR USE IN TRANSFECTING DENDRITIC CELLS TO STIMULATE
SPECIFIC IMMUNITY
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Alexis Barron, Esq.
STREET: Suite 2600 Aramark Tower, 1101 Market Street
CITY: Philadelphia
STATE: PA
COUNTRY: United States of America
ZIP: 19107

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,003A
FILING DATE: 15-Jun-1998
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12012
FILING DATE: 19-JUL-1996
APPLICATION NUMBER: US 60/001,312
FILING DATE: 21-JUL-1995
APPLICATION NUMBER: US 60/007,184
FILING DATE: 01-NOV-1995
APPLICATION NUMBER: US 08/566,286
FILING DATE: 01-DEC-1995

ATTORNEY/AGENT INFORMATION:
NAME: Barron, Alexis
REGISTRATION NUMBER: 22,702
REFERENCE/DOCKET NUMBER: 20,846-K USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 923-4466
TELEFAX: (215) 923-2189

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-000-003A-9

Query Match 91.5%; Score 43; DB 4; Length 10;

Best Local Similarity 88.9%; Pred. No. 0.041; Mismatches 1; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 1 TLGIVAPIC 9
DB 2 TLGIVCPIC 10

RESULT 7

US-09-405-986A-10
; Sequence 10, Application US/09405986A
; Patent No. 6676946
; GENERAL INFORMATION:
; APPLICANT: Bay, Sylvie
; APPLICANT: Cantacuzene, Daniele
; APPLICANT: Leclerc, Claude
; APPLICANT: Lo-Man, Richard
; TITLE OF INVENTION: MULTIPLE ANTIGEN GLYCOPEPTIDE CARBOHYDRATE,
; TITLE OF INVENTION: VACCINE COMPRISING THE SAME AND USE THEREOF
; FILE REFERENCE: 102.166A-1
; CURRENT APPLICATION NUMBER: US/09/405,986A
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 09/049,847
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/041,726
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: HPV16 E7 PEPTIDE
US-09-405-986A-10

Query Match 91.5%; Score 43; DB 4; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.041; Mismatches 1; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 1 TLGIVAPIC 9
DB 2 TLGIVCPIC 10

RESULT 8

US-09-169-425C-31
; Sequence 31, Application US/09169425C
; Patent No. 6183746
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,425C
; FILING DATE: 09-OCT-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/061,657
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/061,657
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...1
; OTHER INFORMATION: where Xaa at position 1 is Met, Ala, Ser,
; OTHER INFORMATION: Arg, Lys, Gly, Gln, Asp, or Glu
US-09-169-425C-31

Query Match 91.5%; Score 43; DB 3; Length 11;
Best Local Similarity 88.9%; Pred. No. 0.046; Mismatches 1; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 1 TLGIVAPIC 9
DB 3 TLGIVCPIC 11

RESULT 9

US-09-169-425C-33
; Sequence 33, Application US/09169425C
; Patent No. 6183746
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,425C
; FILING DATE: 09-OCT-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/061,657
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-169-425C-33

Query Match 91.5%; Score 43; DB 3; Length 11;
Best Local Similarity 88.9%; Pred. No. 0.046;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
Db 3 TLGIVCPIC 11

RESULT 10
US-09-759-960-31

; Sequence 31, Application US/09759960
; Patent No. 6582704

; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,960
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/169,425
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: Other
LOCATION: 1...1
OTHER INFORMATION: where Xaa at position 1 is Met, Ala, Ser,
OTHER INFORMATION: Arg, Lys, Gly, Gln, Asp, or Glu
US-09-759-960-31

Query Match 91.5%; Score 43; DB 4; Length 11;
Best Local Similarity 88.9%; Pred. No. 0.046;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
Db 3 TLGIVCPIC 11

RESULT 11
US-09-759-960-33

; Sequence 33, Application US/09759960
; Patent No. 6582704

; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,960
; FILING DATE:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/169,425
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-759-960-33

Query Match 91.5%; Score 43; DB 4; Length 11;
Best Local Similarity 88.9%; Pred. No. 0.046;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLGIVAPIC 9
Db 3 TLGIVCPIC 11

RESULT 12

US-08-948-378A-16
; Sequence 16, Application US/08948378A
; Patent No. 6013258

; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston

/ STATE: MA
/ COUNTRY: US
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows95
/ SOFTWARE: FastSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/948,378A
/ FILING DATE: 09-OCT-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fraser, Janis K.
/ REGISTRATION NUMBER: 34,819
/ REFERENCE/DOCKET NUMBER: 08191/004001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-542-5070
/ TELEFAX: 617-543-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-948-378A-16

Query Match 91.5%; Score 43; DB 3; Length 12;
Best Local Similarity 88.9%; Pred. No. 0.05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLGIVAPIC 9
DB 4 TLGIVCPIC 12

RESULT 13
US-09-169-425C-16
/ Sequence 16, Application US/09169425C
/ Patent No. 6183746
/ GENERAL INFORMATION:
/ APPLICANT: Urban, Robert G.
/ APPLICANT: Chiciz, Roman M.
/ APPLICANT: Collins, Edward J.
/ APPLICANT: Hedley, Mary Lynn
/ TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
/ TITLE OF INVENTION: PROTEIN
/ NUMBER OF SEQUENCES: 33
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson, P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: US
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows95
/ SOFTWARE: FastSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/169,425C
/ FILING DATE: 09-OCT-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/061,657
/ FILING DATE: 09-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fraser, Janis K.
/ REGISTRATION NUMBER: 34,819
/ REFERENCE/DOCKET NUMBER: 08191/004002

/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-542-5070
/ TELEFAX: 617-543-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-09-169-425C-16

Query Match 91.5%; Score 43; DB 3; Length 12;
Best Local Similarity 88.9%; Pred. No. 0.05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLGIVAPIC 9
DB 4 TLGIVCPIC 12

RESULT 14
US-09-759-960-16
/ Sequence 16, Application US/09759960
/ Patent No. 6582704
/ GENERAL INFORMATION:
/ APPLICANT: Urban, Robert G.
/ APPLICANT: Chiciz, Roman M.
/ APPLICANT: Collins, Edward J.
/ APPLICANT: Hedley, Mary Lynn
/ TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
/ TITLE OF INVENTION: PROTEIN
/ NUMBER OF SEQUENCES: 33
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson, P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: US
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows95
/ SOFTWARE: FastSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/759,960
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/169,425
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fraser, Janis K.
/ REGISTRATION NUMBER: 34,819
/ REFERENCE/DOCKET NUMBER: 08191/004002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-542-5070
/ TELEFAX: 617-543-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-09-759-960-16

Query Match 91.5%; Score 43; DB 4; Length 12;
Best Local Similarity 88.9%; Pred. No. 0.05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLGIVAPIC 9
DB 4 TLGIVCPIC 12

Db 4 TLGIVCPIC 12

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RESULT 15
US-08-948-378A-3
; Sequence 3, Application US/08948378A
; Patent No. 6013258
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM
; TITLE OF INVENTION: THE HPV E7 PROTEIN
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,378A
; FILING DATE: 09-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-948-378A-3

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Query Match 91.5%; Score 43; DB 3; Length 13;
Best Local Similarity 88.9%; Pred. No. 0.055;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 TLGIVAPIC 9
Db 5 TLGIVCPIC 13

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Search completed: June 28, 2005, 19:29:17
Job time : 17.15 secs

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RESULT 2
US-09-872-836-101

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; Sequence 101, Application US/09872836
; Publication No. US20040142475A1
; GENERAL INFORMATION:
; APPLICANT: Barman, Shikha P.
; APPLICANT: McKeever, Una
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 08191-018001
; CURRENT APPLICATION NUMBER: US/09/872,836
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,830
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-836-101

Query Match      100.0%; Score 48; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLPOLCTEL 9
Db      1 KLPOLCTEL 9

RESULT 3
US-10-133-210-278
; Sequence 278, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: DeLisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 278
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-278

Query Match      100.0%; Score 48; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLPOLCTEL 9
Db      1 KLPOLCTEL 9

RESULT 4
US-10-777-053-546
; Sequence 546, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: CONTINUOUS-FLOW METHOD FOR PREPARING MICROPARTICLES
; FILE REFERENCE: 08191-012001
; CURRENT APPLICATION NUMBER: US/10/758,970
; CURRENT FILING DATE: 2004-01-16
; SEQ ID NO 546
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-777-053-546

Query Match      100.0%; Score 48; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLPOLCTEL 9
Db      1 KLPOLCTEL 9

RESULT 5
US-10-837-217-546
; Sequence 546, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: MANK.022C2
; CURRENT APPLICATION NUMBER: US/10/837,217
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 546
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-837-217-546

Query Match      100.0%; Score 48; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLPOLCTEL 9
Db      1 KLPOLCTEL 9

RESULT 6
US-10-758-970-101
; Sequence 101, Application US/10758970
; Publication No. US20050037086A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Hsu, Yung-Yueh
; APPLICANT: Tyo, Michael
; TITLE OF INVENTION: CONTINUOUS-FLOW METHOD FOR PREPARING MICROPARTICLES
; FILE REFERENCE: 08191-012001
; CURRENT APPLICATION NUMBER: US/10/758,970
; CURRENT FILING DATE: 2004-01-16
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-758-970-101

Query Match      100.0%; Score 48; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLPOLCTEL 9
Db      1 KLPOLCTEL 9
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; PRIOR APPLICATION NUMBER: US/09/715,708A
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/166,516
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-758-970-101

Query Match      100.0%; Score 48; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
Db 1 KLPQLCTEL 9

RESULT 7
US-10-484-063-1
; Sequence 1, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-1

Query Match      100.0%; Score 48; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
Db 1 KLPQLCTEL 9

RESULT 8
US-10-751-845-55
; Sequence 55, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16

; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-55

Query Match      100.0%; Score 48; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
Db 1 KLPQLCTEL 9

RESULT 9
US-10-476-570-20
; Sequence 20, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 17-31
US-10-476-570-20

Query Match      100.0%; Score 48; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
Db 2 KLPQLCTEL 10

RESULT 10
US-10-751-845-64
; Sequence 64, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665

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INVENT FILING DATE:	2003-11-04
TITLE OF INVENTION:	Mixture of peptides derived from E6 and/or E7
INVENTOR:	THOMAS J. COOPER, JR.
ATTORNEY:	THOMAS J. COOPER, JR.

; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 32
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-45
US-10-476-570-9

Query Match 100.0%; Score 48; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLPQLCTEL 9
Db 5 KLPQLCTEL 13

RESULT 15
US-10-476-570-19
; Sequence 19, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-46
US-10-476-570-19

Query Match 100.0%; Score 48; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLPQLCTEL 9
Db 5 KLPQLCTEL 13

Search completed: June 29, 2005, 03:24:05
Job time : 58.55 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)
39.174 Million cell updates/sec

Title: US-08-170-344-2

Perfect score: 48

Sequence: 1 KLPOLCTEL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.*
- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
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 - 5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	9	1	US-08-787-547-101
2	48	100.0	9	4	US-09-601-729-274
3	48	100.0	20	2	US-08-934-915-159
4	48	100.0	30	1	US-08-363-586-4
5	48	100.0	30	4	US-09-980-523A-4
6	48	100.0	158	4	US-09-980-523A-2
7	48	100.0	162	1	US-08-316-239B-3
8	48	100.0	162	1	US-08-316-239B-4
9	48	100.0	172	3	US-08-860-165-14
10	48	100.0	172	3	US-09-359-382-14
11	48	100.0	182	1	US-08-117-083-10
12	48	100.0	266	3	US-08-860-165-10
13	48	100.0	266	3	US-09-359-382-10
14	48	100.0	266	4	US-09-367-309A-1
15	48	100.0	273	3	US-09-485-885-4
16	48	100.0	292	3	US-09-485-885-10
17	48	100.0	371	3	US-09-485-885-6
18	48	100.0	390	3	US-09-485-885-14
19	43	89.6	32	1	US-08-466-285-2
20	43	89.6	32	3	US-08-164-788-2
21	43	89.6	158	2	US-08-247-904B-10
22	43	89.6	158	3	US-08-767-942A-19
23	43	89.6	271	1	US-08-117-083-14
24	43	89.6	278	3	US-09-485-885-21
25	43	89.6	383	3	US-09-485-885-23
26	35	72.9	211	4	US-09-543-681A-8111
27	34	70.8	15	1	US-07-909-122-2

28	34	70.8	15	3	US-08-075-541D-52	Sequence 52, Appl
29	34	70.8	23	1	US-08-363-586-3	Sequence 3, Appl
30	34	70.8	161	4	US-09-673-395A-248	Sequence 248, App
31	34	70.8	341	3	US-08-481-968A-11	Sequence 11, Appl
32	34	70.8	341	3	US-08-154-712B-11	Sequence 11, Appl
33	34	70.8	341	4	US-09-947-925A-11	Sequence 11, Appl
34	34	70.8	341	4	US-09-198-452A-1036	Sequence 1036, Ap
35	34	70.8	504	4	US-09-438-185A-966	Sequence 966, App
36	34	70.8	522	4	US-09-949-016-10663	Sequence 10663, A
37	34	70.8	728	4	US-09-747-259-18	Sequence 18, Appl
38	34	70.8	728	4	US-09-816-744-18	Sequence 31445, A
39	33	68.8	163	4	US-09-252-991A-31445	Sequence 16504, A
40	33	68.8	304	4	US-09-248-796A-16504	Sequence 60, Appl
41	33	68.8	308	4	US-09-369-247-60	Sequence 7117, Ap
42	33	68.8	476	4	US-09-543-681A-7117	Sequence 3, Appl
43	33	68.8	536	2	US-08-551-211-3	Sequence 1, Appl
44	33	68.8	620	4	US-09-673-198-1	Sequence 13113, A
45	33	68.8	626	4	US-09-489-039A-13113	

ALIGNMENTS

RESULT 1
US-08-787-547-101
; Sequence 101, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Curley, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-787-547-101

Query Match 100.0%; Score 48; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
Db 1 KLPQLCTEL 9

RESULT 2
US-09-601-729-274
; Sequence 274, Application US/09601729
; Patent No. 6683052
; GENERAL INFORMATION:
; APPLICANT: THIAM, KADER
; APPLICANT: AURIAULT, CLAUDE
; APPLICANT: GRAS-MASSE, HELENE
; APPLICANT: LOING, ESTELLE
; APPLICANT: VERWAERDE, CLAUDE
; APPLICANT: GUILLET, JEAN GERARD
; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
; TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: USB-97-AU-IN
; CURRENT APPLICATION NUMBER: US/09/601,729
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: PCT/FR99/00259
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 98 01439
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 274
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-601-729-274

Query Match 100.0%; Score 48; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
Db 1 KLPQLCTEL 9

RESULT 3
US-08-934-915-159
; Sequence 159, Application US/08934915
; Patent No. 5912412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, WHEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 15, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-159

Query Match 100.0%; Score 48; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
Db 2 KLPQLCTEL 10

RESULT 4
US-08-363-586-4
; Sequence 4, Application US/08363586
; Patent No. 5629161
; GENERAL INFORMATION:
; APPLICANT: Mueller, Martin
; APPLICANT: Gissmann, Iutz
; TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
; TITLE OF INVENTION: Peptides for the Diagnostic Purpose
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,586
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/909,296
; FILING DATE: 09-JUL-1992
; APPLICATION NUMBER: EP 9111720.8
; FILING DATE: 13-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wadler, Linda A.
; REGISTRATION NUMBER: 33,218
; REFERENCE/DOCKET NUMBER: 02481-1195-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; MOLECULE TYPE: peptide
US-08-363-586-4
Query Match      100.0%; Score 48; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
Db 11 KLPQLCTEL 19

RESULT 5
US-09-980-523A-4
; Sequence 4, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-4
Query Match      100.0%; Score 48; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
Db 4 KLPQLCTEL 12

RESULT 6
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
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; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2
Query Match      100.0%; Score 48; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
Db 18 KLPQLCTEL 26

RESULT 7
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3
Query Match      100.0%; Score 48; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
Db 18 KLPQLCTEL 26

RESULT 8
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
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APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNWE-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 48; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPOLCTEL 9
Db 18 KLPQLCTEL 26

RESULT 9
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion

US-08-860-165-14
Query Match 100.0%; Score 48; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KLPOLCTEL 9
Db 87 KLPOLCTEL 95
RESULT 10
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match 100.0%; Score 48; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPOLCTEL 9
Db 87 KLPOLCTEL 95

RESULT 11
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note="Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-10

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Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
Db 19 KLPQLCTEL 27

RESULT 12
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 48; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
Db 18 KLPQLCTEL 26

RESULT 13
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
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; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 48; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
Db 18 KLPQLCTEL 26

RESULT 14
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 48; DB 4; Length 266;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPQLCTEL 9
Db 18 KLPQLCTEL 26

RESULT 15
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Tereza
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
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; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

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Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 KLPQLCTEL 9
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Job time : 18.15 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2005, 01:35:30 ; Search time 57.55 Seconds
(without alignments)
60.138 Million cell updates/sec

Title: US-08-170-344-19
Perfect score: 49
Sequence: 1 GTLGIVCFI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	49	100.0	9	9 US-09-759-960-21	Sequence 21, Appl
2	49	100.0	9	9 US-09-891-823-50	Sequence 50, Appl
3	49	100.0	9	14 US-10-128-711-70	Sequence 70, Appl
4	49	100.0	9	14 US-10-365-908-50	Sequence 50, Appl
5	49	100.0	9	16 US-10-472-661-9	Sequence 9, Appl
6	49	100.0	9	16 US-10-777-053-327	Sequence 327, App
7	49	100.0	9	16 US-10-777-053-494	Sequence 494, App
8	49	100.0	9	16 US-10-837-217-327	Sequence 327, App
9	49	100.0	9	16 US-10-837-217-494	Sequence 494, App
10	49	100.0	9	16 US-10-603-062-21	Sequence 21, Appl
11	49	100.0	9	16 US-10-871-138-50	Sequence 50, Appl

12	49	100.0	9	17 US-10-751-845-104	Sequence 104, App
13	49	100.0	10	9 US-09-891-823-46	Sequence 46, Appl
14	49	100.0	10	9 US-09-888-721-8	Sequence 8, Appl
15	49	100.0	10	14 US-10-365-908-46	Sequence 46, Appl
16	49	100.0	10	15 US-10-668-400-10	Sequence 10, Appl
17	49	100.0	10	16 US-10-871-138-46	Sequence 46, Appl
18	49	100.0	10	17 US-10-484-063-18	Sequence 18, Appl
19	49	100.0	11	9 US-09-759-960-31	Sequence 31, Appl
20	49	100.0	11	9 US-09-759-960-33	Sequence 33, Appl
21	49	100.0	11	16 US-10-603-062-31	Sequence 31, Appl
22	49	100.0	11	16 US-10-603-062-33	Sequence 33, Appl
23	49	100.0	12	9 US-09-759-960-16	Sequence 16, Appl
24	49	100.0	12	9 US-09-909-460-108	Sequence 108, App
25	49	100.0	12	11 US-09-872-836-108	Sequence 108, App
26	49	100.0	12	16 US-10-603-062-16	Sequence 16, Appl
27	49	100.0	12	17 US-10-758-970-108	Sequence 108, App
28	49	100.0	12	17 US-10-751-845-62	Sequence 62, Appl
29	49	100.0	13	9 US-09-759-960-3	Sequence 3, Appl
30	49	100.0	13	9 US-09-759-960-4	Sequence 4, Appl
31	49	100.0	13	9 US-09-759-960-19	Sequence 19, Appl
32	49	100.0	13	9 US-09-909-460-110	Sequence 110, App
33	49	100.0	13	11 US-09-872-836-110	Sequence 110, App
34	49	100.0	13	16 US-10-603-062-3	Sequence 3, Appl
35	49	100.0	13	16 US-10-603-062-4	Sequence 4, Appl
36	49	100.0	13	16 US-10-603-062-19	Sequence 19, Appl
37	49	100.0	14	9 US-09-759-960-32	Sequence 32, Appl
38	49	100.0	14	16 US-10-603-062-32	Sequence 32, Appl
39	49	100.0	15	16 US-10-476-570-52	Sequence 52, Appl
40	49	100.0	15	16 US-10-306-541-71	Sequence 71, Appl
41	49	100.0	15	16 US-10-306-541-84	Sequence 84, Appl
42	49	100.0	16	9 US-09-759-960-25	Sequence 25, Appl
43	49	100.0	16	9 US-09-909-460-109	Sequence 109, App
44	49	100.0	16	11 US-09-872-836-109	Sequence 109, App
45	49	100.0	16	16 US-10-603-062-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-09-759-960-21
; Sequence 21, Application US/09759960
; Patent No. US2001000639A1
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF SEQUENCE: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,960
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/169,425
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEFAX: 617-543-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-759-960-21

Query Match 100.0%; Score 49; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
 Db 1 GTLGIVCPI 9

RESULT 2

US-09-891-823-50
 Sequence 50, Application US/09891823
 Publication No. US20020110566A1

GENERAL INFORMATION:

APPLICANT: Neefe, John R.
 APPLICANT: Boux, Leslie J.
 APPLICANT: Winnett, Mark T.
 APPLICANT: Goldstone, Stephen E.
 APPLICANT: Siegel, Marvin
 TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
 FILE REFERENCE: 12071-003001
 CURRENT APPLICATION NUMBER: US/09/891,823
 CURRENT FILING DATE: 2001-10-19
 PRIOR APPLICATION NUMBER: US 60/214,202
 PRIOR FILING DATE: 2000-06-26
 NUMBER OF SEQ ID NOS: 140
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 50
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Human papilloma virus

US-09-891-823-50

Query Match 100.0%; Score 49; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
 Db 1 GTLGIVCPI 9

RESULT 3

US-10-128-711-70
 Sequence 70, Application US/10128711
 Publication No. US20030099634A1

GENERAL INFORMATION:

APPLICANT: VITIELLO, Maria A.
 CHESTNUT, Robert W.
 SETTE, Alessandro D.
 CELIS, Esteban
 GRAY, Howard
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING CTL IMMUNITY
 NUMBER OF SEQUENCES: 153
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: Steuart Street Tower, One Market Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: US

ZIP: 94105-1493
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/128,711
 FILING DATE: 22-Apr-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/197,484
 FILING DATE: 16-FEB-1994
 APPLICATION NUMBER: US 07/935,811
 FILING DATE: 26-AUG-1992
 APPLICATION NUMBER: US 07/874,491
 FILING DATE: 27-APR-1992
 APPLICATION NUMBER: US 07/827,682
 FILING DATE: 29-JAN-1992
 APPLICATION NUMBER: US 07/749,568
 FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.
 REGISTRATION NUMBER: 31,990
 REFERENCE/DOCKET NUMBER: 14137-26-4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 467-9600

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 70:
 US-10-128-711-70

Query Match 100.0%; Score 49; DB 14; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
 Db 1 GTLGIVCPI 9

RESULT 4

US-10-365-908-50
 Sequence 50, Application US/10365908
 Publication No. US20030170268A1

GENERAL INFORMATION:

APPLICANT: Neefe, John R.
 APPLICANT: Boux, Leslie J.
 APPLICANT: Winnett, Mark T.
 APPLICANT: Goldstone, Stephen E.
 APPLICANT: Siegel, Marvin
 TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
 FILE REFERENCE: 12071-003001
 CURRENT APPLICATION NUMBER: US/10/365,908
 CURRENT FILING DATE: 2003-02-13
 PRIOR APPLICATION NUMBER: US/09/891,823
 PRIOR FILING DATE: 2001-10-19
 PRIOR APPLICATION NUMBER: US 60/214,202
 PRIOR FILING DATE: 2000-06-26
 NUMBER OF SEQ ID NOS: 140
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 50
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Human papilloma virus

US-10-365-908-50


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Query Match      100.0%; Score 49; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 1 GTLGIVCPI 9

RESULT 5
US-10-472-661-9
; Sequence 9, Application US/10472661
; Publication No. US20040106551A1
; GENERAL INFORMATION:
; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Kleif, Samir N.
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS IMMUNOREACTIVE
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 14014.040602
; CURRENT APPLICATION NUMBER: US/10/472,661
; CURRENT FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: PCT/US02/09261
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/278,520
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note =
US-10-472-661-9

Query Match      100.0%; Score 49; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 1 GTLGIVCPI 9

RESULT 6
US-10-777-053-327
; Sequence 327, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANK 022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 327
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papillomavirus 16
US-10-777-053-327

Query Match      100.0%; Score 49; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 1 GTLGIVCPI 9

RESULT 7
US-10-777-053-494
; Sequence 494, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANK 022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 494
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-777-053-494

Query Match      100.0%; Score 49; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 1 GTLGIVCPI 9

RESULT 8
US-10-837-217-327
; Sequence 327, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANK 022C2
; CURRENT APPLICATION NUMBER: US/10/837,217
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 327
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papillomavirus 16
US-10-837-217-327

Query Match      100.0%; Score 49; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 1 GTLGIVCPI 9
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Db      1 GTLGIVCPI 9
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RESULT 9
US-10-837-217-494
; Sequence 494, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANKO.022C2
; CURRENT APPLICATION NUMBER: US/10/837,217
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 494
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-837-217-494

Query Match      100.0%; Score 49; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GTLGIVCPI 9
|||||
Db      1 GTLGIVCPI 9
|||||

RESULT 10
US-10-603-062-21
; Sequence 21, Application US/10603062
; Publication No. US2004022980A1
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/603,062
; FILING DATE: 24-Jun-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,425C
; FILING DATE: 09-OCT-1998
; APPLICATION NUMBER: 60/061,657
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
```

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;
;
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-603-062-21

Query Match      100.0%; Score 49; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GTLGIVCPI 9
|||||
Db      1 GTLGIVCPI 9
|||||

RESULT 11
US-10-871-138-50
; Sequence 50, Application US/10871138
; Publication No. US20040235741A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/871,138
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-871-138-50

Query Match      100.0%; Score 49; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GTLGIVCPI 9
|||||
Db      1 GTLGIVCPI 9
|||||

RESULT 12
US-10-751-845-104
; Sequence 104, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
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; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-104

Query Match      100.0%; Score 49; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 1 GTLGIVCPI 9

RESULT 13
US-09-891-823-46
; Sequence 46, Application US/09891823
; Publication No. US20020110566A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-891-823-46

Query Match      100.0%; Score 49; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 2 GTLGIVCPI 10

RESULT 14
US-09-888-721-8
; Sequence 8, Application US/09888721
; Patent No. US20020132990A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scherman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-09-888-721-8

Query Match      100.0%; Score 49; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 1 GTLGIVCPI 9

RESULT 15
US-10-365-908-46
; Sequence 46, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-46

Query Match      100.0%; Score 49; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 2 GTLGIVCPI 10

Search completed: June 29, 2005, 03:24:12
Job time : 58.55 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)
39.174 Million cell updates/sec

Title: US-08-170-344-19

Perfect score: 49

Sequence: 1 GTLGIVCP1 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	9	3	US-09-169-425C-21
2	49	100.0	9	4	US-08-197-484-70
3	49	100.0	9	4	US-09-759-960-21
4	49	100.0	9	4	US-10-365-908-50
5	49	100.0	9	5	PCT-US95-02121-70
6	49	100.0	10	4	US-09-000-003A-9
7	49	100.0	10	4	US-09-405-985A-10
8	49	100.0	10	4	US-10-363-908-46
9	49	100.0	11	3	US-09-169-425C-31
10	49	100.0	11	3	US-09-169-425C-33
11	49	100.0	11	4	US-09-759-960-31
12	49	100.0	11	4	US-09-759-960-33
13	49	100.0	12	3	US-08-948-378A-16
14	49	100.0	12	3	US-09-169-425C-16
15	49	100.0	12	4	US-09-759-960-16
16	49	100.0	13	3	US-08-948-378A-3
17	49	100.0	13	3	US-08-948-378A-4
18	49	100.0	13	3	US-08-948-378A-19
19	49	100.0	13	3	US-08-159-339A-1167
20	49	100.0	13	3	US-09-169-425C-3
21	49	100.0	13	3	US-09-169-425C-4
22	49	100.0	13	3	US-09-169-425C-19
23	49	100.0	13	4	US-09-759-960-3
24	49	100.0	13	4	US-09-759-960-4
25	49	100.0	13	4	US-09-759-960-19
26	49	100.0	14	3	US-09-169-425C-32
27	49	100.0	14	4	US-09-759-960-32

28 49 100.0 15 3 US-08-159-339A-1168 Sequence 1168, Ap
29 49 100.0 16 3 US-09-169-425C-25 Sequence 25, Appl
30 49 100.0 16 4 US-09-759-960-25 Sequence 25, Appl
31 49 100.0 19 4 US-09-980-523A-18 Sequence 18, Appl
32 49 100.0 20 3 US-08-075-541D-50 Sequence 50, Appl
33 49 100.0 21 2 US-08-934-915-50 Sequence 50, Appl
34 49 100.0 21 2 US-08-934-915-157 Sequence 157, Appl
35 49 100.0 21 4 US-09-980-177A-76 Sequence 76, Appl
36 49 100.0 26 3 US-08-075-541D-40 Sequence 5, Appl
37 49 100.0 28 4 US-09-486-394-5 Sequence 54, Appl
38 49 100.0 30 2 US-08-934-915-54 Sequence 6, Appl
39 49 100.0 38 3 US-08-948-378A-6 Sequence 6, Appl
40 49 100.0 38 3 US-09-169-425C-6 Sequence 6, Appl
41 49 100.0 38 4 US-09-759-960-6 Sequence 6, Appl
42 49 100.0 98 1 US-08-406-248-6 Sequence 42, Appl
43 49 100.0 98 3 US-08-075-541D-42 Sequence 42, Appl
44 49 100.0 98 3 US-09-382-616A-1 Sequence 1, Appl
45 49 100.0 98 3 US-08-944-368A-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-169-425C-21
; Sequence 21, Application US/09169425C
; Patent No. 6183746

; GENERAL INFORMATION:

; APPLICANT: Urban, Robert G.

; APPLICANT: Chicz, Roman M.

; APPLICANT: Collins, Edward J.

; APPLICANT: Hedley, Mary Lynn

; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: PastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/169,425C

; FILING DATE: 09-OCT-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/061,657

; FILING DATE: 09-OCT-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Fraser, Janis K.

; REGISTRATION NUMBER: 34,819

; REFERENCE/DOCKET NUMBER: 08191/004002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-543-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-09-169-425C-21

Query Match 100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GTLGIVCPI 9
Db      1 GTLGIVCPI 9

RESULT 2
US-08-197-484-70
; Sequence 70, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Bateban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Stuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-70

Query Match      100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 GTLGIVCPI 9
Db      1 GTLGIVCPI 9

RESULT 4
US-10-365-908-50
; Sequence 50, Application US/10365908
; Patent No. 6797491
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0

Query Match      100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 GTLGIVCPI 9
Db      1 GTLGIVCPI 9

RESULT 3
US-09-759-960-21
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; SEQ ID NO 50
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-50

Query Match      100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 1 GTLGIVCPI 9

RESULT 5
PCT-US95-02121-70
; Sequence 70, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-70

Query Match      100.0%; Score 49; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 1 GTLGIVCPI 9

RESULT 6
US-09-000-003A-9
; Sequence 9, Application US/09000003A
; Patent No. 6652850
; GENERAL INFORMATION:
; APPLICANT: Philip, Ramila
; Lebkowski, Jane S.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRAL LIPOSOMES AND
; THEIR USE IN TRANSFECTING DENDRITIC CELLS TO STIMULATE
; SPECIFIC IMMUNITY
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alexis Barron, Esq.
; STREET: Suite 2600 Aramark Tower, 1101 Market Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/000,003A
; FILING DATE: 15-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12012
; FILING DATE: 19-JUL-1996
; APPLICATION NUMBER: US 60/001,312
; FILING DATE: 21-JUL-1995
; APPLICATION NUMBER: US 60/007,184
; FILING DATE: 01-NOV-1995
; APPLICATION NUMBER: US 08/566,286
; FILING DATE: 01-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barton, Alexis
; REGISTRATION NUMBER: 22,702
; REFERENCE/DOCKET NUMBER: 20,846-K USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 923-4466
; TELEFAX: (215) 923-2189
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-000-003A-9

Query Match      100.0%; Score 49; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 1 GTLGIVCPI 9

RESULT 7
US-09-405-986A-10
; Sequence 10, Application US/09405986A
; Patent No. 6676946
; GENERAL INFORMATION:
; APPLICANT: Bay, Sylvie
; APPLICANT: Cantacuzene, Daniele
; APPLICANT: Leclerc, Claude
; APPLICANT: Lo-Man, Richard
; TITLE OF INVENTION: MULTIPLE ANTIGEN GLYCOPEPTIDE CARBOHYDRATE,
; TITLE OF INVENTION: VACCINE COMPRISING THE SAME AND USE THEREOF
; FILE REFERENCE: 102.166A-1
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; CURRENT APPLICATION NUMBER: US/09/405,986A
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 09/049,847
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/041,726
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; FEATURE:
; NAME/KEY: MISC_FEATURE
; OTHER INFORMATION: HPV16 E7 PEPTIDE
US-09-405-986A-10

```

```

Query Match          100.0%; Score 49; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GTLGVCP1 9
Db 1 GTLGVCP1 9

```

RESULT 8

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US-10-365-908-46
; Sequence 46, Application US/10365908
; Patent No. 6797491
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-46

```

```

Query Match          100.0%; Score 49; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GTLGVCP1 9
Db 2 GTLGVCP1 10

```

RESULT 9

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US-09-169-425C-31
; Sequence 31, Application US/09169425C
; Patent No. 6183746
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; NUMBER OF SEQUENCES: 33

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,425C
; FILING DATE: 09-OCT-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/061,657
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...1
; OTHER INFORMATION: where Xaa at position 1 is Met, Ala, Ser,
; Arg, Lys, Gly, Gln, Asp, or Glu
US-09-169-425C-31

```

```

Query Match          100.0%; Score 49; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GTLGVCP1 9
Db 2 GTLGVCP1 10

```

RESULT 10

```

US-09-169-425C-33
; Sequence 33, Application US/09169425C
; Patent No. 6183746
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/09/169,425C
/ FILING DATE: 09-OCT-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/061,657
/ FILING DATE: 09-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fraser, Janis K.
/ REGISTRATION NUMBER: 34,819
/ REFERENCE/DOCKET NUMBER: 08191/004002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-542-5070
/ TELEFAX: 617-543-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-09-169-425C-33

Query Match 100.0%; Score 49; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTLGIVCPI 9
Db 2 GTLGIVCPI 10

RESULT 11
US-09-759-960-31
; Sequence 31, Application US/09759960
; Patent No. 6582704
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,960
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/169,425
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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```
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Other
/ LOCATION: 1...1
/ OTHER INFORMATION: where Xaa at position 1 is Met, Ala, Ser,
/ OTHER INFORMATION: Arg, Lys, Gly, Gln, Asp, or Glu
/ US-09-759-960-31

Query Match 100.0%; Score 49; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTLGIVCPI 9
Db 2 GTLGIVCPI 10

RESULT 12
US-09-759-960-33
; Sequence 33, Application US/09759960
; Patent No. 6582704
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,960
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/169,425
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
/ US-09-759-960-33

Query Match 100.0%; Score 49; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTLGIVCPI 9
Db 2 GTLGIVCPI 10

RESULT 13
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US-08-948-378A-16
; Sequence 16, Application US/08948378A
; Patent No. 6013258
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM
; THE HPV E7 PROTEIN
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,378A
; FILING DATE: 09-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-948-378A-16

Query Match 100.0%; Score 49; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 3 GTLGIVCPI 11

RESULT 14
US-09-169-425C-16
; Sequence 16, Application US/09169425C
; Patent No. 6183746
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; THE HPV E7 PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,425C
; FILING DATE: 09-OCT-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/061,657
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-169-425C-16

Query Match 100.0%; Score 49; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
Db 3 GTLGIVCPI 11

RESULT 15
US-09-759-960-16
; Sequence 16, Application US/09759960
; Patent No. 6582704
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; THE HPV E7 PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,960
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/169,425
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906

; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide.
US-09-759-960-16

Query Match 100.0%; Score 49; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTLGIVCPI 9
|||
Db 3 GTLGIVCPI 11

Search completed: June 28, 2005, 19:29:17
Job time : 17.15 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	42	100.0	9	9	US-09-759-960-1	Sequence 1, Appli
2	42	100.0	9	9	US-09-891-823-5	Sequence 5, Appli
3	42	100.0	9	9	US-09-909-460-106	Sequence 106, App
4	42	100.0	9	11	US-09-872-836-106	Sequence 106, App
5	42	100.0	9	11	US-09-872-836-111	Sequence 111, App
6	42	100.0	9	11	US-10-128-711-65	Sequence 65, Appl
7	7	42	100.0	9	US-10-133-210-275	Sequence 275, App
8	42	100.0	9	14	US-10-052-578-314	Sequence 314, App
9	42	100.0	9	14	US-10-053-520-314	Sequence 314, App
10	42	100.0	9	14	US-10-365-908-5	Sequence 5, Appli
11	42	100.0	9	14	US-10-053-498B-314	Sequence 314, App

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-759-960-1
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Query Match 100.0%; Score 42; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 LLMGTLGIV 9
Db 1 LLMGTLGIV 9
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RESULT 2

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US-09-891-823-5
; Sequence 5, Application US/09891823
; Publication No. US20020110566A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/09/891,823
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-891-823-5
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```
Query Match 100.0%; Score 42; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 LLMGTLGIV 9
Db 1 LLMGTLGIV 9
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RESULT 3

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US-09-909-460-106
; Sequence 106, Application US/09909460
; Publication No. US20020182258A1
; GENERAL INFORMATION:
; APPLICANT: Lunsford, Lynn B.
; APPLICANT: Putnam, David
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
; TITLE OF INVENTION: ACID
; FILE REFERENCE: 08191/014001
; CURRENT APPLICATION NUMBER: US/09/909,460
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 9
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; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-909-460-106
```

```
Query Match 100.0%; Score 42; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 LLMGTLGIV 9
Db 1 LLMGTLGIV 9
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RESULT 4

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US-09-872-836-106
; Sequence 106, Application US/09872836
; Publication No. US20040142475A1
; GENERAL INFORMATION:
; APPLICANT: Barman, Shikha P.
; APPLICANT: McKeever, Una
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 08191-018001
; CURRENT APPLICATION NUMBER: US/09/872,836
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,830
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-836-106
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Query Match 100.0%; Score 42; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 LLMGTLGIV 9
Db 1 LLMGTLGIV 9
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RESULT 5

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US-09-872-836-111
; Sequence 111, Application US/09872836
; Publication No. US20040142475A1
; GENERAL INFORMATION:
; APPLICANT: Barman, Shikha P.
; APPLICANT: McKeever, Una
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 08191-018001
; CURRENT APPLICATION NUMBER: US/09/872,836
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,830
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-836-111
```

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Query Match 100.0%; Score 42; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 LLMGTLGIV 9
Db 1 LLMGTLGIV 9
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RESULT 6

US-10-128-711-65
; Sequence 65, Application US/10128711
; Publication No. US2003009934A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourlie and Crew
; STREET: Stuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 28-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 28-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-10-128-711-65

Query Match 100.0%; Score 42; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMGTLGIV 9
DB 1 LLMGTLGIV 9

RESULT 7

US-10-133-210-275
; Sequence 275, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:

; APPLICANT: DeLisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 275
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-275

Query Match 100.0%; Score 42; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMGTLGIV 9
DB 1 LLMGTLGIV 9

RESULT 8

US-10-052-578-314
; Sequence 314, Application US/10052578
; Publication No. US20030134787A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathak
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 314
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-052-578-314

Query Match 100.0%; Score 42; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMGTLGIV 9
DB 1 LLMGTLGIV 9

RESULT 9

US-10-053-520-314
; Sequence 314, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:

; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 314
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-520-314

Query Match 100.0%; Score 42; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
Db 1 LLMGTLGIV 9

RESULT 10
US-10-365-908-5
; Sequence 5, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-5

Query Match 100.0%; Score 42; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
Db 1 LLMGTLGIV 9

RESULT 11
US-10-053-498B-314
; Sequence 314, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:

; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 314
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-498B-314

Query Match 100.0%; Score 42; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
Db 1 LLMGTLGIV 9

RESULT 12
US-10-367-580-88
; Sequence 88, Application US/10367580
; Publication No. US20040071720A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461061
; CURRENT APPLICATION NUMBER: US/10/367,580
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,832
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-580-88

Query Match 100.0%; Score 42; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9


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Db      1 LLMGTLGIV 9
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RESULT 13
US-10-367-593-88
; Sequence 88, Application US/10367593
; Publication NO. US20040071721A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461012
; CURRENT APPLICATION NUMBER: US/10/367,593
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-593-88
Query Match      100.0%; Score 42; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LLMGTLGIV 9
|||||
Db      1 LLMGTLGIV 9
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RESULT 14
US-10-367-594-88
; Sequence 88, Application US/10367594
; Publication NO. US20040071722A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461041
; CURRENT APPLICATION NUMBER: US/10/367,594
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/680,806
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-594-88
Query Match      100.0%; Score 42; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LLMGTLGIV 9
|||||
Db      1 LLMGTLGIV 9
|||||
RESULT 15
US-10-367-654-88
; Sequence 88, Application US/10367654
; Publication NO. US20040071723A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461032
; CURRENT APPLICATION NUMBER: US/10/367,654
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 10/171,734
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/636,295
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-654-88
Query Match      100.0%; Score 42; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db      1 LLMGTLGIV 9
|||||
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Job time : 57.55 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)
39.174 Million cell updates/sec

Title: US-08-170-344-18
Perfect score: 42
Sequence: 1 LLMGTGLIV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	100.0	9	1 US-08-787-547-106	Sequence 106, Appl
2	42	100.0	9	3 US-08-948-378A-1	Sequence 1, Appl
3	42	100.0	9	3 US-09-124-671-9	Sequence 9, Appl
4	42	100.0	9	3 US-09-169-425C-1	Sequence 1, Appl
5	42	100.0	9	4 US-08-197-484-65	Sequence 65, Appl
6	42	100.0	9	4 US-09-759-960-1	Sequence 1, Appl
7	42	100.0	9	4 US-09-601-723-271	Sequence 271, Appl
8	42	100.0	9	4 US-10-365-908-5	Sequence 5, Appl
9	42	100.0	9	5 PCT-US95-02121-65	Sequence 65, Appl
10	42	100.0	10	4 US-10-365-908-47	Sequence 47, Appl
11	42	100.0	13	3 US-08-948-378A-3	Sequence 3, Appl
12	42	100.0	13	3 US-09-169-425C-3	Sequence 3, Appl
13	42	100.0	13	4 US-09-759-960-3	Sequence 25, Appl
14	42	100.0	16	3 US-09-169-425C-25	Sequence 25, Appl
15	42	100.0	16	4 US-09-759-960-25	Sequence 18, Appl
16	42	100.0	19	4 US-09-980-523A-18	Sequence 50, Appl
17	42	100.0	20	3 US-08-075-541D-50	Sequence 12, Appl
18	42	100.0	20	4 US-09-794-529B-12	Sequence 13, Appl
19	42	100.0	20	4 US-09-794-529B-13	Sequence 13, Appl
20	42	100.0	20	4 US-09-794-517A-12	Sequence 12, Appl
21	42	100.0	20	4 US-09-794-517A-13	Sequence 13, Appl
22	42	100.0	20	4 US-09-011-645E-12	Sequence 12, Appl
23	42	100.0	20	4 US-09-011-645E-13	Sequence 13, Appl
24	42	100.0	20	4 US-09-794-832-12	Sequence 12, Appl
25	42	100.0	20	4 US-09-794-832-13	Sequence 13, Appl
26	42	100.0	20	4 US-09-680-806A-12	Sequence 12, Appl
27	42	100.0	20	4 US-09-680-806A-13	Sequence 13, Appl

28	42	100.0	20	4 US-09-552-868-12	Sequence 12, Appl
29	42	100.0	20	4 US-09-552-868-13	Sequence 13, Appl
30	42	100.0	20	4 US-09-636-295-12	Sequence 12, Appl
31	42	100.0	20	4 US-09-636-295-13	Sequence 13, Appl
32	42	100.0	21	2 US-08-934-915-50	Sequence 50, Appl
33	42	100.0	21	2 US-08-934-915-57	Sequence 157, Appl
34	42	100.0	21	4 US-09-580-177A-76	Sequence 76, Appl
35	42	100.0	26	3 US-08-075-541D-40	Sequence 40, Appl
36	42	100.0	28	4 US-09-486-394-5	Sequence 5, Appl
37	42	100.0	30	2 US-08-934-915-54	Sequence 54, Appl
38	42	100.0	30	4 US-09-486-394-4	Sequence 4, Appl
39	42	100.0	59	3 US-09-390-027-6	Sequence 6, Appl
40	42	100.0	98	1 US-08-406-248-6	Sequence 6, Appl
41	42	100.0	98	3 US-08-075-541D-42	Sequence 42, Appl
42	42	100.0	98	3 US-09-382-616A-1	Sequence 1, Appl
43	42	100.0	98	3 US-08-944-368A-4	Sequence 4, Appl
44	42	100.0	98	3 US-09-820-764-4	Sequence 4, Appl
45	42	100.0	98	4 US-09-613-303-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-787-547-106
; Sequence 106, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Curley, Joanne M.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-787-547-106

Query Match 100.0%; Score 42; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.le+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LLMGTLGIV 9
      |||||
Db      1 LLMGTLGIV 9

RESULT 2
US-08-948-378A-1
; Sequence 1, Application US/08948378A
; Patent No. 6013258
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM
; THE HPV E7 PROTEIN
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,378A
; FILING DATE: 09-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-948-378A-1

Query Match      100.0%; Score 42; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LLMGTLGIV 9
      |||||
Db      1 LLMGTLGIV 9

RESULT 3
US-09-124-671-9
; Sequence 9, Application US/09124671A
; Patent No. 6160088
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/09/124,671A
; CURRENT FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42

Query Match      100.0%; Score 42; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LLMGTLGIV 9
      |||||
Db      1 LLMGTLGIV 9

RESULT 4
US-09-169-425C-1
; Sequence 1, Application US/09169425C
; Patent No. 6183746
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,425C
; FILING DATE: 09-OCT-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/061,657
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-169-425C-1

Query Match      100.0%; Score 42; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LLMGTLGIV 9
      |||||
Db      1 LLMGTLGIV 9

RESULT 5
US-08-197-484-65

Query Match      100.0%; Score 42; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LLMGTLGIV 9
      |||||
Db      1 LLMGTLGIV 9

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: papillomavirus
US-09-124-671-9

Query Match      100.0%; Score 42; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LLMGTLGIV 9
      |||||
Db      1 LLMGTLGIV 9
```

; Sequence 65, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Stuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-65

Query Match 100.0%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
Db 1 LLMGTLGIV 9

RESULT 6
US-09-759-960-1
; Sequence 1, Application US/09759960
; Patent No. 6582704
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn

; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,960
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/169,425
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Frazer, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-759-960-1

Query Match 100.0%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
Db 1 LLMGTLGIV 9

RESULT 7
US-09-601-729-271
; Sequence 271, Application US/09601729
; Patent No. 6683052
; GENERAL INFORMATION:
; APPLICANT: THIAM, KADER
; APPLICANT: AURIAULT, CLAUDE
; APPLICANT: GRAS-MASSE, HELENE
; APPLICANT: LOING, ESTELLE
; APPLICANT: VERWAERDE, CLAUDIE
; APPLICANT: GUILLET, JEAN GERARD
; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
; TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: USB-97-AU-IN
; CURRENT APPLICATION NUMBER: US/09/601,729
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: PCT/FR99/00259
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 98 01439
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 271
; LENGTH: 9
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 US-09-601-729-271

Query Match 100.0%; Score 42; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMGTLGIV 9
 |||||
 DB 1 LLMGTLGIV 9

RESULT 8

US-10-365-908-5
 ; Sequence 5, Application US/10365908
 ; Patent No. 6797491
 ; GENERAL INFORMATION:
 ; APPLICANT: Neefe, John R.
 ; APPLICANT: Boux, Leslie J.
 ; APPLICANT: Winnett, Mark T.
 ; APPLICANT: Goldstone, Stephen E.
 ; APPLICANT: Siegel, Marvin
 ; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
 ; FILE REFERENCE: 12071-003001
 ; CURRENT APPLICATION NUMBER: US/10/365,908
 ; CURRENT FILING DATE: 2003-02-13
 ; PRIOR APPLICATION NUMBER: US/09/891,823
 ; PRIOR FILING DATE: 2001-10-19
 ; PRIOR APPLICATION NUMBER: US 60/214,202
 ; PRIOR FILING DATE: 2000-06-26
 ; NUMBER OF SEQ ID NOS: 140
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Human papilloma virus
 US-10-365-908-5

Query Match 100.0%; Score 42; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMGTLGIV 9
 |||||
 DB 1 LLMGTLGIV 9

RESULT 9

PCT-US95-02121-65
 ; Sequence 65, Application PC/TUS9502121
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
 ; TITLE OF INVENTION: CTL IMMUNITY
 ; NUMBER OF SEQUENCES: 153
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/02121
 ; FILING DATE: 16-FEB-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/197,484
 ; FILING DATE: 16-FEB-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/935,811
 ; FILING DATE: 26-AUG-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/874,491

; FILING DATE: 27-APR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/827,682
 ; FILING DATE: 29-JAN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/749,568
 ; FILING DATE: 26-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parmelee, Steven W.
 ; REGISTRATION NUMBER: 31,990
 ; REFERENCE/DOCKET NUMBER: 14137-26-4PC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 467-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 65:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 PCT-US95-02121-65

Query Match 100.0%; Score 42; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMGTLGIV 9
 |||||
 DB 1 LLMGTLGIV 9

RESULT 10

US-10-365-908-47
 ; Sequence 47, Application US/10365908
 ; Patent No. 6797491
 ; GENERAL INFORMATION:
 ; APPLICANT: Neefe, John R.
 ; APPLICANT: Boux, Leslie J.
 ; APPLICANT: Winnett, Mark T.
 ; APPLICANT: Goldstone, Stephen E.
 ; APPLICANT: Siegel, Marvin
 ; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
 ; FILE REFERENCE: 12071-003001
 ; CURRENT APPLICATION NUMBER: US/10/365,908
 ; CURRENT FILING DATE: 2003-02-13
 ; PRIOR APPLICATION NUMBER: US/09/891,823
 ; PRIOR FILING DATE: 2001-10-19
 ; PRIOR APPLICATION NUMBER: US 60/214,202
 ; PRIOR FILING DATE: 2000-06-26
 ; NUMBER OF SEQ ID NOS: 140
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 47
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Human papilloma virus
 US-10-365-908-47

Query Match 100.0%; Score 42; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.04;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMGTLGIV 9
 |||||
 DB 2 LLMGTLGIV 10

RESULT 11

US-08-948-378A-3
 ; Sequence 3, Application US/08948378A
 ; Patent No. 6013258
 ; GENERAL INFORMATION:
 ; APPLICANT: Urban, Robert G.

APPLICANT: Chiciz, Roman M.
APPLICANT: Collins, Edward J.
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM
THE HPV E7 PROTEIN
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,378A
FILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-543-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-08-948-378A-3

Query Match 100.0%; Score 42; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMGTLGIV 9
DB 1 LLMGTLGIV 9

RESULT 12
US-09-169-425C-3
Sequence 3, Application US/09169425C
Patent No. 6183746
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chiciz, Roman M.
APPLICANT: Collins, Edward J.
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/169,425C
FILING DATE: 09-OCT-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/061,657
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/004002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-543-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-169-425C-3

Query Match 100.0%; Score 42; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMGTLGIV 9
DB 1 LLMGTLGIV 9

RESULT 13
US-09-759-960-3
Sequence 3, Application US/09759960
Patent No. 6582704
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chiciz, Roman M.
APPLICANT: Collins, Edward J.
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,960
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/169,425
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/004002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-543-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid

;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-759-960-3

Query Match 100.0%; Score 42; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
| | | | | | | |
Db 1 LLMGTLGIV 9

RESULT 14
US-09-169-425C-25

; Sequence 25, Application US/09169425C
; Patent No. 6183746
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09169,425C
; FILING DATE: 09-OCT-1998

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/061,657
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-169-425C-25

Query Match 100.0%; Score 42; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
| | | | | | | |
Db 1 LLMGTLGIV 9

RESULT 15

US-09-759-960-25
; Sequence 25, Application US/09759960
; Patent No. 6582704
; GENERAL INFORMATION:

; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09759,960
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/169,425
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-759-960-25

Query Match 100.0%; Score 42; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMGTLGIV 9
| | | | | | | |
Db 1 LLMGTLGIV 9

Search completed: June 28, 2005, 19:29:17
Job time : 18.15 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-17
Perfect score: 44
Sequence: 1 TLEDLLMGT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	44	100.0	26	2	Q84267	Q84267 human papill
2	44	100.0	93	2	Q9QDH2	Q9qdh2 human papill
3	44	100.0	93	2	Q9QDH4	Q9qdh4 human papill
4	44	100.0	93	2	Q9QDH6	Q9qdh6 human papill
5	44	100.0	93	2	Q9QDH8	Q9qdh8 human papill
6	44	100.0	94	2	Q8B5P6	Q8B5p6 human papill
7	44	100.0	98	1	VE7_HPV16	P03129 human papill
8	44	100.0	98	2	O11650	O11650 human papill
9	44	100.0	98	2	O12337	O12337 human papill
10	44	100.0	98	2	O12338	O12338 human papill
11	44	100.0	98	2	Q8QRD2	Q8qrd2 human papill
12	44	100.0	98	2	Q8QRD3	Q8qrd3 human papill
13	44	100.0	98	2	Q8QRD4	Q8qrd4 human papill
14	44	100.0	98	2	Q8V1J0	Q8v1j0 human papill
15	44	100.0	98	2	Q778H3	Q778h3 human papill
16	44	100.0	98	2	Q778H5	Q778h5 human papill
17	39	88.6	99	1	VE7_HPV35	P27230 human papill
18	39	88.6	99	2	Q76WP2	Q76wp2 human papill
19	39	88.6	113	1	VE7_RHPV1	P22161 rhesus papill
20	37	84.1	98	2	Q8JTG7	Q8jtg7 human papill
21	36	81.8	99	2	Q705H9	Q705h9 human papill
22	36	81.8	147	2	Q9MYV6	Q9myv6 sus scrofa
23	36	81.8	156	2	Q983E3	Q983e3 rhizobium l
24	36	81.8	687	2	Q9C8K2	Q9c8k2 arabidopsis
25	36	81.8	6420	2	Q7QZU9	Q7quz9 giardia lam
26	35	79.5	98	1	VE7_HPV58	P26557 human papill
27	35	79.5	98	2	Q8QHN7	Q8qhn7 human papill
28	35	79.5	98	2	Q8QHQ2	Q8qhq2 human papill
29	35	79.5	98	2	Q8QSE8	Q8qse8 human papill
30	35	79.5	98	2	Q8QSE9	Q8qse9 human papill
31	35	79.5	98	2	Q8QSF0	Q8qsf0 human papill

ALIGNMENTS

RESULT 1

Q84267 PRELIMINARY; PRT; 26 AA.
 AC Q84267;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE E7 ORF (Fragment).
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89095007; PubMed=2536104;
 RA Choo K.-B., Cheung W.-P., Liew L.-N., Lee H.-H., Han S.-H.;
 RT "Presence of Caenated Human Papillomavirus Type 16 Episomes in a
 RT Cervical Carcinoma Cell Line."
 RL J. Virol. 63:782-789(1989).
 DR EMBL; M24215; AAA46944.1;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 FT NON_TER 1
 SQ SEQUENCE 26 AA; 2799 MW; 91C16FD34D18B34 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.061;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLEDLLMGT 9
 |||||
 Db 6 TLEDLLMGT 14

RESULT 2

Q9QDH2 PRELIMINARY; PRT; 93 AA.
 AC Q9QDH2;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE E7 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF197869; AAF13399.1;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 FT NON_TER 93

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SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;
Query Match 100.0%; Score 44; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TLEDLLMGT 9
Db 78 TLEDLLMGT 86

RESULT 3
Q9QDH4
ID Q9QDH4 PRELIMINARY; PRT; 93 AA.
AC Q9QDH4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;
Query Match 100.0%; Score 44; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TLEDLLMGT 9
Db 78 TLEDLLMGT 86

RESULT 4
Q9QDH6
ID Q9QDH6 PRELIMINARY; PRT; 93 AA.
AC Q9QDH6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187867; AAF13395.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 93
SQ SEQUENCE 93 AA; 10513 MW; 92C7054341326A1F CRC64;
Query Match 100.0%; Score 44; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TLEDLLMGT 9
Db 78 TLEDLLMGT 86

RESULT 5
Q9QDH8
ID Q9QDH8 PRELIMINARY; PRT; 93 AA.
AC Q9QDH8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;
Query Match 100.0%; Score 44; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TLEDLLMGT 9
Db 78 TLEDLLMGT 86

RESULT 6
Q8B5P6
ID Q8B5P6 PRELIMINARY; PRT; 94 AA.
AC Q8B5P6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E7 oncoprotein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469197; AAO15692.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 94
SQ SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;
Query Match 100.0%; Score 44; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TLEDLLMGT 9
Db 78 TLEDLLMGT 86

RESULT 7
VE7_HPV16
ID VE7_HPV16 STANDARD; PRT; 98 AA.
AC P03129;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE E7 protein.
DE Name=E7;
GN Name=E7;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

```

OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85246220; PubMed=2990099;
RA Seedorf K., Kramer G., Durst M., Suhai S., Roweamp W.G.;
RT "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185 (1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90218027; PubMed=2157796;
RA Schneider-Maunoury S., Pehau-Arnauudet G., Breithurd F., Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-v cells,
a line derived from a vulvar intraepithelial neoplasia.";
RL J. Gen. Virol. 71:809-817 (1990).
RN [3]
RP SEQUENCE FROM N.A.
RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBSJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RL Beth-Giraldo E., Giraldo G.;
RN Submitted (JUN-1997) to the EMBL/GenBank/DBSJ databases.
RN [5]
RP FUNCTION.
RX MEDLINE=88223347; PubMed=2836062;
RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;
RT "The human papillomavirus type 16 E7 gene encodes transactivation and
transformation functions similar to those of adenovirus E1A.";
RL Cell 53:539-547 (1988).
CC -! FUNCTION: E7 protein has both transforming and trans-activating
activities.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; K02718; AAA46940.1; -
DR EMBL; D00735; BAA00633.1; -
DR EMBL; U76411; AAB18962.1; -
DR EMBL; U76412; AAB18963.1; -
DR EMBL; U76413; AAB18964.1; -
DR EMBL; AF003020; AAB70737.1; -
DR EMBL; AF003023; AAB70740.1; -
DR EMBL; AF003024; AAB70741.1; -
DR EMBL; AF003025; AAB70742.1; -
DR EMBL; AF003026; AAB70743.1; -
DR PIR; A03688; W7WLS.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW Transcription regulation.
FT SITE 58 61 C-XX-C motif-1.
FT SITE 91 94 C-XX-C motif-2.
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 100.0%; Score 44; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TLEDLLMGT 9
Db 78 TLEDLLMGT 86

RESULT 8
O11650
ID O11650 PRELIMINARY; PRT; 98 AA.

O11650;
AC 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DE Putative transforming protein E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
Lee H.P.;
RT "Major sequence variants in E7 gene of human papillomavirus type 16
from cervical cancerous and noncancerous lesions of Korean women.";
RL Gynecol. Oncol. 66:275-281 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
Lee H.-P.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Terai M., Ma Z., Burk R.D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBSJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700 (2002).
RN [5]
RP SEQUENCE FROM N.A.
RA Terai M., Fu L., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; U76404; AAC58243.1; -
DR EMBL; AF472509; AAO15706.1; -
DR EMBL; AF486326; AAL96631.1; -
DR EMBL; AF486327; AAL96632.1; -
DR EMBL; AF486330; AAL96635.1; -
DR EMBL; AF486331; AAL96636.1; -
DR EMBL; AF486332; AAL96637.1; -
DR EMBL; AF486333; AAL96638.1; -
DR EMBL; AF486334; AAL96639.1; -
DR EMBL; AF486336; AAL96641.1; -
DR EMBL; AF486338; AAL96643.1; -
DR EMBL; AF486346; AAL96651.1; -
DR EMBL; AF486350; AAL96655.1; -
DR EMBL; AF486351; AAL96656.1; -
DR EMBL; AF534061; AAQ10404.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 44; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TLEDLLMGT 9
Db 78 TLEDLLMGT 86

RESULT 9
O12337
ID O12337 PRELIMINARY; PRT; 98 AA.
AC O12337;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus
 RT type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 DR EMBL; AF003021; AAB70738.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLEDLLMGT 9
 |||||
 Db 78 TLEDLLMGT 86

RESULT 10

O12338 PRELIMINARY; PRT; 98 AA.
 AC O12338;
 DT 01-JUL-1997 (TRENBLrel. 04, Created)
 DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update).
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus
 RT type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 DR EMBL; AF003021; AAB70738.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 10969 MW; 9BD612534CCEA59B CRC64;

Query Match 100.0%; Score 44; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLEDLLMGT 9
 |||||
 Db 78 TLEDLLMGT 86

RESULT 11

Q8QRD2 PRELIMINARY; PRT; 98 AA.
 ID Q8QRD2;
 AC Q8QRD2;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)

DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22182962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RT "Human papillomavirus type 16 intratypic variant infection and risk
 RT for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700(2002).
 DR EMBL; AF486345; AAL96650.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 100.0%; Score 44; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLEDLLMGT 9
 |||||
 Db 78 TLEDLLMGT 86

RESULT 12

Q8QRD3 PRELIMINARY; PRT; 98 AA.
 ID Q8QRD3;
 AC Q8QRD3;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22182962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RT "Human papillomavirus type 16 intratypic variant infection and risk
 RT for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700(2002).
 DR EMBL; AF486344; AAL96649.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLEDLLMGT 9
 |||||
 Db 78 TLEDLLMGT 86

RESULT 13

Q8QRD4 PRELIMINARY; PRT; 98 AA.
 ID Q8QRD4;
 AC Q8QRD4;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;

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RN SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486329; AAL96634.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11025 MW; 86E24B234CC3281B CRC64;

Query Match 100.0%; Score 44; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLEDLLMGT 9
Db 78 TLEDLLMGT 86

RESULT 14
QSVLJO PRELIMINARY; PRT; 98 AA.
AC QSVLJO;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Jinhu X., Xinxing W., Yun T.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461264; AAL66736.1; -.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10997 MW; 9BD610834CCEA59B CRC64;

Query Match 100.0%; Score 44; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLEDLLMGT 9
Db 78 TLEDLLMGT 86

RESULT 15
Q778H3 PRELIMINARY; PRT; 98 AA.
AC Q778H3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388063; CAB45119.1; -.
DR InterPro; IPR000148; Papvi_E7.
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DR Pfam; PF00527; E7; 1.
FT NON_TER 98 98
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Query Match 100.0%; Score 44; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLEDLLMGT 9
Db 78 TLEDLLMGT 86

Search completed: June 28, 2005, 19:19:29
Job time : 56.3 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 01:35:30 ; Search time 57.55 Seconds
(without alignments)
60.138 Million cell updates/sec

Title: US-08-170-344-17

Perfect score: 44

Sequence: 1 TLEDLLMGT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	44	100.0	9	9 US-09-891-823-6	Sequence 6, Appli
2	44	100.0	9	14 US-10-365-908-6	Sequence 6, Appli
3	44	100.0	9	16 US-10-871-138-6	Sequence 6, Appli
4	44	100.0	10	9 US-09-891-823-18	Sequence 18, Appl
5	44	100.0	10	9 US-09-891-823-42	Sequence 42, Appl
6	44	100.0	10	14 US-10-365-908-18	Sequence 18, Appl
7	44	100.0	10	14 US-10-365-908-42	Sequence 42, Appl
8	44	100.0	10	16 US-10-871-138-18	Sequence 18, Appl
9	44	100.0	10	16 US-10-871-138-42	Sequence 42, Appl
10	44	100.0	15	16 US-10-476-570-50	Sequence 50, Appl
11	44	100.0	15	16 US-10-476-570-51	Sequence 51, Appl

12	44	100.0	15	16	US-10-306-541-68	Sequence 68, Appl
13	44	100.0	15	16	US-10-306-541-75	Sequence 75, Appl
14	44	100.0	15	16	US-10-306-541-78	Sequence 78, Appl
15	44	100.0	15	16	US-10-306-541-79	Sequence 79, Appl
16	44	100.0	15	16	US-10-306-541-95	Sequence 95, Appl
17	44	100.0	20	15	US-10-432-465-50	Sequence 50, Appl
18	44	100.0	20	16	US-10-890-526-75	Sequence 75, Appl
19	44	100.0	20	17	US-10-484-063-19	Sequence 19, Appl
20	44	100.0	21	15	US-10-432-465-51	Sequence 51, Appl
21	44	100.0	21	16	US-10-476-570-18	Sequence 18, Appl
22	44	100.0	21	16	US-10-890-526-76	Sequence 76, Appl
23	44	100.0	23	16	US-10-476-570-17	Sequence 17, Appl
24	44	100.0	98	9	US-09-728-466-1	Sequence 1, Appli
25	44	100.0	98	9	US-09-820-765-4	Sequence 4, Appli
26	44	100.0	98	9	US-09-824-017-4	Sequence 4, Appli
27	44	100.0	98	10	US-09-986-118A-4	Sequence 8, Appli
28	44	100.0	98	14	US-10-267-311-8	Sequence 8, Appli
29	44	100.0	98	14	US-10-177-390-8	Sequence 8, Appli
30	44	100.0	98	14	US-10-201-764-19	Sequence 19, Appl
31	44	100.0	98	15	US-10-392-113-29	Sequence 29, Appl
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33	44	100.0	98	15	US-10-681-410-19	Sequence 19, Appl
34	44	100.0	98	16	US-10-772-988-3	Sequence 3, Appli
35	44	100.0	98	16	US-10-479-541-5	Sequence 5, Appli
36	44	100.0	98	17	US-10-042-526A-4	Sequence 4, Appli
37	44	100.0	98	17	US-10-657-399-1	Sequence 1, Appli
38	44	100.0	98	17	US-10-858-384-12	Sequence 12, Appl
39	44	100.0	98	17	US-10-484-063-26	Sequence 26, Appl
40	44	100.0	98	17	US-10-343-448-5	Sequence 5, Appli
41	44	100.0	98	17	US-10-679-956-8	Sequence 8, Appli
42	44	100.0	98	17	US-10-367-057-17	Sequence 17, Appl
43	44	100.0	99	15	US-10-115-440-7	Sequence 7, Appli
44	44	100.0	111	16	US-10-472-724-4	Sequence 4, Appli
45	44	100.0	121	14	US-10-267-311-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-891-823-6
; Sequence 6, Application US/09891823
; Publication No. US20020110566A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Lealie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/09/891,823
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-891-823-6

Query Match 100.0%; Score 44; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9

Db 1 TLEDLLMGT 9

RESULT 2

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US-10-365-908-6
; Sequence 6, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/09/891.823
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-6

Query Match          100.0%; Score 44; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 1 TLEDLLMGT 9

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US-10-871-138-6
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; Publication No. US20040235741A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/871,138
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/891.823
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-871-138-6

Query Match          100.0%; Score 44; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TLEDLLMGT 9

US-10-365-908-18
; Sequence 18, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/09/891.823
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
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; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-891-823-18

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 TLEDLLMGT 10

US-09-891-823-42
; Sequence 42, Application US/09891823
; Publication No. US20020110566A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/09/891.823
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
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; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-891-823-42

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 1 TLEDLLMGT 9

US-10-365-908-18
; Sequence 18, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/09/891.823
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-891-823-18

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Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 1 TLEDLLMGT 9

US-10-871-138-6
; Sequence 6, Application US/10871138
; Publication No. US20040235741A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/871,138
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/891.823
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-871-138-6

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
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US-09-891-823-18
; Sequence 18, Application US/09891823
; Publication No. US20020110566A1

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; FILE REFERENCE: 12071-003001
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US-10-365-908-18

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Db 2 TLEDLLMGT 10

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US-10-365-908-42
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; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
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; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
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; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-42

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TLEDLLMGT 9

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US-10-871-138-18
; Sequence 18, Application US/10871138
; Publication No. US20040235741A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/871,138
; CURRENT FILING DATE: 2004-06-18
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; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-871-138-18

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Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 2 TLEDLLMGT 10

RESULT 9
US-10-871-138-42
; Sequence 42, Application US/10871138
; Publication No. US20040235741A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/871,138
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-871-138-42

Query Match      100.0%; Score 44; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 1 TLEDLLMGT 9

RESULT 10
US-10-476-570-50
; Sequence 50, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
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; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E7 72-86
US-10-476-570-50

Query Match      100.0%; Score 44; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 7 TLEDLLMGT 15

RESULT 11
US-10-476-570-51
; Sequence 51, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLARD, Isabelle
; APPLICANT: POUVELLE-NORVILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCI/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E7 77-91
US-10-476-570-51

Query Match      100.0%; Score 44; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 2 TLEDLLMGT 10

RESULT 12
US-10-306-541-68
; Sequence 68, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 249
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 78
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
; US-10-306-541-78

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Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 68
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
; US-10-306-541-68

Query Match      100.0%; Score 44; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 7 TLEDLLMGT 15

RESULT 13
US-10-306-541-75
; Sequence 75, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 75
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
; US-10-306-541-75

Query Match      100.0%; Score 44; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 1 TLEDLLMGT 9

RESULT 14
US-10-306-541-78
; Sequence 78, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 78
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
; US-10-306-541-78

Query Match      100.0%; Score 44; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TLEDLLMGT 9
Db 6 TLEDLLMGT 14

RESULT 15

US-10-306-541-79
; Sequence 79, Application US/10306541
; Publication NO. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 79
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-79

Query Match 100.0%; Score 44; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLEDLLMGT 9
Db 3 TLEDLLMGT 11

Search completed: June 29, 2005, 03:24:11
Job time : 57.55 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)
39.174 Million cell updates/sec

Title: US-08-170-344-17
Perfect score: 44
Sequence: 1 TLEDLLMGT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	9	US-10-365-908-6	Sequence 6, Appli
2	44	100.0	10	US-10-365-908-18	Sequence 18, Appli
3	44	100.0	10	US-10-365-908-42	Sequence 42, Appli
4	44	100.0	20	US-08-075-541D-49	Sequence 49, Appli
5	44	100.0	20	US-08-075-541D-50	Sequence 50, Appli
6	44	100.0	20	US-09-980-177A-75	Sequence 75, Appli
7	44	100.0	21	US-08-934-915-50	Sequence 50, Appli
8	44	100.0	21	US-09-980-177A-76	Sequence 76, Appli
9	44	100.0	26	US-08-075-541D-40	Sequence 40, Appli
10	44	100.0	28	US-09-486-394-5	Sequence 5, Appli
11	44	100.0	30	US-08-934-915-53	Sequence 53, Appli
12	44	100.0	30	US-08-934-915-54	Sequence 54, Appli
13	44	100.0	30	US-09-486-394-4	Sequence 4, Appli
14	44	100.0	98	US-08-406-248-6	Sequence 6, Appli
15	44	100.0	98	US-08-075-541D-42	Sequence 42, Appli
16	44	100.0	98	US-09-382-616A-1	Sequence 1, Appli
17	44	100.0	98	US-08-944-368A-4	Sequence 4, Appli
18	44	100.0	98	US-09-820-764-4	Sequence 4, Appli
19	44	100.0	98	US-09-613-303-8	Sequence 8, Appli
20	44	100.0	98	US-09-566-420-19	Sequence 19, Appli
21	44	100.0	98	US-09-986-118A-4	Sequence 4, Appli
22	44	100.0	98	US-09-728-466-1	Sequence 1, Appli
23	44	100.0	98	US-09-824-017-4	Sequence 4, Appli
24	44	100.0	98	US-10-267-311-8	Sequence 8, Appli
25	44	100.0	98	US-10-201-764-19	Sequence 19, Appli
26	44	100.0	98	US-09-637-746-3	Sequence 3, Appli
27	44	100.0	98	US-09-501-097A-7	Sequence 7, Appli

28	44	100.0	98	4	US-09-980-523A-12	Sequence 12, Appli
29	44	100.0	121	4	US-09-613-303-12	Sequence 12, Appli
30	44	100.0	121	4	US-10-267-311-12	Sequence 12, Appli
31	44	100.0	172	3	US-08-860-165-14	Sequence 14, Appli
32	44	100.0	172	3	US-09-359-382-14	Sequence 14, Appli
33	44	100.0	198	4	US-09-613-303-35	Sequence 35, Appli
34	44	100.0	198	4	US-10-267-311-35	Sequence 35, Appli
35	44	100.0	220	3	US-09-485-885-1	Sequence 1, Appli
36	44	100.0	220	3	US-09-485-885-12	Sequence 12, Appli
37	44	100.0	239	3	US-09-485-885-18	Sequence 18, Appli
38	44	100.0	253	2	US-08-459-818-20	Sequence 20, Appli
39	44	100.0	253	2	US-08-889-666-20	Sequence 20, Appli
40	44	100.0	253	2	US-08-465-078-20	Sequence 20, Appli
41	44	100.0	253	2	US-08-725-776-20	Sequence 20, Appli
42	44	100.0	253	2	US-08-488-062-20	Sequence 20, Appli
43	44	100.0	263	1	US-08-117-083-9	Sequence 9, Appli
44	44	100.0	266	3	US-08-860-165-10	Sequence 10, Appli
45	44	100.0	266	3	US-09-359-382-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-10-365-908-6
; Sequence 6, Application US/10365908
; Patent No. 6797491
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-6
Query Match 100.0%; Score 44; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TLEDLLMGT 9
Db 1 TLEDLLMGT 9
RESULT 2
US-10-365-908-18
; Sequence 18, Application US/10365908
; Patent No. 6797491
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823

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; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-18

Query Match      100.0%; Score 44; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TLEDLLMGT 9
Db      2 TLEDLLMGT 10

RESULT 3
US-10-365-908-42
; Sequence 42, Application US/10365908
; Patent No. 6797491
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-42

Query Match      100.0%; Score 44; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TLEDLLMGT 9
Db      1 TLEDLLMGT 9

RESULT 4
US-08-075-541D-49
; Sequence 49, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-49

Query Match      100.0%; Score 44; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TLEDLLMGT 9
Db      9 TLEDLLMGT 17

RESULT 5
US-08-075-541D-50
; Sequence 50, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-075-541D-50

Query Match 100.0%; Score 44; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 4 TLEDLLMGT 12

RESULT 6
US-09-980-177A-75
; Sequence 75, Application US/09980177A
; Patent No. 6838084
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus Li-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/09/980,177A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; US-09-980-177A-75

Query Match 100.0%; Score 44; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 12 TLEDLLMGT 20

RESULT 7
US-08-934-915-50
; Sequence 50, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-50

Query Match 100.0%; Score 44; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 1 TLEDLLMGT 9

RESULT 8
US-09-980-177A-76
; Sequence 76, Application US/09980177A
; Patent No. 6838084
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus Li-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/09/980,177A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; US-09-980-177A-76

Query Match 100.0%; Score 44; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
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Db 1 TLEDLLMGT 9
RESULT 9
US-08-075-541D-40
; Sequence 40, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075.541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-40
Query Match 100.0%; Score 44; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TLEDLLMGT 9
Db 7 TLEDLLMGT 15
RESULT 10
US-09-486-394-5
; Sequence 5, Application US/09486394
; Patent No. 6478749
; GENERAL INFORMATION:
; APPLICANT: Hopfl, Reinhard
; TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
; FILE REFERENCE: 032929-001
; CURRENT APPLICATION NUMBER: US/09/486.394
; CURRENT FILING DATE: 2000-05-20
; PRIOR APPLICATION NUMBER: PCT/EP98/04773

; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: DE 197 37 409.3
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(28)
; OTHER INFORMATION: E7 peptide.
US-09-486-394-5
Query Match 100.0%; Score 44; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TLEDLLMGT 9
Db 8 TLEDLLMGT 16
RESULT 11
US-08-934-915-53
; Sequence 53, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-53
Query Match 100.0%; Score 44; DB 2; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.022; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 21 TLEDLLMGT 29

RESULT 12

US-08-934-915-54
; Sequence 54, Application US/08934915
; Patent No. 5932412

GENERAL INFORMATION:

APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Fouch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:

INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-934-915-54

Query Match 100.0%; Score 44; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 10 TLEDLLMGT 18

RESULT 13

US-09-486-394-4
; Sequence 4, Application US/09486394
; Patent No. 6478749

GENERAL INFORMATION:

APPLICANT: Hopfl, Reinhard
TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
FILE REFERENCE: 032929-001

CURRENT APPLICATION NUMBER: US/09/486,394
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/04773
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: DE 197 37 409.3
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 30

TYPE: PRT
ORGANISM: Human papillomavirus type 16

FEATURES:

NAME/KEY: PEPTIDE
LOCATION: (1)..(30)
OTHER INFORMATION: E7 peptide.
US-09-486-394-4

Query Match 100.0%; Score 44; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9
Db 18 TLEDLLMGT 26

RESULT 14

US-08-406-248-6
; Sequence 6, Application US/08406248
; Patent No. 5736318

GENERAL INFORMATION:

APPLICANT: Munger, Karl
APPLICANT: Jones, D. Leanne
TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
TITLE OF INVENTION: TRANSFORMED CELLS
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Kusmer
STREET: 200 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,248
FILING DATE:

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: Mcdaniels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: HAZ-011
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-406-248-6

Query Match 100.0%; Score 44; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLLMGT 9

Db 78 TLEDLMGT 86
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RESULT 15
US-08-075-541D-42
; Sequence 42, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-42

Query Match 100.0%; Score 44; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLEDLMGT 9
|||||
Db 78 TLEDLMGT 86

Search completed: June 28, 2005, 19:29:16
JOB time : 17.15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-16
Perfect score: 48
Sequence: 1 RLCVQSTHV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	100.0	77	2	Q8B5P5	Q8B5P5 human papil
2	48	100.0	93	2	Q9QDH2	Q9QDH2 human papil
3	48	100.0	93	2	Q9QDH4	Q9QDH4 human papil
4	48	100.0	93	2	Q9QDH6	Q9QDH6 human papil
5	48	100.0	93	2	Q9QDH8	Q9QDH8 human papil
6	48	100.0	94	2	Q8B5P6	Q8B5P6 human papil
7	48	100.0	98	1	VE7_HPV16	P03129 human papil
8	48	100.0	98	2	O11650	P03129 human papil
9	48	100.0	98	2	O12337	O12337 human papil
10	48	100.0	98	2	O12338	O12338 human papil
11	48	100.0	98	2	Q9QDH2	Q9QDH2 human papil
12	48	100.0	98	2	Q9QDH3	Q9QDH3 human papil
13	48	100.0	98	2	Q8V1J0	Q8V1J0 human papil
14	48	100.0	98	2	Q778H3	Q778H3 human papil
15	48	100.0	98	2	Q778H5	Q778H5 human papil
16	47	97.9	99	1	VE7_HPV35	P27230 human papil
17	47	97.9	99	2	Q76W22	Q76W22 human papil
18	43	89.6	98	2	Q9QRD4	Q9QRD4 human papil
19	40	83.3	98	1	VE7_HPV31	P17387 human papil
20	40	83.3	98	2	Q6T377	Q6T377 human papil
21	39	81.2	95	1	Q6W4J4	Q6W4J4 hordeum vul
22	38	79.2	95	1	VE7_HPV54	Q81019 human papil
23	38	79.2	95	2	Q8B5X6	Q8B5X6 human papil
24	38	79.2	127	2	Q9GKW5	Q9GKW5 macaca fasc
25	37	77.1	347	2	Q6AYF7	Q6AYF7 rattus norv
26	37	77.1	349	2	Q922T2	Q922T2 mus musculu
27	37	77.1	349	2	Q8BHK5	Q8BHK5 m mus muscu
28	37	77.1	918	2	Q6F301	Q6F301 oryza sativ
29	36	75.0	595	2	Q18900	Q18900 caenorhabdi
30	36	75.0	1672	1	K21A_MOUSE	Q9qxl2 mus musculu
31	35	72.9	96	2	Q6LPE4	Q6LPE4 photobacter

32	35	72.9	262	2	Q72EN9	Q72en9 desulfovibr
33	35	72.9	338	2	Q02336	Q02336 caenorhabdi
34	35	72.9	357	2	O6SLC4	O6slc4 coenliobolu
35	35	72.9	538	2	O7XXA3	O7xxa3 oryza sativ
36	35	72.9	555	2	O8T5I3	O8t5i3 anopheles g
37	35	72.9	555	2	Q7PXU4	Q7pxu4 anopheles g
38	35	72.9	653	2	Q8BDI3	Q8bd13 homo sapien
39	35	72.9	1300	2	Q80AC2	Q80ac2 human herpe
40	35	72.9	1302	2	Q80AB9	Q80ab9 human herpe
41	35	72.9	1306	2	Q80AC0	Q80ac0 human herpe
42	35	72.9	1306	2	Q80AC4	Q80ac4 human herpe
43	35	72.9	1310	1	ICP4_VZVD	P09310 varicella-z
44	35	72.9	1310	2	Q98WV4	Q98wv4 human herpe
45	35	72.9	1310	2	Q98WV5	Q98wv5 human herpe

ALIGNMENTS

RESULT 1
Q8B5P5 PRELIMINARY; PRT; 77 AA.
AC Q8B5P5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP Ponglikitmongkol M., Vaeteewoontacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469198; AAOL5694.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 77
SQ SEQUENCE 77 AA; 8782 MW; C5DE3A7E546AC31B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RLCVQSTHV 9
Db ||||| 74
66 RLCVQSTHV 74

RESULT 2
Q9QDH2 PRELIMINARY; PRT; 93 AA.
AC Q9QDH2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187869; AAF13399.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;
Query Match 100.0%; Score 48; DB 2; Length 93;

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Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 66 RLCVQSTHV 74

RESULT 3
Q9QDH4 PRELIMINARY; PRT; 93 AA.
AC Q9QDH4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON TER 93
FT SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 48; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 66 RLCVQSTHV 74

RESULT 4
Q9QDH6 PRELIMINARY; PRT; 93 AA.
AC Q9QDH6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187867; AAF13395.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON TER 93
FT SEQUENCE 93 AA; 10513 MW; 92C7054341326A1F CRC64;

Query Match 100.0%; Score 48; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 66 RLCVQSTHV 74

RESULT 5
Q9QDH8 PRELIMINARY; PRT; 93 AA.
AC Q9QDH8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON TER 93
FT SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 48; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 66 RLCVQSTHV 74

RESULT 6
Q8B5P6 PRELIMINARY; PRT; 94 AA.
AC Q8B5P6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E7 oncoprotein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469197; AAC15892.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON TER 94
FT SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;

Query Match 100.0%; Score 48; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 66 RLCVQSTHV 74

RESULT 7
VE7 HPV16 STANDARD; PRT; 98 AA.
AC P03129;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
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AC Q9QDH8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON TER 93
FT SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 48; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 66 RLCVQSTHV 74

RESULT 6
Q8B5P6 PRELIMINARY; PRT; 94 AA.
AC Q8B5P6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E7 oncoprotein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469197; AAC15892.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON TER 94
FT SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;

Query Match 100.0%; Score 48; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 66 RLCVQSTHV 74

RESULT 7
VE7 HPV16 STANDARD; PRT; 98 AA.
AC P03129;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
```

RP SEQUENCE FROM N.A.
RX MEDLINE=85246220; PubMed=2990099;
RA Seedorf K., Kramer G., Duret M., Suhai S., Rowekamp W.G.;
RT "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90218027; PubMed=2157796;
RA Schneider-Maunoury S., Pehau-Arnaut G., Breitburd F., Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-v cells,
a line derived from a vulvar intraepithelial neoplasia.";
RL J. Gen. Virol. 71:809-817 (1990).
RN [3]
RP SEQUENCE FROM N.A.
RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Girardo E., Giraldo G.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP FUNCTION.
RX MEDLINE=88223347; PubMed=2836062;
RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;
RT "The human papillomavirus type 16 E7 gene encodes transactivation and
transformation functions similar to those of adenovirus E1A.";
RL Cell 53:539-547 (1988).
CC !- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K02718; AAA46940.1; -
DR EMBL; D00735; BAA00633.1; -
DR EMBL; U76411; AAB18962.1; -
DR EMBL; U76412; AAB18963.1; -
DR EMBL; U76413; AAB18964.1; -
DR EMBL; AF003020; AAB70737.1; -
DR EMBL; AF003023; AAB70740.1; -
DR EMBL; AF003024; AAB70741.1; -
DR EMBL; AF003025; AAB70742.1; -
DR EMBL; AF003026; AAB70743.1; -
DR FIR; A03688; W7MLHS.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW Transcription regulation.
FT SITE 58 61 C-XX-C motif-1.
FT SITE 91 94 C-XX-C motif-2.
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 100.0%; Score 48; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 66 RLCVQSTHV 74
|||||
RESULT 8
ID O11650 PRELIMINARY; PRT; 98 AA.
AC O11650;
AC O11650;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transforming protein E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
RA Lee H.P.;
RT "Major sequence variants in E7 gene of human papillomavirus type 16
from cervical cancerous and noncancerous lesions of Korean women.";
RL Gynecol. Oncol. 66:275-281 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
RA Lee H.-P.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Terai M., Ma Z., Burk R.D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700 (2002).
RN [5]
RP SEQUENCE FROM N.A.
RA Terai M., Fu L., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U76404; AAC58243.1; -
DR EMBL; AF472509; AAO15706.1; -
DR EMBL; AF486326; AAL96631.1; -
DR EMBL; AF486327; AAL96632.1; -
DR EMBL; AF486330; AAL96635.1; -
DR EMBL; AF486331; AAL96636.1; -
DR EMBL; AF486332; AAL96637.1; -
DR EMBL; AF486333; AAL96638.1; -
DR EMBL; AF486334; AAL96639.1; -
DR EMBL; AF486336; AAL96641.1; -
DR EMBL; AF486338; AAL96643.1; -
DR EMBL; AF486346; AAL96651.1; -
DR EMBL; AF486350; AAL96655.1; -
DR EMBL; AF486351; AAL96656.1; -
DR EMBL; AF534061; AAQ10404.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 66 RLCVQSTHV 74
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RESULT 9
ID O12337 PRELIMINARY; PRT; 98 AA.
AC O12337;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

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OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Torneello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003021; AAB70738.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 66 RLCVQSTHV 74

RESULT 10
O12338 PRELIMINARY; PRT; 98 AA.
AC O12338;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Torneello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Jinhu X., Xinxiang W., Yun T.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003022; AAB70739.1; -.
DR EMBL; AF477385; AAM03025.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10969 MW; 9BD612534CCEA59B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 66 RLCVQSTHV 74

RESULT 11
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AC O8QRD2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

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OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486345; AAL96650.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 66 RLCVQSTHV 74

RESULT 12
O8QRD3 PRELIMINARY; PRT; 98 AA.
AC O8QRD3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486344; AAL96649.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 66 RLCVQSTHV 74

RESULT 13
O8VIJ0 PRELIMINARY; PRT; 98 AA.
AC O8VIJ0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Jinhu X., Xinxiang W., Yun T.;

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RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF461264; AAL66736.1; -

DR Pfam; PF00527; E7; 1.

SQ SEQUENCE 98 AA; 10997 MW; 9BD610834CCEA59B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.056;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9

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Db 66 RLCVQSTHV 74

RESULT 14

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ID Q778H3 PRELIMINARY; PRT; 98 AA.

AC Q778H3;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE E7 protein (Fragment).

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10581;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20112892; PubMed=10644829;

RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,

RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

RT "Analysis of human papillomavirus type 16 E6 variants in relation to

RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";

RL J. Gen. Virol. 81:317-325(2000).

DR EMBL; AJ388063; CAB45119.1; -

DR InterPro; IPR000148; Papvi_E7.

DR Pfam; PF00527; E7; 1.

DR NON_TER 98

FT NON_TER 98

SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.056;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9

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Db 66 RLCVQSTHV 74

RESULT 15

Q778H5

ID Q778H5 PRELIMINARY; PRT; 98 AA.

AC Q778H5;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE E7 protein (Fragment).

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10581;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20112892; PubMed=10644829;

RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,

RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

RT "Analysis of human papillomavirus type 16 E6 variants in relation to

RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";

RL J. Gen. Virol. 81:317-325(2000).

DR EMBL; AJ388062; CAB45117.1; -

DR InterPro; IPR000148; Papvi_E7.

DR Pfam; PF00527; E7; 1.

DR NON_TER 98

FT NON_TER 98

SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.056;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9

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Db 66 RLCVQSTHV 74

Search completed: June 28, 2005, 19:19:28

Job time : 57.3 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 01:35:30 ; Search time 57.55 Seconds
(without alignments)
60.138 Million cell updates/sec

Title: US-08-170-344-16

Perfect score: 48

Sequence: 1 RLCVQSTHV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	48	100.0	9	14	US-10-161-097-41
2	48	100.0	9	14	US-10-133-210-274
3	48	100.0	9	17	US-10-484-063-16
4	48	100.0	10	9	US-09-891-823-17
5	48	100.0	10	14	US-10-365-908-17
6	48	100.0	10	16	US-10-871-138-17
7	48	100.0	15	16	US-10-476-570-16
8	48	100.0	15	16	US-10-476-570-48
9	48	100.0	15	16	US-10-306-541-77
10	48	100.0	15	16	US-10-306-541-83
11	48	100.0	15	16	US-10-306-541-89
					Sequence 41, Appl
					Sequence 274, App
					Sequence 16, Appl
					Sequence 17, Appl
					Sequence 17, Appl
					Sequence 16, Appl
					Sequence 48, Appl
					Sequence 77, Appl
					Sequence 83, Appl
					Sequence 89, Appl

Query Match 100.0% Score 48; DB 14; Length 9;

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12 48 100.0 15 16 US-10-306-541-93 Sequence 93, Appl
13 48 100.0 15 16 US-10-306-541-94 Sequence 94, Appl
14 48 100.0 18 15 US-10-355-268-16 Sequence 16, Appl
15 48 100.0 19 9 US-09-888-721-7 Sequence 7, Appl
16 48 100.0 19 15 US-10-668-400-9 Sequence 9, Appl
17 48 100.0 19 16 US-10-479-541-1 Sequence 1, Appl
18 48 100.0 20 10 US-09-828-645-4 Sequence 4, Appl
19 48 100.0 20 15 US-10-432-465-49 Sequence 49, Appl
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22 48 100.0 20 17 US-10-827-083-4 Sequence 4, Appl
23 48 100.0 23 16 US-10-476-570-17 Sequence 17, Appl
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25 48 100.0 98 9 US-09-820-765-4 Sequence 4, Appl
26 48 100.0 98 9 US-09-824-017-4 Sequence 4, Appl
27 48 100.0 98 10 US-09-986-118A-4 Sequence 4, Appl
28 48 100.0 98 14 US-10-267-311-8 Sequence 8, Appl
29 48 100.0 98 14 US-10-177-390-8 Sequence 8, Appl
30 48 100.0 98 14 US-10-501-764-19 Sequence 19, Appl
31 48 100.0 98 15 US-10-392-113-29 Sequence 29, Appl
32 48 100.0 98 15 US-10-654-129-4 Sequence 4, Appl
33 48 100.0 98 15 US-10-681-410-19 Sequence 19, Appl
34 48 100.0 98 16 US-10-772-988-3 Sequence 3, Appl
35 48 100.0 98 16 US-10-479-541-5 Sequence 5, Appl
36 48 100.0 98 17 US-10-042-526A-4 Sequence 4, Appl
37 48 100.0 98 17 US-10-657-399-1 Sequence 1, Appl
38 48 100.0 98 17 US-10-858-384-12 Sequence 12, Appl
39 48 100.0 98 17 US-10-484-063-26 Sequence 26, Appl
40 48 100.0 98 17 US-10-343-448-5 Sequence 5, Appl
41 48 100.0 98 17 US-10-679-956-8 Sequence 8, Appl
42 48 100.0 98 17 US-10-367-057-17 Sequence 17, Appl
43 48 100.0 99 15 US-10-115-440-7 Sequence 7, Appl
44 48 100.0 111 16 US-10-472-724-4 Sequence 4, Appl
45 48 100.0 121 14 US-10-267-311-12 Sequence 12, Appl

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ALIGNMENTS

RESULT 1

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; US-10-161-097-41
; Sequence 41, Application US/10161097
; Publication No. US20030096404A1
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADDEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
; TITLE OF INVENTION: DEVICES
; FILE REFERENCE: C1005/7012/KA/ERG
; CURRENT APPLICATION NUMBER: US/10161097
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US/09/574,749
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Papilloma source
US-10-161-097-41

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Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 1 RLCVQSTHV 9

RESULT 2
US-10-133-210-274
; Sequence 274, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: DeLisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Zhao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-03SAX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 274
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-274

Query Match 100.0%; Score 48; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 1 RLCVQSTHV 9

RESULT 3
US-10-484-063-16
; Sequence 16, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-16

Query Match 100.0%; Score 48; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9

Db 1 RLCVQSTHV 9

RESULT 4
US-09-891-823-17
; Sequence 17, Application US/09891823
; Publication No. US20020110566A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/09/891,823
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-891-823-17

Query Match 100.0%; Score 48; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 RLCVQSTHV 10

RESULT 5
US-10-365-908-17
; Sequence 17, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-17

Query Match 100.0%; Score 48; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 2 RLCVQSTHV 10

RESULT 6

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US-10-871-138-17
; Sequence 17, Application US/10871138
; Publication No. US20040235741A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/871,138
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-871-138-17

Query Match 100.0%; Score 48; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 2 RLCVQSTHV 10

RESULT 7
US-10-476-570-16
; Sequence 16, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E7 65-79
US-10-476-570-16

Query Match 100.0%; Score 48; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 2 RLCVQSTHV 10

RESULT 9
US-10-306-541-77
; Sequence 77, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 77
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-77

Query Match 100.0%; Score 48; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 1 RLCVQSTHV 9

RESULT 10
US-10-306-541-83
; Sequence 83, Application US/10306541
; Publication No. US20040171081A1
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; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 83
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-83

Query Match      100.0%; Score 48; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 5 RLCVQSTHV 13

RESULT 11
US-10-306-541-89
; Sequence 89, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 89
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-89

Query Match      100.0%; Score 48; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 6 RLCVQSTHV 14

RESULT 12
US-10-306-541-93
; Sequence 93, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 93
; LENGTH: 15
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; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-93

Query Match      100.0%; Score 48; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 7 RLCVQSTHV 15

RESULT 13
US-10-306-541-94
; Sequence 94, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 94
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-94

Query Match      100.0%; Score 48; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 4 RLCVQSTHV 12

RESULT 14
US-10-355-268-16
; Sequence 16, Application US/10355268
; Publication No. US20030211996A1
; GENERAL INFORMATION:
; APPLICANT: GOWANS, Eric J.
; TITLE OF INVENTION: IMPROVED VIRUS LIKE PARTICLES BASED ON SMALL ENVELOPE PROTEIN FROM
; TITLE OF INVENTION: HEPATITIS B
; FILE REFERENCE: P07848U00/BAS
; CURRENT APPLICATION NUMBER: US/10/355,268
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: PCT/AU01/00935
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: AU PQ9120
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-355-268-16

Query Match      100.0%; Score 48; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 5 RLCVQSTHV 13
```

RESULT 15
US-09-888-721-7
; Sequence 7, Application US/09888721
; Patent No. US20020132990A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Matasco, Wayne A.
; APPLICANT: Scherman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-09-888-721-7

Query Match 100.0%; Score 48; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
| | | | |
Db 7 RLCVQSTHV 15

Search completed: June 29, 2005, 03:24:11
Job time : 58.55 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)
39.174 Million cell updates/sec

Title: US-08-170-344-16

Perfect score: 48

Sequence: 1 RLCVQSTHV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA.*
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6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	9	4	US-09-574-749B-41
2	48	100.0	10	4	US-10-365-908-17
3	48	100.0	17	3	US-08-075-541D-48
4	48	100.0	19	3	US-08-075-541D-39
5	48	100.0	19	4	US-09-000-003A-8
6	48	100.0	19	4	US-09-405-986A-9
7	48	100.0	20	4	US-09-828-645-4
8	48	100.0	20	4	US-09-980-177A-74
9	48	100.0	21	2	US-08-934-915-49
10	48	100.0	21	2	US-08-934-915-156
11	48	100.0	25	3	US-08-075-541D-47
12	48	100.0	30	2	US-08-934-915-53
13	48	100.0	30	4	US-09-486-394-4
14	48	100.0	98	1	US-08-406-248-6
15	48	100.0	98	3	US-08-075-541D-42
16	48	100.0	98	3	US-09-382-616A-1
17	48	100.0	98	3	US-08-944-368A-4
18	48	100.0	98	3	US-09-820-764-4
19	48	100.0	98	4	US-09-613-303-8
20	48	100.0	98	4	US-09-566-420-19
21	48	100.0	98	4	US-09-986-118A-4
22	48	100.0	98	4	US-09-728-466-1
23	48	100.0	98	4	US-09-824-017-4
24	48	100.0	98	4	US-10-267-311-8
25	48	100.0	98	4	US-10-201-764-19
26	48	100.0	98	4	US-09-637-746-3
27	48	100.0	98	4	US-09-501-097A-7

28	48	100.0	98	4	US-09-980-523A-12	Sequence 12, Appl
29	48	100.0	121	4	US-09-613-303-12	Sequence 12, Appl
30	48	100.0	121	4	US-10-267-311-12	Sequence 12, Appl
31	48	100.0	172	3	US-08-860-165-14	Sequence 14, Appl
32	48	100.0	172	3	US-09-359-382-14	Sequence 14, Appl
33	48	100.0	198	4	US-09-613-303-35	Sequence 35, Appl
34	48	100.0	198	4	US-10-267-311-35	Sequence 35, Appl
35	48	100.0	220	3	US-09-485-885-1	Sequence 1, Appl
36	48	100.0	220	3	US-09-485-885-8	Sequence 1, Appl
37	48	100.0	239	3	US-09-485-885-12	Sequence 12, Appl
38	48	100.0	253	2	US-08-459-818-20	Sequence 20, Appl
39	48	100.0	253	2	US-08-889-666-20	Sequence 20, Appl
40	48	100.0	253	2	US-08-465-078-20	Sequence 20, Appl
41	48	100.0	253	2	US-08-725-776-20	Sequence 20, Appl
42	48	100.0	253	2	US-08-488-062-20	Sequence 20, Appl
43	48	100.0	263	1	US-08-117-083-9	Sequence 9, Appl
44	48	100.0	266	3	US-08-860-165-10	Sequence 10, Appl
45	48	100.0	266	3	US-09-359-382-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-574-749B-41
; Sequence 41, Application US/09574749B
; Patent No. 6548299
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADDEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
; TITLE OF INVENTION: DEVICES
; FILE REFERENCE: C1005/7012/KA/ERG
; CURRENT APPLICATION NUMBER: US/09/574,749B
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Papilloma source
US-09-574-749B-41

Query Match 100.0%; Score 48; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9

Db 1 RLCVQSTHV 9

RESULT 2

US-10-365-908-17
; Sequence 17, Application US/10365908
; Patent No. 6797491
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin

;; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
;; FILE REFERENCE: 12071-003001
;; CURRENT APPLICATION NUMBER: US/10/365,908
;; CURRENT FILING DATE: 2003-02-13
;; PRIOR APPLICATION NUMBER: US/09/891,823
;; PRIOR FILING DATE: 2001-10-19
;; PRIOR APPLICATION NUMBER: US 60/214,202
;; PRIOR FILING DATE: 2000-06-26
;; NUMBER OF SEQ ID NOS: 140
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 17
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Human papilloma virus
US-10-365-908-17

Query Match 100.0%; Score 48; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 2 RLCVQSTHV 10

RESULT 3
US-08-075-541D-48
; Sequence 48, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2991
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-48

Query Match 100.0%; Score 48; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 4 RLCVQSTHV 12

RESULT 4
US-08-075-541D-39
; Sequence 39, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-39

Query Match 100.0%; Score 48; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 5 RLCVQSTHV 13

RESULT 5
US-09-000-003A-8
; Sequence 8, Application US/09000003A
; Patent No. 6652850
; GENERAL INFORMATION:


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; PRIOR APPLICATION NUMBER: US 60/041,726
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: HPV 16 E7 PEPTIDE
US-09-405-986A-9

Query Match      100.0%; Score 48; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RLCVQSTHV 9
      |||||
DB      7 RLCVQSTHV 15

RESULT 7
US-09-828-645-4
; Sequence 4, Application US/09828645
; Patent No. 6743593
; GENERAL INFORMATION:
; APPLICANT: Hu, Yao Xiong
; TITLE OF INVENTION: Immunological Methodology for Discerning Human Papillomavirus
; FILE REFERENCE: 146-1-002
; CURRENT APPLICATION NUMBER: US/09/828,645
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/194,796
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E7 early region of HPV-16
US-09-828-645-4

Query Match      100.0%; Score 48; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RLCVQSTHV 9
      |||||
DB      6 RLCVQSTHV 14

RESULT 8
US-09-980-177A-74
; Sequence 74, Application US/09980177A
; Patent No. 6838084
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/09/980,177A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74

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; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-980-177A-74

Query Match      100.0%; Score 48; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 11 RLCVQSTHV 19

RESULT 9
US-08-934-915-49
; Sequence 49, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-49

Query Match      100.0%; Score 48; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 5 RLCVQSTHV 13

RESULT 10
US-08-934-915-156
```

```
; Sequence 156, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 156:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-156

Query Match      100.0%; Score 48; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 5 RLCVQSTHV 13

RESULT 11
US-08-075-541D-47
; Sequence 47, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-075-541D-47

Query Match 100.0%; Score 48; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 17 RLCVQSTHV 25

RESULT 12
US-08-934-915-53
Sequence 53, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-53

Query Match 100.0%; Score 48; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 9 RLCVQSTHV 17

RESULT 13
US-09-486-394-4
Sequence 4, Application US/09486394
Patent No. 6478749
GENERAL INFORMATION:
APPLICANT: Hopfl, Reinhard
TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
FILE REFERENCE: 032929-001
CURRENT APPLICATION NUMBER: US/09/486,394
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/04773
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: DE 197 37 409.3
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 30
TYPE: PRT
ORGANISM: Human papillomavirus type 16
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(30)
OTHER INFORMATION: E7 peptide.
US-09-486-394-4

Query Match 100.0%; Score 48; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 6 RLCVQSTHV 14

RESULT 14
US-08-406-248-6
Sequence 6, Application US/08406248
Patent No. 5736318
GENERAL INFORMATION:
APPLICANT: Munger, Karl
APPLICANT: Jones, D. Leanne
TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
TITLE OF INVENTION: TRANSFORMED CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Kusmer
STREET: 200 State Street
CITY: Boston

STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406.248
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: McDaniels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: HAZ-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-406-248-6

Query Match 100.0%; Score 48; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 66 RLCVQSTHV 74
|||||

RESULT 15
US-08-075-541D-42
Sequence 42, Application US/08075541D
Patent No. 6183745
GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
STATE: PENNSYLVANIA
COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075.541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4

TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-075-541D-42

Query Match 100.0%; Score 48; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCVQSTHV 9
Db 66 RLCVQSTHV 74
|||||

Search completed: June 28, 2005, 19:29:16
Job time : 18.15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-15
Perfect score: 46
Sequence: 1 MLDLQPETT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	43	2 Q91194	Q91194 human papil
2	46	100.0	65	2 Q8B563	Q8B563 human papil
3	46	100.0	77	2 Q8B5P5	Q8B5P5 human papil
4	46	100.0	93	2 Q9QDH2	Q9QDH2 human papil
5	46	100.0	93	2 Q9QDH4	Q9QDH4 human papil
6	46	100.0	93	2 Q9QDH6	Q9QDH6 human papil
7	46	100.0	93	2 Q9QDH8	Q9QDH8 human papil
8	46	100.0	94	2 Q8B5P6	Q8B5P6 human papil
9	46	100.0	98	1 V57 HPV16	P03129 human papil
10	46	100.0	98	2 O11550	O11650 human papil
11	46	100.0	98	2 O12337	O12337 human papil
12	46	100.0	98	2 O12338	O12338 human papil
13	46	100.0	98	2 Q8QRD2	Q8QRD2 human papil
14	46	100.0	98	2 Q8QRD3	Q8QRD3 human papil
15	46	100.0	98	2 Q8QRD4	Q8QRD4 human papil
16	46	100.0	98	2 Q8V1J0	Q8V1J0 human papil
17	46	100.0	98	2 Q778H3	Q778H3 human papil
18	46	100.0	98	2 Q778H5	Q778H5 human papil
19	42	91.3	99	1 V3E7 HPV52	P36831 human papil
20	41	89.1	99	1 RS24_PYRAB	Q8U420 pyrococcus
21	41	89.1	99	1 RS24_PYRBU	Q8U442 pyrococcus
22	41	89.1	99	1 RS24_PYRHO	P58746 pyrococcus
23	38	82.6	99	2 Q90724	O90724 human papil
24	38	82.6	336	2 Q65SD0	Q65SD0 manheimia
25	37	80.4	99	1 V5E7 HPV31	P17387 human papil
26	37	80.4	599	2 Q9KED7	Q9KED7 bacillus ha
27	36	78.3	18	2 Q919A8	Q919A8 human papil
28	36	78.3	18	2 Q919B3	Q919B3 human papil
29	36	78.3	18	2 Q919B5	Q919B5 human papil
30	36	78.3	18	2 Q919B7	Q919B7 human papil
31	36	78.3	18	2 Q919B9	Q919B9 human papil

32 36 78.3 18 2 Q919C5 Q919C5 human papil
33 36 78.3 18 2 Q919C7 Q919C7 human papil
34 36 78.3 18 2 Q919C9 Q919C9 human papil
35 36 78.3 18 2 Q919D1 Q919D1 human papil
36 36 78.3 18 2 Q919D3 Q919D3 human papil
37 36 78.3 18 2 Q919D5 Q919D5 human papil
38 36 78.3 416 2 Q8BPO5 Q8BPO5 mus musculus
39 36 78.3 616 2 Q810D3 Q810D3 mus musculus
40 36 78.3 1218 2 Q810D2 Q810D2 mus musculus
41 36 78.3 1301 2 Q8KUD6 Q8KUD6 enterococu
42 36 78.3 1305 2 Q838H0 Q838H0 enterococu
43 36 78.3 2780 2 Q912S2 Q912S2 mus musculus
44 36 78.3 6298 2 Q8VHN7 Q8VHN7 mus musculus
45 36 78.3 10917 2 Q93NM6 Q93NM6 streptomyce

ALIGNMENTS

RESULT 1
Q91194 PRELIMINARY; PRT; 43 AA.
AC Q91194;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DB Truncated E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhao M., Wu X.X., Ding X.H.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF393782; AAK84003.1; -
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 43 AA; 4903 MW; 19A57D4E52FB14D6 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
|||
Db 12 MLDLQPETT 20

RESULT 2
Q8B563 PRELIMINARY; PRT; 65 AA.
ID Q8B563
AC Q8B563;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DB E7 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaetsewoottacharn K.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF548023; AA016240.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 65
SQ SEQUENCE 65 AA; 7373 MW; E9D74D7923700195 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MLDLQPETT 9
    |||||
Db 12 MLDLQPETT 20

RESULT 3
Q8B5P5 PRELIMINARY; PRT; 77 AA.
AC Q8B5P5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469198; AAO15694.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 77
SQ SEQUENCE 77 AA; 8782 MW; C5DE3A7E546AC31B CRC64;

Query Match 100.0%; Score 46; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
    |||||
Db 12 MLDLQPETT 20

RESULT 4
Q9QDH2 PRELIMINARY; PRT; 93 AA.
AC Q9QDH2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187869; AAF13399.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 46; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
    |||||
Db 12 MLDLQPETT 20

RESULT 5
Q9QDH4 PRELIMINARY; PRT; 93 AA.
AC Q9QDH4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

```

```

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187868; AAF13397.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 46; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
    |||||
Db 12 MLDLQPETT 20

RESULT 6
Q9QDH6 PRELIMINARY; PRT; 93 AA.
AC Q9QDH6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187867; AAF13395.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10513 MW; 92C7054341326A1F CRC64;

Query Match 100.0%; Score 46; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
    |||||
Db 12 MLDLQPETT 20

RESULT 7
Q9QDH8 PRELIMINARY; PRT; 93 AA.
AC Q9QDH8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 46; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 12 MLDLQPETT 20

RESULT 8
Q8B5P6 PRELIMINARY; PRT; 94 AA.
AC Q8B5P6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-JUN-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E7 oncoprotein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteswoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469197; AAO15692.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 94
SQ SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;

Query Match 100.0%; Score 46; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 12 MLDLQPETT 20

RESULT 9
VE7_HPV16 STANDARD; PRT; 98 AA.
AC P03129;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85246220; PubMed=2990099;
RA Seedorf K., Krammer G., Durst M., Suhai S., Roweckamp W.G.;
RL "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90218027; PubMed=2157796;
RA Schneider-Maunoury S., Pehau-Arnaut G., Breitburd F., Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-v cells, a line derived from a vulvar intraepithelial neoplasia.";
RL J. Gen. Virol. 71:809-817(1990).
RN [3]

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RP SEQUENCE FROM N.A.
RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Girardo E., Giraldo G.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP FUNCTION.
RX MEDLINE=88223347; PubMed=2836062;
RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;
RT "The human papillomavirus type 16 E7 gene encodes transactivation and
RT transformation functions similar to those of adenovirus E1A.";
RL Cell 53:539-547(1988).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; K02718; AAA46940.1; -.
CC EMBL; D00735; BAA00633.1; -.
CC EMBL; U76411; AAB18962.1; -.
CC EMBL; U76412; AAB18963.1; -.
CC EMBL; U76413; AAB18964.1; -.
CC EMBL; AF003020; AAB70737.1; -.
CC EMBL; AF003023; AAB70740.1; -.
CC EMBL; AF003024; AAB70741.1; -.
CC EMBL; AF003025; AAB70742.1; -.
CC EMBL; AF003026; AAB70743.1; -.
CC PIR; A03688; W7MLHS.
CC InterPro; IPR000148; Papvi_E7.
CC Pfam; PF00527; E7; 1.
CC DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW Transcription regulation.
FT SITE 58 61 C-XX-C motif-1.
FT SITE 91 94 C-XX-C motif-2.
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 100.0%; Score 46; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 12 MLDLQPETT 20

RESULT 10
O11650 PRELIMINARY; PRT; 98 AA.
AC O11650;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transforming protein E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
RA Lee H.P.;
RT "Major sequence variants in E7 gene of human papillomavirus type 16
RT from cervical cancerous and noncancerous lesions of Korean women.";
RN [2]

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RL Gynecol. Oncol. 66:275-281(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
RA Lee H.-P.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Terai M., Ma Z., Burk R.D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
RN [5]
RP SEQUENCE FROM N.A.
RA Terai M., Fu L., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U76404; AAC58243.1; -
DR EMBL; AF472509; AAO15706.1; -
DR EMBL; AF486326; AAL96631.1; -
DR EMBL; AF486327; AAL96632.1; -
DR EMBL; AF486330; AAL96635.1; -
DR EMBL; AF486331; AAL96636.1; -
DR EMBL; AF486332; AAL96637.1; -
DR EMBL; AF486333; AAL96638.1; -
DR EMBL; AF486334; AAL96639.1; -
DR EMBL; AF486336; AAL96641.1; -
DR EMBL; AF486338; AAL96643.1; -
DR EMBL; AF486346; AAL96651.1; -
DR EMBL; AF486350; AAL96655.1; -
DR EMBL; AF486351; AAL96656.1; -
DR EMBL; AF534061; AAO10404.1; -
DR InterPro: IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 46; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 12 MLDLQPETT 20

RESULT 11
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AC O12337
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Girardo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003021; AAB70738.1; -
DR InterPro: IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.

Query Match 100.0%; Score 46; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 12 MLDLQPETT 20

RESULT 13
Q8QRD2 PRELIMINARY; PRT; 98 AA.
AC Q8QRD2
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486345; AAL96650.1; -
DR InterPro: IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
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SQ SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 100.0%; Score 46; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLDLQPETT 9
DB 12 MLDLQPETT 20

RESULT 14

Q8QRD3 PRELIMINARY; PRT; 98 AA.
AC Q8QRD3;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486344; AAL96649.1; -;
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLDLQPETT 9
DB 12 MLDLQPETT 20

RESULT 15

Q8QRD4 PRELIMINARY; PRT; 98 AA.
AC Q8QRD4;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486329; AAL96634.1; -;
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11025 MW; 86E24B234CC3281B CRC64;

Query Match 100.0%; Score 46; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLDLQPETT 9
DB 12 MLDLQPETT 20

Search completed: June 28, 2005, 19:19:26
Job time : 56.3 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 01:35:30 ; Search time 57.55 Seconds
(without alignments)
60.138 Million cell updates/sec

Title: US-08-170-344-15

Perfect score: 46

Sequence: 1 MLDLPETT 9

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	9	14	US-10-128-711-71
2	46	100.0	9	16	US-10-777-053-328
3	46	100.0	9	16	US-10-777-053-496
4	46	100.0	9	16	US-10-777-053-913
5	46	100.0	9	16	US-10-837-217-328
6	46	100.0	9	16	US-10-837-217-496
7	46	100.0	9	16	US-10-837-217-913
8	46	100.0	9	17	US-10-484-063-12
9	46	100.0	9	17	US-10-751-845-101
10	46	100.0	10	9	US-09-847-185-19
11	46	100.0	10	9	US-09-835-853-22

12	46	100.0	10	11	US-09-739-466C-13	Sequence 13, Appl
13	46	100.0	10	14	US-10-133-210-271	Sequence 271, Appl
14	46	100.0	10	14	US-10-224-286-19	Sequence 19, Appl
15	46	100.0	10	14	US-10-177-390-33	Sequence 33, Appl
16	46	100.0	10	15	US-10-406-317-30	Sequence 30, Appl
17	46	100.0	10	15	US-10-297-168-30	Sequence 30, Appl
18	46	100.0	10	16	US-10-777-053-329	Sequence 329, Appl
19	46	100.0	10	16	US-10-777-053-542	Sequence 542, Appl
20	46	100.0	10	16	US-10-837-217-329	Sequence 329, Appl
21	46	100.0	10	16	US-10-837-217-542	Sequence 542, Appl
22	46	100.0	10	16	US-10-890-526-19	Sequence 19, Appl
23	46	100.0	10	17	US-10-751-845-105	Sequence 105, Appl
24	46	100.0	11	14	US-10-062-710-206	Sequence 206, Appl
25	46	100.0	15	16	US-10-476-570-45	Sequence 45, Appl
26	46	100.0	15	16	US-10-476-570-46	Sequence 46, Appl
27	46	100.0	15	16	US-10-306-541-72	Sequence 72, Appl
28	46	100.0	15	16	US-10-306-541-80	Sequence 80, Appl
29	46	100.0	15	16	US-10-306-541-92	Sequence 92, Appl
30	46	100.0	19	17	US-10-751-845-67	Sequence 67, Appl
31	46	100.0	20	15	US-10-432-465-44	Sequence 44, Appl
32	46	100.0	20	15	US-10-432-465-45	Sequence 45, Appl
33	46	100.0	20	16	US-10-476-570-14	Sequence 14, Appl
34	46	100.0	20	16	US-10-890-526-69	Sequence 69, Appl
35	46	100.0	20	16	US-10-890-526-70	Sequence 70, Appl
36	46	100.0	21	16	US-10-476-570-15	Sequence 15, Appl
37	46	100.0	23	16	US-10-476-570-57	Sequence 57, Appl
38	46	100.0	23	17	US-10-858-384-14	Sequence 14, Appl
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41	46	100.0	30	17	US-10-827-007-3	Sequence 3, Appl
42	46	100.0	30	17	US-10-827-007-7	Sequence 7, Appl
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44	46	100.0	30	17	US-10-827-083-7	Sequence 7, Appl
45	46	100.0	31	11	US-09-739-466C-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1

US-10-128-711-71

; Sequence 71, Application US/10128711

; Publication No. US20030099634A1

; GENERAL INFORMATION:

; APPLICANT: VITIELLO, Maria A.

; CHESTNUT, Robert W.

; SETTE, Alessandro D.

; CELIS, Esteban

; GRAY, Howard

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING

; CTL IMMUNITY

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: Steuart Street Tower, One Market Plaza

; CITY: San Francisco

; STATE: California

; COUNTRY: US

; ZIP: 94105-1493

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10128.711

; FILING DATE: 22-Apr-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/197.484

; FILING DATE: 16-FEB-1994

; APPLICATION NUMBER: US 07/935.811

; FILING DATE: 26-AUG-1992

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; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-128-711-71
Query Match 100.0%; Score 46; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 1 MLDLQPETT 9

RESULT 2
US-10-777-053-328
; Sequence 328, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: MANK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 328
; LENGTH: 9
; TYPE: PPT
; ORGANISM: Human Papillomavirus 16
US-10-777-053-328
Query Match 100.0%; Score 46; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 1 MLDLQPETT 9

RESULT 3
US-10-777-053-496
; Sequence 496, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: MANK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 328
; LENGTH: 9
; TYPE: PPT
; ORGANISM: Human Papillomavirus 16
US-10-777-053-328
Query Match 100.0%; Score 46; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 1 MLDLQPETT 9

RESULT 4
US-10-777-053-913
; Sequence 913, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: MANK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 913
; LENGTH: 9
; TYPE: PPT
; ORGANISM: Homo Sapien
US-10-777-053-913
Query Match 100.0%; Score 46; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 1 MLDLQPETT 9

RESULT 5
US-10-837-217-328
; Sequence 328, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
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; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANNK.022C2
; CURRENT APPLICATION NUMBER: US/10/837,217
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 328
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papillomavirus 16
US-10-837-217-328

Query Match      100.0%; Score 46; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 1 MLDLQPETT 9

RESULT 6
US-10-837-217-496
; Sequence 496, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANNK.022C2
; CURRENT APPLICATION NUMBER: US/10/837,217
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 496
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-837-217-496

Query Match      100.0%; Score 46; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 1 MLDLQPETT 9

RESULT 7
US-10-837-217-913
; Sequence 913, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANNK.022C2
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; CURRENT APPLICATION NUMBER: US/10/837,217
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 913
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-837-217-913

Query Match      100.0%; Score 46; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 1 MLDLQPETT 9

RESULT 8
US-10-484-063-12
; Sequence 12, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE OF INVENTION: PRB-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC-560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-12

Query Match      100.0%; Score 46; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 1 MLDLQPETT 9

RESULT 9
US-10-751-845-101
; Sequence 101, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
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; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-101

Query Match      100.0%; Score 46; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLDLQPTT 9
DB      1 MLDLQPTT 9

RESULT 10
US-09-847-185-19
; Sequence 19, Application US/09847185
; Patent No. US20020076392A1
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/847,185
; FILING DATE: 01-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,931
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-1M 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-847-185-19
Query Match      100.0%; Score 46; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLDLQPTT 9
DB      2 MLDLQPTT 10

; PRIOR APPLICATION NUMBER: US 09/835,853
; Sequence 22, Application US/09835853
; Patent No. US20020165136A1
; GENERAL INFORMATION:
; APPLICANT: BASERGA, Renato L.
; APPLICANT: RESNICOFF, Mariana
; APPLICANT: HUANG, Ziwei
; TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE and DORR LLP
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/835,853
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/704,344
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, Henry N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.196
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 942-8459
; TELEFAX: (202) 942-8484
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-835-853-22

Query Match      100.0%; Score 46; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLDLQPTT 9
DB      2 MLDLQPTT 10

RESULT 12
US-09-739-466C-13
; Sequence 13, Application US/09739466C
; Publication No. US20050107585A1
; GENERAL INFORMATION:
; APPLICANT: MURRAY, JOSEPH S
; APPLICANT: STAHAN, TERUNA J
; APPLICANT: HU, YONGBO
; TITLE OF INVENTION: SIGNAL-1/SIGNAL-2 BIFUNCTIONAL PEPTIDE INHIBITORS
; FILE REFERENCE: 23902-08805
; CURRENT APPLICATION NUMBER: US/09/739,466C
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 10
; TYPE: PRT
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; ORGANISM: Human papillomavirus
US-09-739-466C-13

Query Match      100.0%; Score 46; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 2 MLDLQPETT 10

RESULT 13
US-10-133-210-271
; Sequence 271, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: DeLisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 271
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-271

Query Match      100.0%; Score 46; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 2 MLDLQPETT 10

RESULT 14
US-10-224-286-19
; Sequence 19, Application US/10224286
; Publication No. US20030108517A1
; GENERAL INFORMATION:
; APPLICANT: Soc Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/224,286
; FILING DATE: 19-Aug-2002
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,516
; FILING DATE: 29-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-224-286-19

Query Match      100.0%; Score 46; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 2 MLDLQPETT 10

RESULT 15
US-10-177-390-33
; Sequence 33, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Influenza virus
US-10-177-390-33

Query Match      100.0%; Score 46; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 2 MLDLQPETT 10

Search completed: June 29, 2005, 03:24:10
Job time : 57.55 secs
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)
39.174 Million cell updates/sec

Title: US-08-170-344-15

Perfect score: 46

Sequence: 1 MLDLQPTT 9

Scoring table: BLOSUM62

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents_AA.*
- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	9	1	US-08-217-188A-62
2	46	100.0	9	1	US-08-687-226-62
3	46	100.0	9	3	US-08-667-725B-62
4	46	100.0	9	3	US-09-007-748-62
5	46	100.0	9	4	US-08-197-484-71
6	46	100.0	9	5	PCT-US95-02121-71
7	46	100.0	10	2	US-08-902-516-19
8	46	100.0	10	3	US-08-704-344-22
9	46	100.0	10	4	US-09-847-185-19
10	46	100.0	10	4	US-09-601-729-270
11	46	100.0	10	4	US-09-980-177A-19
12	46	100.0	18	3	US-08-075-541D-35
13	46	100.0	18	3	US-08-075-541D-45
14	46	100.0	20	2	US-08-934-915-46
15	46	100.0	20	3	US-08-075-541D-43
16	46	100.0	20	3	US-08-075-541D-44
17	46	100.0	20	4	US-09-980-177A-69
18	46	100.0	20	4	US-09-980-177A-70
19	46	100.0	23	4	US-09-980-523A-14
20	46	100.0	30	1	US-08-363-586-1
21	46	100.0	30	2	US-08-934-915-51
22	46	100.0	30	4	US-09-486-394-1
23	46	100.0	30	4	US-09-828-645-3
24	46	100.0	30	4	US-09-828-645-7
25	46	100.0	59	3	US-09-390-027-6
26	46	100.0	98	1	US-08-406-248-6
27	46	100.0	98	3	US-08-075-541D-42

28	46	100.0	98	3	US-09-382-616A-1	Sequence 1, Appli
29	46	100.0	98	3	US-08-944-368A-4	Sequence 4, Appli
30	46	100.0	98	3	US-09-820-764-4	Sequence 4, Appli
31	46	100.0	98	4	US-09-613-303-8	Sequence 8, Appli
32	46	100.0	98	4	US-09-566-420-19	Sequence 19, Appli
33	46	100.0	98	4	US-09-986-118A-4	Sequence 4, Appli
34	46	100.0	98	4	US-09-728-466-1	Sequence 1, Appli
35	46	100.0	98	4	US-09-824-017-4	Sequence 4, Appli
36	46	100.0	98	4	US-10-267-311-8	Sequence 8, Appli
37	46	100.0	98	4	US-10-201-764-19	Sequence 19, Appli
38	46	100.0	98	4	US-09-637-746-3	Sequence 3, Appli
39	46	100.0	98	4	US-09-501-097A-7	Sequence 7, Appli
40	46	100.0	98	4	US-09-980-523A-12	Sequence 12, Appli
41	46	100.0	121	4	US-09-613-303-12	Sequence 12, Appli
42	46	100.0	121	4	US-10-267-311-12	Sequence 12, Appli
43	46	100.0	172	3	US-08-860-165-12	Sequence 12, Appli
44	46	100.0	172	3	US-09-359-382-12	Sequence 12, Appli
45	46	100.0	198	4	US-09-613-303-35	Sequence 35, Appli

ALIGNMENTS

RESULT 1
US-08-217-188A-62
; Sequence 62, Application US/08217188A
; Patent No. 5554724
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,188A
; FILING DATE: 24-MARCH-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5554724man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-217-188A-62

Query Match 100.0%; Score 46; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPTT 9
| | | | |

Db 1 MLDLQPETT 9

RESULT 2

US-08-687-226-62
; Sequence 62, Application US/08687226
; Patent No. 5686068

; GENERAL INFORMATION:

; APPLICANT: Melief, Cornelis J. M.; Visseren, M. W.;
; APPLICANT: van der Burg, Sjoerd; van der Bruggen, Pierre;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Derived From
; TITLE OF INVENTION: MAGE-2, Cytolytic T Cells Specific To Complexes Of
; TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/687,226
; FILING DATE: 25-JULY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-MARCH-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, No. 5686068man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 62:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-687-226-62

Query Match 100.0%; Score 46; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9

Db 1 MLDLQPETT 9

RESULT 3

US-08-667-725B-62
; Sequence 62, Application US/08667725B
; Patent No. 6063300

; GENERAL INFORMATION:

; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry

; TITLE OF INVENTION: Isolated Tumor Rejection Antigen

; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP

; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,725B
; FILING DATE: 21 June 1996
; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, No. 6063300man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340.1 DIV (081585)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958

; INFORMATION FOR SEQ ID NO: 62:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-667-725B-62

Query Match 100.0%; Score 46; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9

Db 1 MLDLQPETT 9

RESULT 4

US-09-007-748-62
; Sequence 62, Application US/09007748
; Patent No. 6147187

; GENERAL INFORMATION:

; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,748
; FILING DATE: 15 January 1998
; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, No. 6147187man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340.2 DIV (081572)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000

TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-007-748-62

Query Match 100.0%; Score 46; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 1 MLDLQPETT 9

RESULT 5
US-08-197-484-71
; Sequence 71, Application US/08197484
; Patent No. 641931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-08-197-484-71

Query Match 100.0%; Score 46; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 1 MLDLQPETT 9

RESULT 6
PCT-US95-02121-71
; Sequence 71, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-02121-71

Query Match 100.0%; Score 46; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 1 MLDLQPETT 9

RESULT 7
US-08-902-516-19
; Sequence 19, Application US/08902516
; Patent No. 5891432
; GENERAL INFORMATION:

APPLICANT: Soo Hoo, William
TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
TITLE OF INVENTION: RESPONSE USING SAME
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,516
FILING DATE: 29-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 2442
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-902-516-19

Query Match 100.0%; Score 46; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPTT 9
Db 2 MLDLQPTT 10

RESULT 8
US-08-704-344-22
Sequence 22, Application US/08704344
Patent No. 6218363
GENERAL INFORMATION:
APPLICANT: BASERGA, Renato L.
APPLICANT: RESNICOFF, Mariana
APPLICANT: HUANG, Ziwei
TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE and DORR LLP
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,344
FILING DATE: 28-AUG-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, Henry N.

REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.196
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 942-8459
TELEFAX: (202) 942-8484
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-704-344-22

Query Match 100.0%; Score 46; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPTT 9
Db 2 MLDLQPTT 10

RESULT 9
US-09-847-185-19
Sequence 19, Application US/09847185
Patent No. 6482407
GENERAL INFORMATION:
APPLICANT: Soo Hoo, William
TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
RESPONSE USING SAME
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/847,185
FILING DATE: 01-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/201,931
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 2442
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-847-185-19

Query Match 100.0%; Score 46; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLDLQPETT 9
Db      2 MLDLQPETT 10

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
US-09-601-729-270
; Sequence 270, Application US/09601729
; Patent No. 6683052
; GENERAL INFORMATION:
; APPLICANT: THIAM, KADER
; APPLICANT: AURIAULT, CLAUDE
; APPLICANT: GRAS-MASSE, HELENE
; APPLICANT: LOING, ESTELLE
; APPLICANT: VERWAERDE, CLAUDE
; APPLICANT: GUILLET, JEAN GERARD
; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
; TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: USB-97-AU-IN
; CURRENT APPLICATION NUMBER: US/09/601,729
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: PCT/FR99/00259
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 98 01439
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 270
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-601-729-270

Query Match      100.0%; Score 46; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLDLQPETT 9
Db      2 MLDLQPETT 10

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
US-09-980-177A-19
; Sequence 19, Application US/09980177A
; Patent No. 6838084
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus Li-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/09/980,177A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-980-177A-19

Query Match      100.0%; Score 46; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLDLQPETT 9
Db      2 MLDLQPETT 10

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
US-08-075-541D-35
; Sequence 35, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-35

Query Match      100.0%; Score 46; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLDLQPETT 9
Db      4 MLDLQPETT 12

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
US-08-075-541D-45
; Sequence 45, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN

```

; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-45

Query Match 100.0%; Score 46; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 1 MLDLQPETT 9

RESULT 14
US-08-934-915-46
; Sequence 46, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-46

Query Match 100.0%; Score 46; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDLQPETT 9
Db 11 MLDLQPETT 19

RESULT 15
US-08-075-541D-43
; Sequence 43, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020

```
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 20 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-075-541D-43

Query Match      100.0%; Score 46; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLDLQPETT 9
        |||||
Db      12 MLDLQPETT 20
```

Search completed: June 28, 2005, 19:29:15
Job time : 17.15 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-14
Perfect score: 48
Sequence: 1 YMLDLQPET 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	43	2 Q91194	Q91194 human papil
2	48	100.0	65	2 Q8B563	Q8B563 human papil
3	48	100.0	77	2 Q8B5P5	Q8B5P5 human papil
4	48	100.0	93	2 Q9QDH2	Q9QDH2 human papil
5	48	100.0	93	2 Q9QDH4	Q9QDH4 human papil
6	48	100.0	93	2 Q9QDH6	Q9QDH6 human papil
7	48	100.0	93	2 Q9QDH8	Q9QDH8 human papil
8	48	100.0	94	2 Q8B5P6	Q8B5P6 human papil
9	48	100.0	98	1 V87 HPV16	P03129 human papil
10	48	100.0	98	2 O11650	O11650 human papil
11	48	100.0	98	2 O12337	O12337 human papil
12	48	100.0	98	2 O12338	O12338 human papil
13	48	100.0	98	2 Q9QRD2	Q9QRD2 human papil
14	48	100.0	98	2 Q9QRD3	Q9QRD3 human papil
15	48	100.0	98	2 Q9QRD4	Q9QRD4 human papil
16	48	100.0	98	2 Q8V1J0	Q8V1J0 human papil
17	48	100.0	98	2 Q778H3	Q778H3 human papil
18	48	100.0	98	2 Q778H5	Q778H5 human papil
19	44	91.7	99	1 V87 HPV52	P36831 human papil
20	43	89.6	18	2 Q919A8	Q919A8 human papil
21	43	89.6	18	2 Q919B3	Q919B3 human papil
22	43	89.6	18	2 Q919B5	Q919B5 human papil
23	43	89.6	18	2 Q919B7	Q919B7 human papil
24	43	89.6	18	2 Q919B9	Q919B9 human papil
25	43	89.6	18	2 Q919C5	Q919C5 human papil
26	43	89.6	18	2 Q919C7	Q919C7 human papil
27	43	89.6	18	2 Q919C9	Q919C9 human papil
28	43	89.6	18	2 Q919D1	Q919D1 human papil
29	43	89.6	18	2 Q919D3	Q919D3 human papil
30	43	89.6	18	2 Q919D5	Q919D5 human papil
31	41	85.4	225	2 Q7MRN2	Q7MRN2 wolinnella s

32	40	83.3	99	2	O90724	human papil
33	40	83.3	589	1	PHBC ALCEU	P23608 a poly-beta
34	39	81.2	98	1	VE7 HPV31	P17387 human papil
35	39	81.2	371	2	O65T55	mannheimia
36	39	81.2	545	2	Q7VZ00	Q7vz00 bordetella
37	39	81.2	545	2	Q7WSU2	Q7wsu2 bordetella
38	39	81.2	545	2	Q7WGU3	Q7wgj3 bordetella
39	39	81.2	566	2	P94189	P94189 aicalligenes
40	39	81.2	576	2	P75003	P75003 zoogloea ra
41	39	81.2	601	2	Q63UR2	Q63ur2 burkholderi
42	39	81.2	625	2	Q9RB82	Q9rb82 burkholderi
43	39	81.2	632	2	Q62JY7	Q62jy7 burkholderi
44	38	79.2	17	2	Q919B0	Q919b0 human papil
45	38	79.2	18	2	Q919C1	Q919c1 human papil

ALIGNMENTS

RESULT 1

Q91194 PRELIMINARY; PRT; 43 AA.

AC Q91194;

DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)

DE Truncated E7 protein.

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10581;

RN [1]

RP SEQUENCE FROM N.A.

RA Zhao M., Wu X.X., Ding X.H.;

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF93782; AAR84003.1; -.

DR Pflam; PF00527; E7; 1.

SQ SEQUENCE 43 AA; 4903 MW; 19A57D4E52FB14D6 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
| | | | | | | |
Db 11 YMLDLQPET 19

RESULT 2

Q8B563 PRELIMINARY; PRT; 65 AA.

AC Q8B563;

DT 01-MAR-2003 (Tremblrel. 23, Created)

DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)

DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)

DE E7 protein (Fragment).

OS Human papillomavirus.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10566;

RN [1]

RP SEQUENCE FROM N.A.

RA Ponglikitmongkol M., Vaeteewootacharn K.;

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF548023; AAOL6240.1; -.

DR InterPro; IPR00148; Papvi_E7.

DR Pflam; PF00527; E7; 1.

FT NON TER 65 65

SQ SEQUENCE 65 AA; 7373 MW; E9D74D7923700195 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 YMLDLQPET 9
Db 11 YMLDLQPET 19

RESULT 3
Q8B5P5
ID Q8B5P5 PRELIMINARY; PRT; 77 AA.
AC Q8B5P5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DR EMBL; AF469198; AAO15694.1; -.
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE E7 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469198; AAO15694.1; -.
DR InterPro: IPR000148; Papvi_E7.
DR Pfam: PF00527; E7; 1.
DR NON TER 77
FT SEQUENCE 77 AA; 8782 MW; C5DE3A7E546AC31B CRC64;
SQ

Query Match 100.0%; Score 48; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 11 YMLDLQPET 19

RESULT 4
Q9QDH2
ID Q9QDH2 PRELIMINARY; PRT; 93 AA.
AC Q9QDH2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DR EMBL; AF187869; AAF13399.1; -.
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187869; AAF13399.1; -.
DR InterPro: IPR000148; Papvi_E7.
DR Pfam: PF00527; E7; 1.
DR NON TER 93
FT SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;
SQ

Query Match 100.0%; Score 48; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 11 YMLDLQPET 19

RESULT 5
Q9QDH4
ID Q9QDH4 PRELIMINARY; PRT; 93 AA.
AC Q9QDH4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187868; AAF13397.1; -.
DR InterPro: IPR000148; Papvi_E7.
DR Pfam: PF00527; E7; 1.
DR NON TER 93
FT SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;
SQ

Query Match 100.0%; Score 48; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 11 YMLDLQPET 19

RESULT 6
Q9QDH6
ID Q9QDH6 PRELIMINARY; PRT; 93 AA.
AC Q9QDH6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187867; AAF13395.1; -.
DR InterPro: IPR000148; Papvi_E7.
DR Pfam: PF00527; E7; 1.
DR NON TER 93
FT SEQUENCE 93 AA; 10513 MW; 92C7054341326A1F CRC64;
SQ

Query Match 100.0%; Score 48; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 11 YMLDLQPET 19

RESULT 7
Q9QDH8
ID Q9QDH8 PRELIMINARY; PRT; 93 AA.
AC Q9QDH8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR00148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AB2C8A1F CRC64;

Query Match 100.0%; Score 48; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YMLDLQPET 9
Db 11 YMLDLQPET 19

RESULT 8
Q8B5P6 PRELIMINARY; PRT; 94 AA.
AC Q8B5P6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E7 oncoprotein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M.; Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469197; AAO15692.1; -.
DR InterPro; IPR00148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 94
SQ SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AB2C8A CRC64;

Query Match 100.0%; Score 48; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YMLDLQPET 9
Db 11 YMLDLQPET 19

RESULT 9
VE7_HPV16 STANDARD; PRT; 98 AA.
AC P03129;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Seedorf K.; Kramer G.; Durst M.; Suhai S.; Rowekamp W.G.;
RT "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185 (1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90218027; PubMed=2157796;
RA Schneider-Maunoury S.; Pehau-Arnaut G.; Breitburd F.; Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-v cells,
a line derived from a vulvar intraepithelial neoplasia.";
RT J. Gen. Virol. 71:809-817 (1990).
RN [3]

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RP SEQUENCE FROM N.A.
RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP FUNCTION.
RX MEDLINE=8823347; PubMed=2836062;
RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;
RT "The human papillomavirus type 16 E7 gene encodes transactivation and
transformation functions similar to those of adenovirus E1A.";
RL Cell 53:539-547 (1988).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating
activities.
CC -----
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CC EMBL; U76411; AAB18962.1; -.
CC EMBL; U76412; AAB18963.1; -.
CC EMBL; U76413; AAB18964.1; -.
CC EMBL; AF003020; AAB70737.1; -.
CC EMBL; AF003023; AAB70740.1; -.
CC EMBL; AF003024; AAB70741.1; -.
CC EMBL; AF003025; AAB70742.1; -.
CC EMBL; AF003026; AAB70743.1; -.
CC PIR; A03688; W7MLHS.
CC InterPro; IPR00148; Papvi_E7.
CC Pfam; PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW Transcription regulation.
FT SITE 58 61 C-XX-C motif-1.
FT SITE 91 94 C-XX-C motif-2.
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 100.0%; Score 48; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YMLDLQPET 9
Db 11 YMLDLQPET 19

RESULT 10
O11650 PRELIMINARY; PRT; 98 AA.
AC O11650;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transforming protein E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
RA Lee H.P.;
RT "Major sequence variants in E7 gene of human papillomavirus type 16
from cervical cancerous and noncancerous lesions of Korean women.";
RT

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RL Gynecol. Oncol. 66:275-281(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
RA Lee H.-P.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Terai M., Ma Z., Burk R.D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RN J. Infect. Dis. 186:696-700(2002).
RN [5]
RP SEQUENCE FROM N.A.
RA Terai M., Fu L., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; U76404; AAC58243.1; -
DR EMBL; AF472509; AAO15706.1; -
DR EMBL; AF486326; AAL96631.1; -
DR EMBL; AF486327; AAL96632.1; -
DR EMBL; AF486330; AAL96635.1; -
DR EMBL; AF486331; AAL96636.1; -
DR EMBL; AF486332; AAL96637.1; -
DR EMBL; AF486333; AAL96638.1; -
DR EMBL; AF486334; AAL96639.1; -
DR EMBL; AF486336; AAL96641.1; -
DR EMBL; AF486338; AAL96643.1; -
DR EMBL; AF486346; AAL96651.1; -
DR EMBL; AF486350; AAL96655.1; -
DR EMBL; AF486351; AAL96656.1; -
DR EMBL; AF534061; AAO10404.1; -
DR InterPro: IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10995 MW; 81853B534CC3281B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 11 YMLDLQPET 19

RESULT 11
O12337 PRELIMINARY; PRT; 98 AA.
AC Q8QRD2;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Toranesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RN J. Gen. Virol. 78:2199-2208(1997).
RL EMBL; AF003021; AAB70738.1; -
DR InterPro: IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.

Query Match 100.0%; Score 48; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 11 YMLDLQPET 19

RESULT 12
O12338 PRELIMINARY; PRT; 98 AA.
AC Q12338;
DT 01-JUN-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Toranesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RN J. Gen. Virol. 78:2199-2208(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Jinhu X., Xinxiang W., Yun T.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF003022; AAB70739.1; -
DR EMBL; AF477385; AAM03025.1; -
DR InterPro: IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10969 MW; 9BD612534CCEA59B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 11 YMLDLQPET 19

RESULT 13
Q8QRD2 PRELIMINARY; PRT; 98 AA.
AC Q8QRD2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RN J. Infect. Dis. 186:696-700(2002).
RL EMBL; AF486345; AAL96650.1; -
DR InterPro: IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
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RL Gynecol. Oncol. 66:275-281(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
RA Lee H.-P.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Terai M., Ma Z., Burk R.D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RN J. Infect. Dis. 186:696-700(2002).
RN [5]
RP SEQUENCE FROM N.A.
RA Terai M., Fu L., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; U76404; AAC58243.1; -
DR EMBL; AF472509; AAO15706.1; -
DR EMBL; AF486326; AAL96631.1; -
DR EMBL; AF486327; AAL96632.1; -
DR EMBL; AF486330; AAL96635.1; -
DR EMBL; AF486331; AAL96636.1; -
DR EMBL; AF486332; AAL96637.1; -
DR EMBL; AF486333; AAL96638.1; -
DR EMBL; AF486334; AAL96639.1; -
DR EMBL; AF486336; AAL96641.1; -
DR EMBL; AF486338; AAL96643.1; -
DR EMBL; AF486346; AAL96651.1; -
DR EMBL; AF486350; AAL96655.1; -
DR EMBL; AF486351; AAL96656.1; -
DR EMBL; AF534061; AAO10404.1; -
DR InterPro: IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
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Query Match 100.0%; Score 48; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 11 YMLDLQPET 19

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AC Q8QRD2;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Toranesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RN J. Gen. Virol. 78:2199-2208(1997).
RL EMBL; AF003021; AAB70738.1; -
DR InterPro: IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.

Query Match 100.0%; Score 48; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 11 YMLDLQPET 19

RESULT 12
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AC Q12338;
DT 01-JUN-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Toranesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RN J. Gen. Virol. 78:2199-2208(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Jinhu X., Xinxiang W., Yun T.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF003022; AAB70739.1; -
DR EMBL; AF477385; AAM03025.1; -
DR InterPro: IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10969 MW; 9BD612534CCEA59B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 11 YMLDLQPET 19

RESULT 13
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AC Q8QRD2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RN J. Infect. Dis. 186:696-700(2002).
RL EMBL; AF486345; AAL96650.1; -
DR InterPro: IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
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SQ SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 11 YMLDLQPET 19

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DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486344; AAL96649.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 11 YMLDLQPET 19

RESULT 15

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AC Q8QRD4;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
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RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486329; AAL96634.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11025 MW; 86E24B234CC3281B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 11 YMLDLQPET 19

Search completed: June 28, 2005, 19:19:25
Job time : 56.3 secs

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2005, 01:35:30 ; Search time 57.55 Seconds
(without alignments)
60.138 Million cell updates/sec

Title: US-08-170-344-14

Perfect score: 48

Sequence: 1 YMLDLPET 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	48	100.0	9	9	US-09-891-823-3
3	48	100.0	9	9	US-09-909-460-104
4	48	100.0	9	11	US-09-872-836-104
5	48	100.0	9	14	US-10-128-711-66
6	48	100.0	9	14	US-10-365-908-3
7	48	100.0	9	16	US-10-603-062-17
8	48	100.0	9	15	US-10-871-138-3
9	48	100.0	9	17	US-10-758-370-104
10	48	100.0	9	17	US-10-751-845-58
11	48	100.0	10	9	US-09-847-185-19
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					Sequence 3, Appl
					Sequence 104, App
					Sequence 104, App
					Sequence 66, Appl
					Sequence 3, Appl
					Sequence 17, Appl
					Sequence 3, Appl
					Sequence 104, App
					Sequence 58, Appl
					Sequence 19, Appl

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Sequence 7, Appl
Sequence 46, Appl
Sequence 1, Appl

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US-10-133-210-271
US-10-324-286-19
US-10-177-390-33
US-10-406-317-30
US-10-297-168-30
US-10-777-053-329
US-10-777-053-542
US-10-837-217-329
US-10-837-217-542
US-10-890-526-19
US-10-751-845-105
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US-09-739-466C-46
US-09-728-466C-1

ALIGNMENTS

RESULT 1
US-09-759-960-17
; Sequence 17, Application US/09759960
; Patent No. US2001000639A1
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09759,960
; FILING DATE:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 09/169,425
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-759-960-17

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Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 YMLDLQPET 9
Db 1 YMLDLQPET 9

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RESULT 2

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US-09-891-823-3
; Sequence 3, Application US/09891823
; Publication No. US20020110566A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/09/891,823
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-891-823-3

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Best Local Similarity 100.0%; Pred. No. 1.5e+06;
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Qy 1 YMLDLQPET 9
Db 1 YMLDLQPET 9

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RESULT 3

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US-09-909-460-104
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; Publication No. US20020182258A1
; GENERAL INFORMATION:
; APPLICANT: Lunsford, Lynn B.
; APPLICANT: Putnam, David
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
; ACID
; FILE REFERENCE: 08191/014001
; CURRENT APPLICATION NUMBER: US/09/909,460
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 9

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; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-909-460-104

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Query Match      100.0%; Score 48; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
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Qy 1 YMLDLQPET 9
Db 1 YMLDLQPET 9

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RESULT 4

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US-09-872-836-104
; Sequence 104, Application US/09872836
; Publication No. US20040142475A1
; GENERAL INFORMATION:
; APPLICANT: Barman, Shikha P.
; APPLICANT: McKeever, Una
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 08191-018001
; CURRENT APPLICATION NUMBER: US/09/872,836
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,830
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-836-104

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Qy 1 YMLDLQPET 9
Db 1 YMLDLQPET 9

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RESULT 5

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US-10-128-711-66
; Sequence 66, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>

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; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
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US-10-128-711-66
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Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YMLDLQPET 9

RESULT 6
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; Sequence 3, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-3
Query Match 100.0%; Score 48; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 17, Application US/10603062
; Publication No. US20040229809A1
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; Chicz, Roman M.
; Collins, Edward J.
; Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/603,062
; FILING DATE: 24-Jun-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,425C
; FILING DATE: 09-OCT-1998
; APPLICATION NUMBER: 60/061,657
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-603-062-17
Query Match 100.0%; Score 48; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 1 YMLDLQPET 9

RESULT 8
US-10-871-138-3
; Sequence 3, Application US/10871138
; Publication No. US20040235741A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/871,138
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-06-26
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; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-871-138-3

Query Match 100.0%; Score 48; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLPET 9
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Db 1 YMLDLPET 9

RESULT 9
US-10-758-970-104
; Sequence 104, Application US/10758970
; Publication No. US20050037086A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Hsu, Yung-Yueh
; APPLICANT: Tyo, Michael
; TITLE OF INVENTION: CONTINUOUS-FLOW METHOD FOR PREPARING MICROPARTICLES
; FILE REFERENCE: 08191-012001
; CURRENT APPLICATION NUMBER: US/10/758,970
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US/09/715,708A
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/166,516
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-758-970-104

Query Match 100.0%; Score 48; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLPET 9
| | | | |
Db 1 YMLDLPET 9

RESULT 10
US-10-751-845-58
; Sequence 58, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-58

Query Match 100.0%; Score 48; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLPET 9
| | | | |
Db 1 YMLDLPET 9

RESULT 11
US-09-847-185-19
; Sequence 19, Application US/09847185
; Patent No. US20020076392A1
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/847,185
; FILING DATE: 01-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,931
; FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 2442
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-847-185-19
Query Match 100.0%; Score 48; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLPET 9
| | | | |
Db 1 YMLDLPET 9

RESULT 12
US-09-835-853-22
; Sequence 22, Application US/09835853
; Patent No. US20020165136A1
; GENERAL INFORMATION:

APPLICANT: BASERGA, Renato L.
APPLICANT: RESNICOFF, Mariana
APPLICANT: HUANG, Ziwei
TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE and DORR LLP
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/835,853
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/704,344
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, Henry N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.196
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 942-8459
TELEFAX: (202) 942-8484
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-835-853-22

Query Match 100.0%; Score 48; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 1 YMLDLQPET 9

RESULT 13
US-09-739-466C-13
Sequence 13, Application US/09739466C
Publication No. US20050107585A1
GENERAL INFORMATION:
APPLICANT: MURRAY, JOSEPH S
APPLICANT: SIAHAAN, TERUNA J
APPLICANT: HU, YONGBO
TITLE OF INVENTION: SIGNAL-1/SIGNAL-2 BIFUNCTIONAL PEPTIDE INHIBITORS
FILE REFERENCE: 23902-08805
CURRENT APPLICATION NUMBER: US/09/739,466C
CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 13
LENGTH: 10
TYPE: PRT
ORGANISM: Human papillomavirus
US-09-739-466C-13
Query Match 100.0%; Score 48; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YMLDLQPET 9
Db 1 YMLDLQPET 9

RESULT 14
US-10-133-210-271
Sequence 271, Application US/10133210
Publication No. US20030103964A1
GENERAL INFORMATION:
APPLICANT: Delisi, Charles
APPLICANT: Berzofsky, Jay
APPLICANT: Gulukota, Kamalakara
APPLICANT: Vaccaro, Dennis
APPLICANT: Weng, Zhiping
APPLICANT: Zhang, Chao
TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
FILE REFERENCE: BU-035AX
CURRENT APPLICATION NUMBER: US/10/133,210
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 281
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 271
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-271

Query Match 100.0%; Score 48; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 1 YMLDLQPET 9

RESULT 15
US-10-224-286-19
Sequence 19, Application US/10224286
Publication No. US20030108517A1
GENERAL INFORMATION:
APPLICANT: Soo Hoo, William
TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
RESPONSE USING SAME
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/224,286
FILING DATE: 19-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/902,516
FILING DATE: 29-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

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/
/   REGISTRATION NUMBER: 31,815
/   REFERENCE/DOCKET NUMBER: P-IM 2442
/   TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (619)535-9001
/   TELEFAX: (619)535-8949
/   INFORMATION FOR SEQ ID NO: 19:
/   SEQUENCE CHARACTERISTICS:
/   LENGTH: 10 amino acids
/   TYPE: amino acid
/   TOPOLOGY: linear
/   MOLECULE TYPE: peptide
/   SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-224-286-19

Query Match      100.0%; Score 48; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YMLDLQPET 9
        |||||
Db      1 YMLDLQPET 9
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Search completed: June 29, 2005, 03:24:10
Job time : 57.55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)
39.174 Million cell updates/sec

Title: US-08-170-344-14
Perfect score: 48
Sequence: 1 YMLDLQPET 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pcp:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pcp:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pcp:*
6: /cgn2_6/ptodata/1/iaa/backfiles.pcp:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	9	1	US-08-787-547-104
2	48	100.0	9	3	US-08-948-378A-17
3	48	100.0	9	3	US-09-169-425C-17
4	48	100.0	9	4	US-08-197-484-66
5	48	100.0	9	4	US-09-759-960-17
6	48	100.0	9	4	US-10-365-908-3
7	48	100.0	9	5	PCT-US95-02121-66
8	48	100.0	10	2	US-08-902-516-19
9	48	100.0	10	3	US-08-704-344-22
10	48	100.0	10	4	US-09-847-185-19
11	48	100.0	10	4	US-09-601-729-270
12	48	100.0	10	4	US-09-980-177A-19
13	48	100.0	18	3	US-08-075-541D-35
14	48	100.0	20	2	US-08-934-915-46
15	48	100.0	20	3	US-08-075-541D-43
16	48	100.0	20	3	US-08-075-541D-44
17	48	100.0	20	4	US-09-980-177A-69
18	48	100.0	23	4	US-09-980-523A-14
19	48	100.0	30	1	US-08-363-586-1
20	48	100.0	30	2	US-08-934-915-51
21	48	100.0	30	4	US-09-486-394-1
22	48	100.0	30	4	US-09-828-645-3
23	48	100.0	30	4	US-09-828-645-7
24	48	100.0	59	3	US-09-390-027-6
25	48	100.0	98	1	US-08-408-248-6
26	48	100.0	98	3	US-08-075-541D-42
27	48	100.0	98	3	US-09-382-616A-1

28	48	100.0	98	3	US-08-944-368A-4	Sequence 4, Appli
29	48	100.0	98	3	US-09-820-764-4	Sequence 4, Appli
30	48	100.0	98	4	US-09-613-303-8	Sequence 8, Appli
31	48	100.0	98	4	US-09-566-420-19	Sequence 19, Appli
32	48	100.0	98	4	US-09-986-118A-4	Sequence 4, Appli
33	48	100.0	98	4	US-09-728-466-1	Sequence 1, Appli
34	48	100.0	98	4	US-09-824-017-4	Sequence 4, Appli
35	48	100.0	98	4	US-10-267-311-8	Sequence 8, Appli
36	48	100.0	98	4	US-10-201-764-19	Sequence 19, Appli
37	48	100.0	98	4	US-09-637-746-3	Sequence 3, Appli
38	48	100.0	98	4	US-09-501-097A-7	Sequence 7, Appli
39	48	100.0	98	4	US-09-980-523A-12	Sequence 12, Appli
40	48	100.0	121	4	US-09-613-303-12	Sequence 12, Appli
41	48	100.0	121	4	US-10-267-311-12	Sequence 12, Appli
42	48	100.0	172	3	US-08-860-165-12	Sequence 12, Appli
43	48	100.0	172	3	US-09-359-382-12	Sequence 12, Appli
44	48	100.0	198	4	US-09-613-303-35	Sequence 35, Appli
45	48	100.0	198	4	US-10-267-311-35	Sequence 35, Appli

ALIGNMENTS

RESULT 1
US-08-787-547-104
; Sequence 104, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Curley, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-787-547-104

Query Match 100.0%; Score 48; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
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 Db 1 YMLDLQPET 9

RESULT 2

US-08-948-378A-17
 ; Sequence 17, Application US/08948378A
 ; Patent No. 6013258
 ; GENERAL INFORMATION:
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiciz, Roman M.
 ; APPLICANT: Collins, Edward J.
 ; APPLICANT: Hedley, Mary Lynn
 ; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM
 ; THE HPV E7 PROTEIN
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson, P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/948,378A
 ; FILING DATE: 09-OCT-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fraser, Janis K.
 ; REGISTRATION NUMBER: 34,819
 ; REFERENCE/DOCKET NUMBER: 08191/004001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-542-5070
 ; TELEFAX: 617-543-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-948-378A-17

Query Match 100.0%; Score 48; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
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 Db 1 YMLDLQPET 9

RESULT 3

US-09-169-425C-17
 ; Sequence 17, Application US/09169425C
 ; Patent No. 6183746
 ; GENERAL INFORMATION:
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiciz, Roman M.
 ; APPLICANT: Collins, Edward J.
 ; APPLICANT: Hedley, Mary Lynn
 ; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/169,425C
 ; FILING DATE: 09-OCT-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/061,657
 ; FILING DATE: 09-OCT-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fraser, Janis K.
 ; REGISTRATION NUMBER: 34,819
 ; REFERENCE/DOCKET NUMBER: 08191/004002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-542-5070
 ; TELEFAX: 617-543-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-169-425C-17

Query Match 100.0%; Score 48; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
 |||||
 Db 1 YMLDLQPET 9

RESULT 4

US-08-197-484-66
 ; Sequence 66, Application US/08197484
 ; Patent No. 6419931
 ; GENERAL INFORMATION:
 ; APPLICANT: VITIELLO, Maria A.
 ; APPLICANT: CHESTNUT, Robert W.
 ; APPLICANT: SETTE, Alessandro D.
 ; APPLICANT: CELIS, Esteban
 ; APPLICANT: GRAY, Howard
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
 ; CTL IMMUNITY
 ; NUMBER OF SEQUENCES: 153
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
 ; STREET: Steuart Street Tower, One Market Plaza
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94105-1493
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/197,484
 ; FILING DATE: 16-FEB-1994
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/935,811

; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-197-484-66

Query Match 100.0%; Score 48; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 1 YMLDLQPET 9

RESULT 5
US-09-759-960-17
; Sequence 17, Application US/09759960
; Patent No. 6582704
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiczo, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/169,425
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-759-960-17

Query Match 100.0%; Score 48; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 1 YMLDLQPET 9

RESULT 6
US-10-365-908-3
; Sequence 3, Application US/10365908
; Patent No. 6797491
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
; US-10-365-908-3

Query Match 100.0%; Score 48; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 1 YMLDLQPET 9

RESULT 7
PCT-US95-02121-66
; Sequence 66, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pamelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-66

Query Match 100.0%; Score 48; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 1 YMLDLQPET 9

RESULT 8
US-08-902-516-19
; Sequence 19, Application US/08902516
; Patent No. 5891432
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESS: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,516
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-902-516-19

Query Match 100.0%; Score 48; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 1 YMLDLQPET 9

RESULT 9
US-08-704-344-22
; Sequence 22, Application US/08704344
; Patent No. 6218363
; GENERAL INFORMATION:
; APPLICANT: BASERGA, Renato L.
; APPLICANT: RESNICOFF, Mariana
; APPLICANT: HUANG, Ziwei
; TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE and DORR LLP
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,344
; FILING DATE: 28-AUG-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, Henry N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.196
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 942-8459
; TELEFAX: (202) 942-8484
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-704-344-22

Query Match 100.0%; Score 48; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMLDLQPET 9
Db 1 YMLDLQPET 9

RESULT 10
US-09-847-185-19
; Sequence 19, Application US/09847185
; Patent No. 6482407
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS


```

; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME
;
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/847,185
; FILING DATE: 01-May-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,931
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-847-185-19
;
; Query Match 100.0%; Score 48; DB 4; Length 10;
; Best Local Similarity 100.0%; Pred. No. 0.0027;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 YMLDLQPET 9
; Db 1 YMLDLQPET 9
;
; RESULT 11
; US-09-601-729-270
; Sequence 270, Application US/09601729
; Patent No. 6683052
; GENERAL INFORMATION:
; APPLICANT: THIAM, KADER
; APPLICANT: AURIAULT, CLAUDE
; APPLICANT: GRAS-MASSE, HELENE
; APPLICANT: LOING, ESTELLE
; APPLICANT: VERWAERDE, CLAUDE
; APPLICANT: GUILLET, JEAN GERARD
; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
; TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: USB-97-AU-IN
; CURRENT APPLICATION NUMBER: US/09/601,729
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: PCT/FR99/00259
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 98 01439
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 270
; LENGTH: 10
; TYPE: PPT
; ORGANISM: Artificial Sequence
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-09-601-729-270
;
; Query Match 100.0%; Score 48; DB 4; Length 10;
; Best Local Similarity 100.0%; Pred. No. 0.0027;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 YMLDLQPET 9
; Db 1 YMLDLQPET 9
;
; RESULT 12
; US-09-980-177A-19
; Sequence 19, Application US/09980177A
; Patent No. 6838884
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus LI-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/09/980.177A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 10
; TYPE: PPT
; ORGANISM: Human papillomavirus type 16
; US-09-980-177A-19
;
; Query Match 100.0%; Score 48; DB 4; Length 10;
; Best Local Similarity 100.0%; Pred. No. 0.0027;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 YMLDLQPET 9
; Db 1 YMLDLQPET 9
;
; RESULT 13
; US-08-075-541D-35
; Sequence 35, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D

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; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-075-541D-35

Query Match 100.0%; Score 48; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMLDLQPET 9
Db 3 YMLDLQPET 11

RESULT 14

US-08-934-915-46
; Sequence 46, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 15, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:

; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-46

Query Match 100.0%; Score 48; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMLDLQPET 9
Db 10 YMLDLQPET 18

RESULT 15

US-08-075-541D-43
; Sequence 43, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-075-541D-43

Query Match 100.0%; Score 48; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMLDLQPET 9
Db 11 YMLDLQPET 19

Search completed: June 28, 2005, 19:29:15
Job time : 17.15 secs

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RESULT 2


```
; SEQ ID NO 270
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-871-138-4

Query Match      100.0%; Score 48; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
Db 1 TLHEYMLDL 9

RESULT 6
US-10-365-908-4
; Sequence 4, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-4

Query Match      100.0%; Score 48; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
Db 1 TLHEYMLDL 9

RESULT 7
US-10-871-138-4
; Sequence 4, Application US/10871138
; Publication No. US20040235741A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/871,138
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4

; SEQ ID NO 270
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-871-138-4

Query Match      100.0%; Score 48; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
Db 1 TLHEYMLDL 9

RESULT 8
US-10-758-970-105
; Sequence 105, Application US/10758970
; Publication No. US20050037086A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Hsu, Yung-Yueh
; APPLICANT: TYO, Michael
; TITLE OF INVENTION: CONTINUOUS-FLOW METHOD FOR PREPARING MICROPARTICLES
; FILE REFERENCE: 08191-012001
; CURRENT APPLICATION NUMBER: US/10/758,970
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US/09/715,708A
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/166,516
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 105
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-758-970-105

Query Match      100.0%; Score 48; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
Db 1 TLHEYMLDL 9

RESULT 9
US-10-751-845-59
; Sequence 59, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-59
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QY 1 TLHEYMLDL 9
| | | | |
Db 2 TLHEYMLDL 10

RESULT 14
US-10-306-541-69
; Sequence 69, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 69
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-69

Query Match 100.0%; Score 48; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
| | | | |
Db 6 TLHEYMLDL 14

RESULT 15
US-10-306-541-92
; Sequence 92, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 92
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-92

Query Match 100.0%; Score 48; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
| | | | |
Db 1 TLHEYMLDL 9

Search completed: June 29, 2005, 03:24:10
Job time : 58.55 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)
39.174 Million cell updates/sec

Title: US-08-170-344-13
Perfect score: 48
Sequence: 1 TLHEYMLDL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	48	100.0	9	1	US-08-787-547-105
2	48	100.0	9	4	US-08-197-484-69
3	48	100.0	9	4	US-10-365-908-4
4	48	100.0	9	5	PCT-US95-02121-69
5	48	100.0	10	4	US-10-365-908-49
6	48	100.0	18	3	US-08-075-541D-34
7	48	100.0	20	2	US-08-934-915-46
8	48	100.0	20	3	US-08-075-541D-43
9	48	100.0	20	3	US-08-075-541D-44
10	48	100.0	20	4	US-09-980-177A-69
11	48	100.0	23	4	US-09-980-523A-14
12	48	100.0	30	1	US-08-363-586-1
13	48	100.0	30	2	US-08-934-915-51
14	48	100.0	30	4	US-09-486-394-1
15	48	100.0	30	4	US-09-828-645-3
16	48	100.0	30	4	US-09-828-645-7
17	48	100.0	30	1	US-08-406-248-6
18	48	100.0	98	3	US-08-075-541D-42
19	48	100.0	98	3	US-09-382-616A-1
20	48	100.0	98	3	US-08-944-368A-4
21	48	100.0	98	3	US-09-820-764-4
22	48	100.0	98	4	US-09-613-303-8
23	48	100.0	98	4	US-09-566-420-19
24	48	100.0	98	4	US-09-986-118A-4
25	48	100.0	98	4	US-09-728-466-1
26	48	100.0	98	4	US-09-824-017-4
27	48	100.0	98	4	US-10-267-311-8

28	48	100.0	98	4	US-10-201-764-19	Sequence 19, Appl
29	48	100.0	98	4	US-09-637-746-3	Sequence 3, Appl
30	48	100.0	98	4	US-09-501-097A-7	Sequence 7, Appl
31	48	100.0	98	4	US-09-980-523A-12	Sequence 12, Appl
32	48	100.0	121	4	US-09-613-303-12	Sequence 12, Appl
33	48	100.0	121	4	US-10-267-311-12	Sequence 12, Appl
34	48	100.0	172	3	US-08-860-165-12	Sequence 12, Appl
35	48	100.0	172	3	US-09-359-382-12	Sequence 12, Appl
36	48	100.0	198	4	US-09-613-303-35	Sequence 35, Appl
37	48	100.0	198	4	US-10-267-311-35	Sequence 35, Appl
38	48	100.0	220	3	US-09-485-885-1	Sequence 1, Appl
39	48	100.0	220	3	US-09-485-885-8	Sequence 8, Appl
40	48	100.0	239	3	US-09-485-885-12	Sequence 12, Appl
41	48	100.0	253	2	US-08-459-818-20	Sequence 20, Appl
42	48	100.0	253	2	US-08-889-666-20	Sequence 20, Appl
43	48	100.0	253	2	US-08-465-078-20	Sequence 20, Appl
44	48	100.0	253	2	US-08-725-776-20	Sequence 20, Appl
45	48	100.0	253	2	US-08-488-062-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-787-547-105
; Sequence 105, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Curley, Joanne M.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/08/787,547
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 105:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-787-547-105

Query Match 100.0%; Score 48; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
Db 1 TLHEYMLDL 9

RESULT 2
US-08-197-484-69
; Sequence 69, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-69

Query Match 100.0%; Score 48; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
Db 1 TLHEYMLDL 9

RESULT 3
US-10-365-908-4

; Sequence 4, Application US/10365908
; Patent No. 6797491
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-4

Query Match 100.0%; Score 48; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
Db 1 TLHEYMLDL 9

RESULT 4
PCT-US95-02121-69
; Sequence 69, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 69:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-69

Query Match      100.0%; Score 48; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
Db 1 TLHEYMLDL 9

RESULT 5
US-10-365-908-49
; Sequence 49, Application US/10365908
; Patent No. 6797491
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; PRIOR FILING DATE: 2003-02-13
; PRIOR FILING DATE: 2001-10-19
; PRIOR FILING DATE: 2001-10-19
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-49

Query Match      100.0%; Score 48; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
Db 2 TLHEYMLDL 10

RESULT 6
US-08-075-541D-34
; Sequence 34, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; COMPUTER: IBM PC compatible.

; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-69

Query Match      100.0%; Score 48; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
Db 1 TLHEYMLDL 9

RESULT 5
US-10-365-908-49
; Sequence 49, Application US/10365908
; Patent No. 6797491
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; PRIOR FILING DATE: 2003-02-13
; PRIOR FILING DATE: 2001-10-19
; PRIOR FILING DATE: 2001-10-19
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-49

Query Match      100.0%; Score 48; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
Db 2 TLHEYMLDL 10

RESULT 6
US-08-075-541D-34
; Sequence 34, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; COMPUTER: IBM PC compatible.

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-34

Query Match      100.0%; Score 48; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
Db 7 TLHEYMLDL 15

RESULT 7
US-08-934-915-46
; Sequence 46, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-46

Query Match 100.0%; Score 48; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
| | | | | | | | | |
Db 6 TLHEYMLDL 14

RESULT 8

US-08-075-541D-43
; Sequence 43, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075.541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2991
; TELEFAX: 215-567-2020
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-43

Query Match 100.0%; Score 48; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
| | | | | | | | | |
Db 7 TLHEYMLDL 15

RESULT 9

US-08-075-541D-44
; Sequence 44, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075.541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-44

Query Match 100.0%; Score 48; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLHEYMLDL 9
| | | | | | | | | |
Db 2 TLHEYMLDL 10

RESULT 10

US-09-980-177A-69
; Sequence 69, Application US/09980177A
; Patent No. 6838084
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and

```

; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/09/980,177A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-980-177A-69

Query Match      100.0%; Score 48; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
Db 7 TLHEYMLDL 15

RESULT 11
US-09-980-523A-14
; Sequence 14, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-14

Query Match      100.0%; Score 48; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
Db 5 TLHEYMLDL 13

RESULT 12
US-08-363-586-1
; Sequence 1, Application US/08363586
; Patent No. 5629161
; GENERAL INFORMATION:
; APPLICANT: Mueller, Martin
; APPLICANT: Giesmann, Lutz
; TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
; TITLE OF INVENTION: Peptides for the Diagnostic Purpose
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,586
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/909,296
; FILING DATE: 09-JUL-1992
; APPLICATION NUMBER: EP 91111720.8
; FILING DATE: 13-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wadler, Linda A.
; REGISTRATION NUMBER: 33,218
; REFERENCE/DOCKET NUMBER: 02481-1195-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO. 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-363-586-1

Query Match      100.0%; Score 48; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
Db 2 TLHEYMLDL 10

RESULT 13
US-08-934-915-51
; Sequence 51, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997

```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-51

Query Match 100.0%; Score 48; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
| | | | |
Db 6 TLHEYMLDL 14

RESULT 14
US-09-486-394-1
; Sequence 1, Application US/09486394
; Patent No. 6478749
; GENERAL INFORMATION:
; APPLICANT: Hopfl, Reinhard
; TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
; FILE REFERENCE: 032929-001
; CURRENT APPLICATION NUMBER: US/09/486,394
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/04773
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: DE 197 37 409.3
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(30)
; OTHER INFORMATION: E7 peptide.
US-09-486-394-1

Query Match 100.0%; Score 48; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
| | | | |
Db 7 TLHEYMLDL 15

RESULT 15
US-09-828-645-3
; Sequence 3, Application US/09828645
; Patent No. 6743593
; GENERAL INFORMATION:
; APPLICANT: Hu, Yao Xiong
; TITLE OF INVENTION: Immunological Methodology for Discerning Human Papillomavirus
; FILE REFERENCE: 146-1-002
; CURRENT APPLICATION NUMBER: US/09/828,645

; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/194,796
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E7 early region of HPV-16
US-09-828-645-3

Query Match 100.0%; Score 48; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLHEYMLDL 9
| | | | |
Db 2 TLHEYMLDL 10

Search completed: June 28, 2005, 19:29:15
Job time : 18.15 secs

Qy 1 PLCDLLIRC 9
| | | | | | | | | |
Db 1 PLCDLLIRC 9

RESULT 2
 US-10-476-570-38
 ; Sequence 38, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: POUVELLE-MORATILLE, Sandra
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 38
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 97-111 -
 US-10-476-570-38

Query Match 100.0%; Score 52; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.046; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

Qy 1 PLCDLLIRC 9
 |||||
 Db 6 PLCDLLIRC 14
 |||||

RESULT 3
 US-10-476-570-39
 ; Sequence 39, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: POUVELLE-MORATILLE, Sandra
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 39
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 101-115
 US-10-476-570-39

Query Match 100.0%; Score 52; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.046; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

Qy 1 PLCDLLIRC 9
 |||||
 Db 2 PLCDLLIRC 10
 |||||

RESULT 4
 US-10-476-570-35
 ; Sequence 35, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: POUVELLE-MORATILLE, Sandra
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 35
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 91-110
 US-10-476-570-35

Query Match 100.0%; Score 52; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.06; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

Qy 1 PLCDLLIRC 9
 |||||
 Db 12 PLCDLLIRC 20
 |||||

RESULT 5
 US-10-484-063-8
 ; Sequence 8, Application US/10484063
 ; Publication No. US20050048467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SASTRY, K. JAGANNADHA
 ; APPLICANT: TORTOLERO-LUNA, GUILLERMO
 ; APPLICANT: FOLLEN, MICHELE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
 ; FILE REFERENCE: UTSC:560US
 ; CURRENT APPLICATION NUMBER: US/10/484,063
 ; CURRENT FILING DATE: 2004-01-16
 ; PRIOR APPLICATION NUMBER: PCT/US02/23198
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 60/306,809
 ; PRIOR FILING DATE: 2001-07-20
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus
 US-10-484-063-8

Query Match 100.0%; Score 52; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.06; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

QY 1 PLCDLLIRC 9
 |||||
 Db 6 PLCDLLIRC 14

RESULT 6

US-10-476-570-13
 ; Sequence 13, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INSTITUT NATIONAL A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: POUVELLE-MORATILLE, Sandra
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; TITLE OF INVENTION: Papillomavirus proteins and uses thereof
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 29
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 91-119
 US-10-476-570-13

Query Match 100.0%; Score 52; DB 16; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.083;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLCDLLIRC 9
 |||||
 Db 12 PLCDLLIRC 20

RESULT 7

US-10-177-390-6
 ; Sequence 6, Application US/10177390
 ; Publication No. US20030143743A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schuler, Gerold
 ; APPLICANT: N.V. Antwerp Innovatiecentrum
 ; TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with Linear
 ; TITLE OF INVENTION: Polynucleotides by Electroporation
 ; FILE REFERENCE: 021505wo/JH/ml
 ; CURRENT APPLICATION NUMBER: US/10/177,390
 ; CURRENT FILING DATE: 2002-06-20
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus type 16
 US-10-177-390-6

Query Match 100.0%; Score 52; DB 14; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLCDLLIRC 9
 |||||
 Db 95 PLCDLLIRC 103

RESULT 8

US-10-484-063-20
 ; Sequence 20, Application US/10484063
 ; Publication No. US20050048467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SASTRY, K. JAGANNADHA
 ; APPLICANT: TORTOLERO-LUNA, GUILLERMO
 ; APPLICANT: FOLLEN, MICHELE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
 ; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
 ; FILE REFERENCE: UTSC:560US
 ; CURRENT APPLICATION NUMBER: US/10/484,063
 ; CURRENT FILING DATE: 2004-01-16
 ; PRIOR APPLICATION NUMBER: PCT/US02/23198
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 60/306,809
 ; PRIOR FILING DATE: 2001-07-20
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus
 US-10-484-063-20

Query Match 100.0%; Score 52; DB 17; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLCDLLIRC 9
 |||||
 Db 95 PLCDLLIRC 103

RESULT 9

US-10-484-063-27
 ; Sequence 27, Application US/10484063
 ; Publication No. US20050048467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SASTRY, K. JAGANNADHA
 ; APPLICANT: TORTOLERO-LUNA, GUILLERMO
 ; APPLICANT: FOLLEN, MICHELE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
 ; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
 ; FILE REFERENCE: UTSC:560US
 ; CURRENT APPLICATION NUMBER: US/10/484,063
 ; CURRENT FILING DATE: 2004-01-16
 ; PRIOR APPLICATION NUMBER: PCT/US02/23198
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 60/306,809
 ; PRIOR FILING DATE: 2001-07-20
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 27
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus type 16
 US-10-484-063-27

Query Match 100.0%; Score 52; DB 17; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLCDLLIRC 9
 |||||
 Db 95 PLCDLLIRC 103

RESULT 10

US-10-858-384-2
 ; Sequence 2, Application US/10858384
 ; Publication No. US2005003025A1
 ; GENERAL INFORMATION:

```
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGALT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match      100.0%; Score 52; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 102 PLCDLLIRC 110

RESULT 11
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match      100.0%; Score 52; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 102 PLCDLLIRC 110

RESULT 12
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
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; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match      100.0%; Score 52; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 107 PLCDLLIRC 115

RESULT 13
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 52; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 102 PLCDLLIRC 110

RESULT 14
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
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; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match      100.0%; Score 52; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 208 PLCDLLIRC 216

RESULT 15
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

Query Match      100.0%; Score 52; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 208 PLCDLLIRC 216

Search completed: June 29, 2005, 03:24:09
Job time : 57.55 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)
39.174 Million cell updates/sec

Title: US-08-170-344-12

Perfect score: 52

Sequence: 1 PLCDLLIRC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents_AA.*
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 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
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 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	20	US-08-934-915-45	Sequence 45, Appl
2	52	100.0	158	US-09-980-523A-2	Sequence 2, Appl
3	52	100.0	162	US-08-316-239B-3	Sequence 3, Appl
4	52	100.0	162	US-08-316-239B-4	Sequence 4, Appl
5	52	100.0	172	US-08-860-165-12	Sequence 12, Appl
6	52	100.0	172	US-09-359-382-12	Sequence 12, Appl
7	52	100.0	266	US-08-860-165-10	Sequence 10, Appl
8	52	100.0	266	US-09-359-382-10	Sequence 10, Appl
9	52	100.0	266	US-09-367-309A-1	Sequence 1, Appl
10	52	100.0	273	US-09-485-885-4	Sequence 4, Appl
11	52	100.0	292	US-09-485-885-10	Sequence 10, Appl
12	52	100.0	371	US-09-485-885-6	Sequence 6, Appl
13	52	100.0	390	US-09-485-885-14	Sequence 14, Appl
14	47	90.4	20	US-08-934-915-164	Sequence 164, App
15	38	73.1	29	US-09-980-523A-8	Sequence 8, Appl
16	36	69.2	172	US-09-248-796A-20508	Sequence 20508, A
17	36	69.2	343	US-09-902-540-12017	Sequence 12017, A
18	35	67.3	348	US-09-489-039A-13746	Sequence 13746, A
19	35	67.3	687	US-09-252-991A-31650	Sequence 31650, A
20	34	65.4	10	US-09-574-749B-43	Sequence 43, Appl
21	34	65.4	104	US-09-270-767-33183	Sequence 33183, A
22	34	65.4	104	US-09-270-767-48400	Sequence 48400, A
23	34	65.4	109	US-09-270-767-34129	Sequence 34129, A
24	34	65.4	109	US-09-270-767-49346	Sequence 49346, A
25	34	65.4	146	US-09-640-211A-1032	Sequence 1032, Ap
26	34	65.4	166	US-09-228-986-113	Sequence 113, App
27	34	65.4	166	US-10-101-464A-113	Sequence 113, App

Query Match 100.0%; Score 52; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0057;

28	34	65.4	321	4	US-09-498-520A-18	Sequence 18, Appl
29	34	65.4	527	1	US-08-246-583-2	Sequence 2, Appl
30	34	65.4	537	4	US-09-949-016-7509	Sequence 7509, Ap
31	34	65.4	538	2	US-08-933-227-5	Sequence 5, Appl
32	34	65.4	538	4	US-09-636-791A-4	Sequence 4, Appl
33	34	65.4	538	4	US-09-538-092-1186	Sequence 1186, Ap
34	34	65.4	540	4	US-09-949-016-8190	Sequence 8190, Ap
35	34	65.4	542	1	US-08-246-583-3	Sequence 3, Appl
36	34	65.4	542	4	US-09-636-791A-5	Sequence 5, Appl
37	34	65.4	542	4	US-09-538-092-672	Sequence 672, App
38	34	65.4	556	4	US-09-248-796A-19179	Sequence 19179, A
39	33	63.5	81	4	US-09-489-039A-12083	Sequence 12083, A
40	33	63.5	120	4	US-09-513-999C-4376	Sequence 4376, Ap
41	33	63.5	155	4	US-09-270-767-35225	Sequence 35225, A
42	33	63.5	155	4	US-09-270-767-50442	Sequence 50442, A
43	33	63.5	293	4	US-09-902-540-12712	Sequence 12712, A
44	33	63.5	313	4	US-09-489-039A-13053	Sequence 13053, A
45	33	63.5	338	3	US-09-199-637A-174	Sequence 174, App

ALIGNMENTS

RESULT 1
US-08-934-915-45
; Sequence 45, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-45

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 11 PLCDLLIRC 19

RESULT 2
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGALT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 52; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 102 PLCDLLIRC 110

RESULT 3
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 52; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 52; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
Db 102 PLCDLLIRC 110

RESULT 4
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 52; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 PLCDLLIRC 9
| | | | |
Db 102 PLCDLLIRC 110

RESULT 5

US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match 100.0%; Score 52; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.052; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
| | | | |
Db 40 PLCDLLIRC 48

RESULT 6

US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match 100.0%; Score 52; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.052; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
| | | | |
Db 40 PLCDLLIRC 48

RESULT 7

US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 52; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9
| | | | |
Db 102 PLCDLLIRC 110

RESULT 8

US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 52; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLCDLLIRC 9

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Db      102 PLCDLLIRC 110

RESULT 9
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 52; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PLCDLLIRC 9
Db      102 PLCDLLIRC 110

RESULT 10
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match      100.0%; Score 52; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PLCDLLIRC 9
Db      208 PLCDLLIRC 216

RESULT 11
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match      100.0%; Score 52; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PLCDLLIRC 9
Db      208 PLCDLLIRC 216

RESULT 12
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match      100.0%; Score 52; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PLCDLLIRC 9
Db      227 PLCDLLIRC 235

RESULT 13
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:

```

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; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-14

Query Match      100.0%; Score 52; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  PLCDLLIRC 9
Db      227  PLCDLLIRC 235

RESULT 14
US-08-934-915-164
; Sequence 164, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; TITLE OF INVENTION: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-164

Query Match      90.4%; Score 47; DB 2; Length 20;
Best Local Similarity 88.9%; Pred. No. 0.045;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1  PLCDLLIRC 9
Db      11  PLCDLLIRC 19

RESULT 15
US-09-980-523A-8
; Sequence 8, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCES
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: WO/91 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-8

Query Match      73.1%; Score 38; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  PLCDLLI 7
Db      23  PLCDLLI 29

Search completed: June 28, 2005, 19:29:14
Job time : 18.15 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 01:35:30 ; Search time 57.55 Seconds
(without alignments)
60.138 Million cell updates/sec

Title: US-08-170-344-11
Perfect score: 54
Sequence: 1 KISEYRHYC 9

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	54	100.0	9	17	US-10-751-845-78
2	54	100.0	10	17	US-10-751-845-76
3	54	100.0	15	16	US-10-476-570-31
4	54	100.0	15	16	US-10-476-570-32
5	54	100.0	20	16	US-10-476-570-12
6	54	100.0	23	17	US-10-751-845-66
7	54	100.0	117	17	US-10-751-845-126
8	54	100.0	151	14	US-10-177-390-6
9	54	100.0	151	17	US-10-484-063-20
10	54	100.0	151	17	US-10-484-063-27
11	54	100.0	158	17	US-10-858-384-2

12	54	100.0	158	17	US-10-367-057-16	Sequence 16, Appl
13	54	100.0	171	16	US-10-472-724-2	Sequence 2, Appl
14	54	100.0	236	17	US-10-751-845-157	Sequence 157, App
15	54	100.0	237	17	US-10-751-845-158	Sequence 158, App
16	54	100.0	261	17	US-10-751-845-160	Sequence 160, App
17	54	100.0	266	9	US-09-367-309A-1	Sequence 1, Appl
18	54	100.0	273	13	US-10-000-503-4	Sequence 4, Appl
19	54	100.0	273	17	US-10-899-771-4	Sequence 4, Appl
20	54	100.0	292	13	US-10-000-503-10	Sequence 10, Appl
21	54	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
22	54	100.0	371	13	US-10-000-503-6	Sequence 6, Appl
23	54	100.0	371	17	US-10-899-771-6	Sequence 6, Appl
24	54	100.0	390	13	US-10-000-503-14	Sequence 14, Appl
25	54	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
26	49	90.7	9	17	US-10-751-845-70	Sequence 70, Appl
27	49	90.7	10	17	US-10-751-845-75	Sequence 75, Appl
28	49	90.7	29	16	US-10-476-570-55	Sequence 55, Appl
29	49	90.7	29	17	US-10-858-384-8	Sequence 8, Appl
30	45	83.3	10	17	US-10-751-845-80	Sequence 80, Appl
31	45	83.3	15	16	US-10-476-570-33	Sequence 33, Appl
32	41	75.9	9	14	US-10-239-313A-313	Sequence 313, App
33	41	75.9	9	17	US-10-751-845-86	Sequence 86, Appl
34	41	75.9	10	17	US-10-751-845-93	Sequence 93, Appl
35	39	72.2	112	16	US-10-425-115-249267	Sequence 249267, Sequence 308652,
36	39	72.2	147	16	US-10-425-115-308652	Sequence 308652,
37	38	70.4	28	10	US-09-809-391-640	Sequence 640, App
38	38	70.4	28	10	US-09-882-171-640	Sequence 640, App
39	38	70.4	28	15	US-10-164-861-640	Sequence 640, App
40	38	70.4	113	15	US-10-264-237-2295	Sequence 2295, App
41	38	70.4	180	16	US-10-408-765A-1288	Sequence 1288, App
42	38	70.4	198	13	US-10-001-054-40	Sequence 40, Appl
43	38	70.4	198	14	US-10-028-072-550	Sequence 550, App
44	38	70.4	198	14	US-10-140-808-550	Sequence 550, App
45	38	70.4	198	14	US-10-121-049-550	Sequence 550, App

ALIGNMENTS

RESULT 1

US-10-751-845-78
; Sequence 78, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman W.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-78

Query Match 100.0%; Score 54; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9

Db 1 KISEYRHYC 9

RESULT 2

US-10-751-845-76
 ; Sequence 76, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiciz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 76
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Human Papilloma virus
 ; US-10-751-845-76

Query Match 100.0%; Score 54; DB 17; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0083;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
 Db 1 KISEYRHYC 9

RESULT 3

US-10-476-570-31
 ; Sequence 31, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 31
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 76-90
 ; US-10-476-570-31

Query Match 100.0%; Score 54; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
 Db 4 KISEYRHYC 12

RESULT 4

US-10-476-570-32
 ; Sequence 32, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: POUVELLE-MORATILLE, Sandra
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 32
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 78-92
 ; US-10-476-570-32

Query Match 100.0%; Score 54; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
 Db 2 KISEYRHYC 10

RESULT 5

US-10-476-570-12
 ; Sequence 12, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: POUVELLE-MORATILLE, Sandra
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 12
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 76-95
 ; US-10-476-570-12

Query Match 100.0%; Score 54; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
| | | | |
Db 4 KISEYRHYC 12

RESULT 6
US-10-751-845-66
; Sequence 66, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-66

Query Match 100.0%; Score 54; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
| | | | |
Db 1 KISEYRHYC 9

RESULT 7
US-10-751-845-126
; Sequence 126, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-126

Query Match 100.0%; Score 54; DB 17; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
| | | | |
Db 45 KISEYRHYC 53

RESULT 8
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match 100.0%; Score 54; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
| | | | |
Db 72 KISEYRHYC 80

RESULT 9
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SATRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match 100.0%; Score 54; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
| | | | |
Db 72 KISEYRHYC 80

RESULT 10
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1

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; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match      100.0%; Score 54; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 72 KISEYRHYC 80

RESULT 11
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match      100.0%; Score 54; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 79 KISEYRHYC 87

RESULT 12
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
```

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; APPLICANT: Ooi, Chuan Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: Curasequist version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match      100.0%; Score 54; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 79 KISEYRHYC 87

RESULT 13
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match      100.0%; Score 54; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 84 KISEYRHYC 92

RESULT 14
US-10-751-845-157
; Sequence 157, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
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; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-157

Query Match 100.0%; Score 54; DB 17; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 45 KISEYRHYC 53

RESULT 15
US-10-751-845-158
; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-158

Query Match 100.0%; Score 54; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 46 KISEYRHYC 54

Search completed: June 29, 2005, 03:24:09
Job time : 58.55 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)
39.174 Million cell updates/sec

Title: US-08-170-344-11
Perfect score: 54
Sequence: 1 KISEYRHYC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	54	100.0	20	US-08-934-915-44	Sequence 44, Appl
2	54	100.0	20	US-08-934-915-163	Sequence 163, App
3	54	100.0	158	US-09-980-523A-2	Sequence 2, Appli
4	54	100.0	162	US-08-316-239B-3	Sequence 3, Appli
5	54	100.0	162	US-08-316-239B-4	Sequence 4, Appli
6	54	100.0	172	US-08-860-165-12	Sequence 12, Appl
7	54	100.0	172	US-08-860-165-14	Sequence 14, Appl
8	54	100.0	172	US-09-359-382-12	Sequence 12, Appl
9	54	100.0	172	US-09-359-382-14	Sequence 14, Appl
10	54	100.0	266	US-08-860-165-10	Sequence 10, Appl
11	54	100.0	266	US-09-359-382-10	Sequence 10, Appl
12	54	100.0	266	US-09-367-309A-1	Sequence 1, Appli
13	54	100.0	273	US-09-485-885-4	Sequence 4, Appli
14	54	100.0	292	US-09-485-885-10	Sequence 10, Appl
15	54	100.0	371	US-09-485-885-6	Sequence 6, Appli
16	54	100.0	390	US-09-485-885-14	Sequence 14, Appl
17	49	90.7	9	US-08-159-339A-76	Sequence 76, Appl
18	49	90.7	9	US-09-601-723-277	Sequence 277, App
19	49	90.7	29	US-09-980-523A-8	Sequence 8, Appli
20	49	90.7	182	US-08-117-083-10	Sequence 10, Appl
21	45	83.3	9	US-08-159-339A-234	Sequence 234, App
22	45	83.3	10	US-08-159-339A-75	Sequence 75, Appl
23	41	75.9	370	US-09-454-071-6	Sequence 6, Appli
24	40	74.1	9	US-08-159-339A-134	Sequence 134, App
25	38	70.4	28	US-09-149-476-640	Sequence 640, App
26	37	68.5	124	US-09-270-767-33888	Sequence 33888, A
27	36	66.7	169	US-09-489-039A-13995	Sequence 13995, A

Sequence 3467, Ap
Sequence 7708, Ap
Sequence 28, Appl
Sequence 28, Appl
Sequence 3, Appli
Sequence 58, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 10, Appl
Sequence 4, Appli
Sequence 3, Appli
Sequence 12, Appl
Sequence 3, Appli
Sequence 11, Appl
Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-934-915-44
; Sequence 44, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934.915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-44
Query Match 100.0%; Score 54; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.004;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KISEYRHYC 9
   |||||
Db 3 KISEYRHYC 11

RESULT 2
US-08-934-915-163
; Sequence 163, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Fouch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-163

Query Match 100.0%; Score 54; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KISEYRHYC 9
   |||||
Db 3 KISEYRHYC 11

RESULT 3
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
```

```
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/01 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 54; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KISEYRHYC 9
   |||||
Db 79 KISEYRHYC 87

RESULT 4
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3
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Query Match      100.0%; Score 54; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KISEYRHYC 9
Db      79 KISEYRHYC 87

RESULT 5
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNWE-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match      100.0%; Score 54; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KISEYRHYC 9
Db      79 KISEYRHYC 87

RESULT 6
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

Query Match      100.0%; Score 54; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KISEYRHYC 9
Db      148 KISEYRHYC 156

RESULT 7
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

Query Match      100.0%; Score 54; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KISEYRHYC 9
Db      17 KISEYRHYC 25

RESULT 8
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
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FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 172
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match      100.0%; Score 54; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KISEYRHYC 9
Db      17 KISEYRHYC 25

RESULT 7
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

Query Match      100.0%; Score 54; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KISEYRHYC 9
Db      148 KISEYRHYC 156

RESULT 8
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
```

; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; TYPE: PRT
; LENGTH: 172
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match 100.0%; Score 54; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 17 KISEYRHYC 25

RESULT 9
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397

; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match 100.0%; Score 54; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 148 KISEYRHYC 156

RESULT 10
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557

; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A

; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 54; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 79 KISEYRHYC 87

RESULT 11
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397

; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 54; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 79 KISEYRHYC 87

RESULT 12
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807

; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13

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; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 54; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 79 KISEYRHYC 87

RESULT 13
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match      100.0%; Score 54; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 185 KISEYRHYC 193

RESULT 14
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match      100.0%; Score 54; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 185 KISEYRHYC 193

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Job time : 18.15 secs
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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match      100.0%; Score 54; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 204 KISEYRHYC 212

RESULT 15
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Tereesa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match      100.0%; Score 54; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KISEYRHYC 9
Db 185 KISEYRHYC 193

Search completed: June 28, 2005, 19:29:13
Job time : 18.15 secs
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OM protein - protein search, using sw model

Run on: June 29, 2005, 01:35:30 ; Search time 57.55 Seconds
(without alignments)
60.138 Million cell updates/sec

Title: US-08-170-344-10

Perfect score: 48

Sequence: 1 FAFRDLCLIV 9

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Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	9	9	US-09-909-460-103
2	48	100.0	9	11	US-09-872-836-103
3	48	100.0	9	14	US-10-128-711-67
4	48	100.0	9	14	US-10-133-210-281
5	48	100.0	9	17	US-10-758-970-103
6	48	100.0	9	17	US-10-751-845-57
7	48	100.0	15	16	US-10-476-570-29
8	48	100.0	22	17	US-10-858-384-6
9	48	100.0	24	17	US-10-751-845-65
10	48	100.0	117	17	US-10-751-845-126
11	48	100.0	151	14	US-10-177-390-6
					Sequence 103, App
					Sequence 103, App
					Sequence 67, Appl
					Sequence 281, App
					Sequence 103, App
					Sequence 57, Appl
					Sequence 29, Appl
					Sequence 6, Appl
					Sequence 65, Appl
					Sequence 126, App
					Sequence 6, Appli

12	48	100.0	151	17	US-10-484-063-20	Sequence 20, Appl
13	48	100.0	151	17	US-10-484-063-27	Sequence 27, Appl
14	48	100.0	158	17	US-10-858-384-2	Sequence 2, Appli
15	48	100.0	158	17	US-10-367-057-16	Sequence 16, Appli
16	48	100.0	171	16	US-10-472-724-2	Sequence 2, Appli
17	48	100.0	236	17	US-10-751-845-157	Sequence 157, App
18	48	100.0	237	17	US-10-751-845-158	Sequence 158, App
19	48	100.0	261	17	US-10-751-845-160	Sequence 160, App
20	48	100.0	266	9	US-09-367-309A-1	Sequence 1, Appli
21	48	100.0	273	13	US-10-000-903-4	Sequence 4, Appli
22	48	100.0	273	17	US-10-899-771-4	Sequence 4, Appli
23	48	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
24	48	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
25	48	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
26	48	100.0	371	17	US-10-899-771-6	Sequence 14, Appli
27	48	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
28	48	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
29	48	100.0	536	15	US-10-367-095-10	Sequence 10, Appl
30	48	100.0	536	15	US-10-368-046-10	Sequence 10, Appl
31	48	100.0	536	16	US-10-367-367-10	Sequence 10, Appl
32	48	100.0	536	17	US-10-918-337-10	Sequence 10, Appl
33	44	91.7	9	17	US-10-751-845-89	Sequence 89, Appl
34	40	83.3	10	17	US-10-484-063-5	Sequence 5, Appli
35	40	83.3	10	17	US-10-751-845-94	Sequence 94, Appl
36	37	77.1	162	15	US-10-351-334-160	Sequence 160, App
37	37	77.1	205	15	US-10-264-237-2326	Sequence 2326, Ap
38	37	77.1	207	15	US-10-351-334-320	Sequence 320, App
39	37	77.1	242	16	US-10-425-115-251824	Sequence 251824,
40	37	77.1	445	16	US-10-839-882-8	Sequence 8, Appli
41	37	77.1	473	16	US-10-437-963-179845	Sequence 179845,
42	37	77.1	492	9	US-09-978-295A-7	Sequence 7, Appli
43	37	77.1	492	9	US-09-978-697-7	Sequence 7, Appli
44	37	77.1	492	9	US-09-978-192A-7	Sequence 7, Appli
45	37	77.1	492	9	US-09-999-832A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-909-460-103
; Sequence 103, Application US/09909460
; Publication No. US20020182258A1
; GENERAL INFORMATION:
; APPLICANT: Lunsford, Lynn B.
; APPLICANT: Putnam, David
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
; TITLE OF INVENTION: ACID
; FILE REFERENCE: 08191/014001
; CURRENT APPLICATION NUMBER: US/09/909,460
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 103
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-909-460-103

Query Match 100.0%; Score 48; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFRDLCLIV 9
| | | | | | | | | |
Db 1 FAFRDLCLIV 9

RESULT 2
US-09-872-836-103

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; Sequence 103, Application US/09872836
; Publication No. US20040142475A1
; GENERAL INFORMATION:
; APPLICANT: Barman, Shikha P.
; APPLICANT: McKeever, Una
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 08191-018001
; CURRENT APPLICATION NUMBER: US/09/872,836
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,830
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-836-103

Query Match      100.0%; Score 48; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FAFRDLCIV 9
Db      1 FAFRDLCIV 9

RESULT 3
US-10-128-711-67
; Sequence 67, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Beteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Stuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 28-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4

; Sequence 103, Application US/09872836
; Publication No. US20040142475A1
; GENERAL INFORMATION:
; APPLICANT: Barman, Shikha P.
; APPLICANT: McKeever, Una
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 08191-018001
; CURRENT APPLICATION NUMBER: US/09/872,836
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,830
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-836-103

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-128-711-67

Query Match      100.0%; Score 48; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FAFRDLCIV 9
Db      1 FAFRDLCIV 9

RESULT 4
US-10-133-210-281
; Sequence 281, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 281
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-281

Query Match      100.0%; Score 48; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FAFRDLCIV 9
Db      1 FAFRDLCIV 9

RESULT 5
US-10-758-970-103
; Sequence 103, Application US/10758970
; Publication No. US20050037086A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Hsu, Yung-Yueh
; APPLICANT: Tyo, Michael
; TITLE OF INVENTION: CONTINUOUS-FLOW METHOD FOR PREPARING MICROPARTICLES
; FILE REFERENCE: 08191-012001
; CURRENT APPLICATION NUMBER: US/10/758,970
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US/09/715,708A
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/166,516
; PRIOR FILING DATE: 1999-11-19
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; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 103
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-758-970-103

Query Match          100.0%; Score 48; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFRDLCLIV 9
Db 1 FAFRDLCLIV 9

RESULT 6
US-10-751-845-57
; Sequence 57, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-57

Query Match          100.0%; Score 48; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFRDLCLIV 9
Db 1 FAFRDLCLIV 9

RESULT 7
US-10-476-570-29
; Sequence 29, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: Papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63

; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 50-64
US-10-476-570-29

Query Match          100.0%; Score 48; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFRDLCLIV 9
Db 3 FAFRDLCLIV 11

RESULT 8
US-10-858-384-6
; Sequence 6, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E6 of HPV
US-10-858-384-6

Query Match          100.0%; Score 48; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFRDLCLIV 9
Db 7 FAFRDLCLIV 15

RESULT 9
US-10-751-845-65
; Sequence 65, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
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; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-65

Query Match 100.0%; Score 48; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFRDLCIV 9
Db 9 FAFRDLCIV 17

RESULT 10

US-10-751-845-126
; Sequence 126, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiccz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-126

Query Match 100.0%; Score 48; DB 17; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFRDLCIV 9
Db 29 FAFRDLCIV 37

RESULT 11

US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N. V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16

US-10-177-390-6

Query Match 100.0%; Score 48; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFRDLCIV 9
Db 45 FAFRDLCIV 53

RESULT 12

US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match 100.0%; Score 48; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFRDLCIV 9
Db 45 FAFRDLCIV 53

RESULT 13

US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match 100.0%; Score 48; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: June 29, 2005, 03:24:08
Job time : 57.55 secs

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Qy      1  FAFRDLCLIV 9
Db      45  FAFRDLCLIV 53

RESULT 14
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858.384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match      100.0%; Score 48; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  FAFRDLCLIV 9
Db      52  FAFRDLCLIV 60

RESULT 15
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match      100.0%; Score 48; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  FAFRDLCLIV 9
Db      52  FAFRDLCLIV 60
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)
39.174 Million cell updates/sec

Title: US-08-170-344-10
Perfect score: 48
Sequence: 1 FAFRDLCLIV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	9	1	US-08-787-547-103
2	48	100.0	9	4	US-08-197-484-67
3	48	100.0	9	5	PCT-US95-02121-67
4	48	100.0	22	4	US-09-980-523A-6
5	48	100.0	23	4	US-09-601-729-276
6	48	100.0	158	4	US-09-980-523A-2
7	48	100.0	162	1	US-08-316-239B-3
8	48	100.0	162	1	US-08-316-239B-4
9	48	100.0	172	3	US-08-860-165-14
10	48	100.0	172	3	US-09-359-382-14
11	48	100.0	266	3	US-08-860-165-10
12	48	100.0	266	3	US-09-359-382-10
13	48	100.0	266	4	US-09-367-309A-1
14	48	100.0	273	3	US-09-485-885-4
15	48	100.0	292	3	US-09-485-885-10
16	48	100.0	371	3	US-09-485-885-6
17	48	100.0	390	3	US-09-485-885-14
18	47	97.9	182	1	US-08-117-083-10
19	43	83.6	20	2	US-08-934-915-161
20	40	83.3	14	1	US-07-909-122-4
21	37	77.1	162	4	US-09-489-847-160
22	37	77.1	207	4	US-09-489-847-320
23	35	72.9	411	4	US-09-949-016-6312
24	35	72.9	414	4	US-09-949-016-9493
25	34	70.8	263	3	US-08-776-059-43
26	34	70.8	264	3	US-08-776-059-33
27	34	70.8	379	4	US-09-252-991A-26698

28	34	70.8	564	3	US-08-776-059-35	Sequence 35, Appl
29	33	68.8	90	4	US-09-543-681A-7008	Sequence 7008, Ap
30	33	68.8	158	2	US-08-247-904B-10	Sequence 10, Appl
31	33	68.8	158	3	US-08-767-942A-19	Sequence 19, Appl
32	33	68.8	271	1	US-08-117-083-14	Sequence 14, Appl
33	33	68.8	278	3	US-09-485-885-21	Sequence 21, Appl
34	33	68.8	349	4	US-09-491-577-96	Sequence 96, Appl
35	33	68.8	383	3	US-09-485-885-23	Sequence 23, Appl
36	33	68.8	415	4	US-09-583-110-4250	Sequence 4250, Ap
37	33	68.8	3074	4	US-09-543-681A-5508	Sequence 5508, Ap
38	32	66.7	109	4	US-09-270-767-31915	Sequence 31915, A
39	32	66.7	133	4	US-09-270-767-37721	Sequence 37721, A
40	32	66.7	133	4	US-09-270-767-52938	Sequence 52938, A
41	32	66.7	231	4	US-09-270-767-61639	Sequence 61639, A
42	32	66.7	274	4	US-09-614-912-160	Sequence 160, App
43	32	66.7	327	1	US-08-118-270-55	Sequence 55, Appl
44	32	66.7	327	5	PCT-US93-08528-55	Sequence 55, Appl
45	32	66.7	335	4	US-09-543-681A-5733	Sequence 5733, Ap

ALIGNMENTS

RESULT 1
US-08-787-547-103
; Sequence 103, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Curley, Joanne M.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/08787,547
; APPLICATION NUMBER: US/08787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-787-547-103

Query Match 100.0%; Score 48; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

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Qy 1 FAFRDLCLIV 9
Db 1 FAFRDLCLIV 9

RESULT 2
US-08-197-484-67
; Sequence 67, Application US/08197484
; Patent No. 641931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-67

Query Match 100.0%; Score 48; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFRDLCLIV 9
Db 1 FAFRDLCLIV 9

RESULT 3
PCT-US95-02121-67
; Sequence 67, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-67

Query Match 100.0%; Score 48; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAFRDLCLIV 9
Db 1 FAFRDLCLIV 9

RESULT 4
US-09-980-523A-6
; Sequence 6, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE 36 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/91 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
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; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-6

Query Match 100.0%; Score 48; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.023; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 FAFRDLCLIV 9
| | | | | | | |
Db 7 FAFRDLCLIV 15

RESULT 5
US-09-601-729-276
; Sequence 276, Application US/09601729
; Patent No. 6683052
; GENERAL INFORMATION:
; APPLICANT: THIAM, KADER
; APPLICANT: AURIAULT, CLAUDE
; APPLICANT: GRAS-MASSE, HELENE
; APPLICANT: LOING, ESTELLE
; APPLICANT: VERWAERDE, CLAUDE
; APPLICANT: GUILLET, JEAN GERARD
; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
; FILE REFERENCE: USB-97-AU-IN
; CURRENT APPLICATION NUMBER: US/09/601,729
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: PCT/FR99/00259
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 98 01439
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 276
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-601-729-276

Query Match 100.0%; Score 48; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.024; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 FAFRDLCLIV 9
| | | | | | | |
Db 8 FAFRDLCLIV 16

RESULT 6
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; FILE REFERENCE: WO81 AO INS

; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 48; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.16; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 FAFRDLCLIV 9
| | | | | | | |
Db 52 FAFRDLCLIV 60

RESULT 7
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 48; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 FAFRDLCLIV 9

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Db          52 FAFRDLCLIV 60
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RESULT 8
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match          100.0%; Score 48; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy          1 FAFRDLCLIV 9
|||||
Db          52 FAFRDLCLIV 60

RESULT 9
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157

; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match          100.0%; Score 48; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy          1 FAFRDLCLIV 9
|||||
Db          121 FAFRDLCLIV 129

RESULT 11
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
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; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match      100.0%; Score 48; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FAFRDLCIV 9
Db      52 FAFRDLCIV 60

RESULT 12
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRASER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; PRIOR FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PNO157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match      100.0%; Score 48; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FAFRDLCIV 9
Db      52 FAFRDLCIV 60

RESULT 13
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JTM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; PRIOR FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 48; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FAFRDLCIV 9
Db      52 FAFRDLCIV 60

RESULT 14
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match      100.0%; Score 48; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FAFRDLCIV 9
Db      158 FAFRDLCIV 166

RESULT 15
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
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/ ORGANISM: Homo sapien
US-09-485-885-10
Query Match      100.0%; Score 48; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FAERDLCIV 9
      |||||
Db      177 FAERDLCIV 185
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Job time : 17.15 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 01:35:30 ; Search time 57.55 Seconds
(without alignments)
60.138 Million cell updates/sec

Title: US-08-170-344-1

Perfect score: 48

Sequence: 1 AMFODPOER 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries.

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	9	14	US-10-133-210-277
2	48	100.0	9	17	US-10-751-845-81
3	48	100.0	20	17	US-10-751-845-64
4	48	100.0	22	16	US-10-476-570-59
5	48	100.0	117	17	US-10-751-845-126
6	48	100.0	158	17	US-10-858-384-2
7	48	100.0	158	17	US-10-367-057-16
8	48	100.0	171	16	US-10-472-724-2
9	48	100.0	236	17	US-10-751-845-157
10	48	100.0	237	17	US-10-751-845-158
11	48	100.0	261	17	US-10-751-845-160

12	48	100.0	266	9	US-09-367-309A-1	Sequence 1, Appli
13	48	100.0	273	13	US-10-000-903-4	Sequence 4, Appli
14	48	100.0	273	17	US-10-899-771-4	Sequence 4, Appli
15	48	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
16	48	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
17	48	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
18	48	100.0	371	17	US-10-899-771-6	Sequence 6, Appli
19	48	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
20	48	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
21	48	100.0	536	15	US-10-367-095-10	Sequence 10, Appl
22	48	100.0	536	15	US-10-368-046-10	Sequence 10, Appl
23	48	100.0	536	16	US-10-367-367-10	Sequence 10, Appl
24	48	100.0	536	17	US-10-918-337-10	Sequence 10, Appl
25	44	91.7	151	14	US-10-177-390-6	Sequence 20, Appli
26	44	91.7	151	17	US-10-484-063-20	Sequence 20, Appli
27	44	91.7	151	17	US-10-484-063-27	Sequence 27, Appl
28	40	83.3	32	14	US-10-118-047-2	Sequence 2, Appli
29	40	83.3	32	16	US-10-118-047-2	Sequence 2, Appli
30	40	83.3	381	16	US-10-859-572-2	Sequence 2, Appli
31	39	81.2	9	17	US-10-751-845-71	Sequence 71, Appl
32	39	81.2	10	17	US-10-739-930-9788	Sequence 74, Appl
33	39	81.2	405	16	US-10-159-257A-149	Sequence 149, App
34	37	77.1	521	16	US-10-159-257A-181	Sequence 181, App
35	37	77.1	521	16	US-10-425-114-68828	Sequence 68828, A
36	36	75.0	354	15	US-10-425-115-330168	Sequence 341903,
37	36	75.0	354	16	US-10-425-115-341903	Sequence 341903,
38	35	72.9	129	16	US-10-282-122A-68570	Sequence 68570, A
39	35	72.9	1144	15	US-09-864-761-45512	Sequence 45512, A
40	34	70.8	29	9	US-10-425-115-203539	Sequence 203539,
41	34	70.8	204	16	US-09-815-453-8	Sequence 8, Appli
42	34	70.8	456	10	US-10-087-192-867	Sequence 867, App
43	34	70.8	484	13	US-10-369-493-4878	Sequence 4878, Ap
44	34	70.8	792	15	US-10-369-493-7637	Sequence 7637, Ap
45	34	70.8	792	15		

ALIGNMENTS

RESULT 1
US-10-133-210-277
; Sequence 277, Application US/10133210
; Publication No. US20030101964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulkota, Kamalakar
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND COMPOSITIONS THEREOF
; FILE REFERENCE: EU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 277
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-277

Query Match 100.0%; Score 48; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFODPOER 9

Db 1 AMFODPOER 9

RESULT 2
 US-10-751-845-81
 ; Sequence 81, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chicz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 81
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Human Papilloma virus
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 1-22
 US-10-751-845-81

Query Match 100.0%; Score 48; DB 17; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
 Db 1 AMFQDPQER 9

RESULT 3
 US-10-751-845-64
 ; Sequence 84, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chicz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 64
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Human Papilloma virus
 ; OTHER INFORMATION: Artificial fusion sequence
 US-10-751-845-64

Query Match 100.0%; Score 48; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
 Db 1 AMFQDPQER 9

RESULT 4
 US-10-476-570-59

; Sequence 59, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: POUVELLE-MORATILLE, Sandra
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 59
 ; LENGTH: 22
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 1-22
 US-10-476-570-59

Query Match 100.0%; Score 48; DB 16; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
 Db 7 AMFQDPQER 15

RESULT 5
 US-10-751-845-126
 ; Sequence 126, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chicz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 126
 ; LENGTH: 117
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial fusion sequence
 US-10-751-845-126

Query Match 100.0%; Score 48; DB 17; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.31;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
 Db 1 AMFQDPQER 9

```
RESULT 6
US-10-858-384-2
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2
Query Match 100.0%; Score 48; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 12 AMFQDPQER 20

RESULT 9
US-10-751-845-157
; Sequence 157, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-157
Query Match 100.0%; Score 48; DB 17; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 1 AMFQDPQER 9

RESULT 10
US-10-751-845-158
; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.

RESULT 7
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Cooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16
Query Match 100.0%; Score 48; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 7 AMFQDPQER 15

RESULT 8
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
```

; APPLICANT: Chicx, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-158

Query Match 100.0%; Score 48; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 2 AMFQDPQER 10
|||||

RESULT 11
US-10-751-845-160
; Sequence 160, Application US/10/751,845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicx, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160

Query Match 100.0%; Score 48; DB 17; Length 261;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 26 AMFQDPQER 34
|||||

RESULT 12
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.

; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 48; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 7 AMFQDPQER 15
|||||

RESULT 13
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match 100.0%; Score 48; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 113 AMFQDPQER 121
|||||

RESULT 14
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27


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; PRIOR APPLICATION NUMBER: US/09/581.976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
; US-10-899-771-4

```

```

Query Match      100.0%; Score 48; DB 17; Length 273;
Best Local Similarity 100.0%; Pred.No. 0.74;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AMFQDPQER 9
DB 113 AMFQDPQER 121

```

```

RESULT 15
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-000-903-10

```

```

Query Match      100.0%; Score 48; DB 13; Length 292;
Best Local Similarity 100.0%; Pred.No. 0.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AMFQDPQER 9
DB 132 AMFQDPQER 140

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Search completed: June 29, 2005, 03:24:04
Job time : 58.55 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)
39.174 Million cell updates/sec

Title: US-08-170-344-1
Perfect score: 48
Sequence: 1 AMFQDPQER 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	9	3	US-08-159-339A-225
2	48	100.0	23	1	US-08-363-586-3
3	48	100.0	158	4	US-09-980-523A-2
4	48	100.0	162	1	US-08-316-239B-3
5	48	100.0	162	1	US-08-316-239B-4
6	48	100.0	172	3	US-08-860-165-14
7	48	100.0	172	3	US-09-359-382-14
8	48	100.0	182	1	US-08-117-083-10
9	48	100.0	266	3	US-08-860-165-10
10	48	100.0	266	3	US-09-359-382-10
11	48	100.0	266	4	US-09-367-309A-1
12	48	100.0	273	3	US-09-485-885-4
13	48	100.0	292	3	US-09-485-885-10
14	48	100.0	371	3	US-09-485-885-6
15	48	100.0	390	3	US-09-485-885-14
16	44	91.7	30	1	US-08-363-586-4
17	43	89.6	20	2	US-08-934-915-158
18	39	81.2	15	1	US-07-909-122-2
19	36	75.0	15	3	US-08-075-541D-52
20	35	72.9	1161	4	US-09-543-681A-6486
21	33	68.8	245	4	US-09-198-452A-37
22	33	68.8	352	4	US-09-252-991A-32932
23	33	68.8	588	4	US-09-438-185A-23
24	33	68.8	910	4	US-09-902-540-16309
25	32	66.7	325	4	US-09-702-705-1816
26	32	66.7	325	4	US-09-736-457-1816
27	32	66.7	325	4	US-09-671-325-1816

28	32	66.7	401	4	US-09-631-863A-2	Sequence 2, Appli
29	32	66.7	529	4	US-09-248-796A-16357	Sequence 16357, A
30	32	66.7	620	4	US-09-489-039A-7923	Sequence 7923, Ap
31	31	64.6	197	4	US-09-270-767-41556	Sequence 41556, A
32	31	64.6	271	2	US-07-857-224B-46	Sequence 46, Appl
33	31	64.6	287	4	US-09-270-767-42416	Sequence 42416, A
34	31	64.6	324	4	US-09-252-991A-29703	Sequence 29703, A
35	31	64.6	338	4	US-09-252-991A-30165	Sequence 30165, A
36	31	64.6	474	4	US-09-252-991A-22590	Sequence 22590, A
37	31	64.6	484	4	US-09-252-991A-19511	Sequence 19511, A
38	31	64.6	534	4	US-09-252-991A-20181	Sequence 20181, A
39	31	64.6	545	4	US-10-237-551-121	Sequence 121, App
40	31	64.6	545	4	US-10-237-551-157	Sequence 157, App
41	31	64.6	547	4	US-10-237-551-215	Sequence 215, App
42	31	64.6	547	4	US-10-237-551-216	Sequence 216, App
43	31	64.6	672	4	US-09-949-016-9511	Sequence 9511, Ap
44	31	64.6	740	4	US-09-252-991A-21575	Sequence 21575, A
45	31	64.6	818	4	US-09-328-352-5208	Sequence 5208, Ap

ALIGNMENTS

RESULT 1
US-08-159-339A-225
; Sequence 225, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cellis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 225:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-225

Query Match 100.0%; Score 48; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 1 AMFQDPQER 9

RESULT 2

US-08-363-586-3
; Sequence 3, Application US/08363586
; Patent No. 5629161
; GENERAL INFORMATION:
; APPLICANT: Mueller, Martin
; APPLICANT: Gissmann, Lutz
; TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
; TITLE OF INVENTION: Peptides for the Diagnostic Purpose
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,586
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/909,296
; FILING DATE: 09-JUL-1992
; APPLICATION NUMBER: EP 9111720.8
; FILING DATE: 13-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wadler, Linda A.
; REGISTRATION NUMBER: 33,218
; REFERENCE/DOCKET NUMBER: 02481-1195-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-363-586-3

Query Match 100.0%; Score 48; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 7 AMFQDPQER 15

RESULT 3

US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE

; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
; US-09-980-523A-2

Query Match 100.0%; Score 48; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 7 AMFQDPQER 15

RESULT 4

US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein

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; HYPOTHETICAL: NO
US-08-316-23B-B-3

Query Match      100.0%; Score 48; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 7 AMFQDPQER 15

RESULT 5
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Farmer, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNNE-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match      100.0%; Score 48; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 7 AMFQDPQER 15

RESULT 6
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
```

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; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match      100.0%; Score 48; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 76 AMFQDPQER 84

RESULT 7
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match      100.0%; Score 48; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 76 AMFQDPQER 84

RESULT 8
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
```

;; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
;; TITLE OF INVENTION: Papilloma Virus Proteins
;; NUMBER OF SEQUENCES: 70
;; CORRESPONDENCE ADDRESS:
;; STREET: 4 Embarcadero Center, Suite 3400
;; CITY: San Francisco
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94111
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/117,083
;; FILING DATE: 10-SEP-1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Dreger, Walter H.
;; REGISTRATION NUMBER: 24,190
;; REFERENCE/DOCKET NUMBER: A-58783
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-781-1989
;; TELEFAX: 415-398-3249
;; TELEX: 910 277299
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 182 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..182
;; OTHER INFORMATION: /note="Xaa refers to stop codon in
;; OTHER INFORMATION: the open reading frame."
US-08-117-084-10

Query Match 100.0%; Score 48; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 8 AMFQDPQER 16

RESULT 9
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence

;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 48; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 7 AMFQDPQER 15

RESULT 10
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 48; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPQER 9
Db 7 AMFQDPQER 15

RESULT 11
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 48; DB 4; Length 266;

Best Local Similarity 100.0%; Pred. No. 0.098; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPOER 9
Db 7 AMFQDPOER 15

RESULT 12

US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 48; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPOER 9
Db 113 AMFQDPOER 121

RESULT 13

US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match 100.0%; Score 48; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 0.098; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPOER 9
Db 7 AMFQDPOER 15

RESULT 14

US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match 100.0%; Score 48; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPOER 9
Db 113 AMFQDPOER 121

RESULT 15

US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match 100.0%; Score 48; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMFQDPOER 9
Db 132 AMFQDPOER 140

Search completed: June 28, 2005, 19:28:59
Job time : 18.15 secs
